

184189

From: Ibrahim, Medina A.
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Thanks

Medina A. Ibrahim
Patent Examiner, GAU-1638
transgenic plants and plant breeding
Remsen-2B07
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Searcher: _____
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Date Searcher Picked up: _____
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Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
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Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
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DIALOG: _____
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Other (Specify): _____

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:06:24 ; Search time 5558.17 Seconds
(without alignments)
9664.530 Million cell updates/sec

Title: US-09-978-274A-1

Perfect score: 945
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_srs:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	945	100.0	945	6	AX427702 Sequence
2	940.2	99.5	1249	15	PAPAPSRIP
3	786.4	83.2	792	6	AX427704 Sequence
4	766.8	81.1	786	15	AB071855 Phytolacc
5	761.4	80.6	1092	6	AX427720 Sequence
6	635.8	67.3	1164	15	AY049785 Phytolacc
7	634	67.1	1195	6	A42103 Sequence 1
8	634	67.1	1195	6	I43835 Sequence 1
9	634	67.1	1195	6	I55866 Sequence 1
10	632.4	66.9	1379	6	AR009535 Sequence
11	632.4	66.9	1379	6	AR136704 Sequence
12	632.4	66.9	1379	6	AX427731 Sequence
13	632.2	66.9	942	15	AY572976 Phytolacc
14	632.2	66.9	1114	15	AF533515 Phytolacc
15	631	66.8	1164	15	PAPAP
16	630.8	66.8	1195	6	A36639
17	630.8	66.8	1379	6	AR141172 Sequence
18	630.4	66.7	1052	15	AY137202 Phytolacc

19	629.2	66.6	1378	6	AX427732	AX427732 Sequence
20	629.2	66.6	1379	6	AR136705	AR136705 Sequence
21	629	66.6	939	15	AY327475	AY327475 Phytolacc
22	629	66.6	942	15	AY547315	AY547315 Phytolacc
23	624.2	66.1	2472	6	E05033	E05033 DNA encodin
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25	588.6	62.3	882	6	A67183	A67183 Sequence 1
26	586.4	62.1	951	6	A67185	A67185 Sequence 3
27	586.4	62.1	2369	15	AR141331	AR141331 Phytolacc
28	581.2	61.5	783	15	AB071854	AB071854 Phytolacc
29	543.8	57.5	918	6	A43003	A43003 Sequence 1
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35	479	50.7	714	15	AY603353	AY603353 Phytolacc
36	478	50.6	711	15	AF338910	AF338910 Phytolacc
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38	459	48.6	465	6	AX427706	AX427706 Sequence
39	339	34.8	333	6	AX427708	AX427708 Sequence
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ALIGNMENTS

RESULT 1	AX427702	945 bp	DNA	linear	PAT 20-JUN-2002
LOCUS	AX427702	Sequence 1 from Patent WO0233107.			
DEFINITION	AX427702				
ACCESSION	AX427702				
VERSION	AX427702.1	GI:21537815			
KEYWORDS					
SOURCE					
ORGANISM	Phytolacca americana (American pokeweed)				
	Phytolacca americana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.				
REFERENCE	1				
AUTHORS	Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.				
TITLE	Plant cell death system				
JOURNAL	Patent: WO 0233107-A 1 25-APR-2002;				
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misc_feature	complement(735..776)				
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variation	750..759				
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misc_feature	complement(922..945)				
	/note="Binding site for primer PPS2SR"				
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Matches 945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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DB	1 ATGAAGGTATGCTGTGTAAGTGTGTGACGTTAATGACGTGCTCAATTCGACCAACT 60				

QY 61 TCAACTTGGCCATAAATAGATCACCTTGTGATGCTGGAATGCCAATTAACTAATAT 120
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QY 301 TCTGATCCCTTCAATGCGAATAGTGTCTTACCAATATATTAATGATATTAACAGACC 360
DB 301 TCTGATCCCTTCAATGCGAATAGTGTCTTACCAATATATTAATGATATTAACAGACC 360
QY 361 GAACGCACTGATGAGAAATATCTTGTGCTCAAGTTCTAGTCTGCTGTGTCATGTC 420
DB 361 GAACGCACTGATGAGAAATATCTTGTGCTCAAGTTCTAGTCTGCTGTGTCATGTC 420
QY 421 ATTAACCAATAGCTTATATCCGACATGAAAAGAAAGCAGAACTCAAGAAAT 480
DB 421 ATTAACCAATAGCTTATATCCGACATGAAAAGAAAGCAGAACTCAAGAAAT 480
QY 481 CAAGTCATATGGGAATTCAAAATCTCAGAGATGACATTTGGAATAATCTCTGAGATTGAT 540
DB 481 CAAGTCATATGGGAATTCAAAATCTCAGAGATGACATTTGGAATAATCTCTGAGATTGAT 540
QY 541 TCATTCCTCTGTAATAAATGAGGCTTTTCTTCTAGTGTGAGCCATCCAAATGTTTCAGAG 600
DB 541 TCATTCCTCTGTAATAAATGAGGCTTTTCTTCTAGTGTGAGCCATCCAAATGTTTCAGAG 600
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DB 661 CCTGATCCCAAGATTAATTTTGGAGAGAAAGTGGGCAAAATCTCTGAGCAATTCAC 720
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DB 721 AATGCCAAGATGAGGCTTTTACCCAAACCACTTGATGATGAGTCCAAAGTATCAAG 780
QY 781 TGGATAGTCTTAGAGTGAATCAATCGTATGAGCACTCCTTAAGTACGTTAAT 840
DB 781 TGGATAGTCTTAGAGTGAATCAATCGTATGAGCACTCCTTAAGTACGTTAAT 840
QY 841 GGAACCTGTCAGACAACTTAACCAAAATGCGATTTCTCAGATTAAATTTTCTACTTAT 900
DB 841 GGAACCTGTCAGACAACTTAACCAAAATGCGATTTCTCAGATTAAATTTTCTACTTAT 900
QY 901 TATTAATTAATGCTAATCTTGTGATCTAATTTGAAGATTTCTAA 945
DB 901 TATTAATTAATGCTAATCTTGTGATCTAATTTGAAGATTTCTAA 945

RESULT 2
LOCUS PAPASRIP 1249 bp mRNA linear PLN 18-APR-2005
DEFINITION P.americana mRNA for pokeweed antiviral protein.
ACCESSION X98079.1 GI:1707648
VERSION PAP-S gene; pokeweed antiviral protein (PAP) ; ribosome-inactivating protein.
KEYWORDS Phytolacca americana (American pokeweed)
SOURCE Phytolacca americana
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
AUTHORS Poyet,J.L. and Hoeveler,A.
TITLE CDNA cloning and expression of pokeweed antiviral protein from seeds in *Bescherichia coli* and its inhibition of protein synthesis in vitro
JOURNAL FEBS Lett. 406 (1-2), 97-100 (1997)
PUBMED 9109394
REFERENCES 2 (bases 1 to 1249)
AUTHORS Poyet,J.L.
TITLE Direct Submission
JOURNAL Submitted (22-MAY-1996) J.L. Poyet, Laboratoire de Biochimie-Biologie Moléculaire, UPR Sciences et Techniques, 16 route de Gray, 25030 Besancon Cedex, FRANCE
REMARK Revised by author 20-SEP-1996
FEATURES
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Matches 942; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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polyA_site
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DB 106 ATGAAGTGATGCTTGTAGTGTGATGACGTTAATAGCGTGCTGATGCTGACCAACT 165
QY 61 TCAACTTGGCCATAAATAGATCACCTTGTATCAAGCGAAGATCCAAACTAATAT 120
DB 166 TCAACTTGGCCATAAATAGATCACCTTGTATCAAGCGAAGATCCAAACTAATAT 225
QY 121 GCCACTTTATGGAATCTCTTGTATCAAGCGAAGATCCAAACTAATATGCTATGGC 180
DB 226 GCCACTTTATGGAATCTCTTGTATCAAGCGAAGATCCAAACTAATATGCTATGGC 285
QY 181 ATACCAATGCTACTGATCTAATATGACCCCTTACCTATATGTTAGTCCAAAGT 240
DB 286 ATACCAATGCTACTGATCTAATATGACCCCTTACCTATATGTTAGTCCAAAGT 345
QY 241 GCAAACTTAAAAACCTTACACTAATGCTGAGAGCAAAATTAATTATACGATGGCTAT 300

Db 346 GCAAACTTAAACCATTAACAATAGCTGAGACGAAATTAATTATAGATGAGGCTAT 405
Qy 301 TCTGATCCCTCAATGGAATAGTGTGTACCAATATTAATGATTAACAAGCAC 360
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Qy 361 GAAAGCATGATGAGAAATATCTTGTCTCAAGTTTAACTGATGCTGATGCTC 420
Db 466 GAAAGCATGATGAGAAATATCTTGTCTCAAGTTTAACTGATGCTGATGCTC 525
Qy 421 ATTAATCAATAGATTAATGATGATGATGATGATGATGATGATGATGATGAT 480
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Qy 481 CAAGTCAATGAGGATTAATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 586 CAAGTCAATGAGGATTAATGATGATGATGATGATGATGATGATGATGATGAT 645
Qy 541 TCATTCCTGTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db 646 TCATTCCTGTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 705
Qy 601 GCAGCGGATTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 706 GCAGCGGATTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 765
Qy 661 CCTGATCCCAATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 766 CCTGATCCCAATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 825
Qy 721 AATGCAAGATGAGGCTTTTACCAACCACTGATGATGATGATGATGATGATGAT 780
Db 826 AATGCAAGATGAGGCTTTTACCAACCACTGATGATGATGATGATGATGATGAT 885
Qy 781 TGAATGATTCCTTAAGTGAATGATGATGATGATGATGATGATGATGATGAT 840
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Qy 841 GGAACCTGTGAGAACTTACCAAAATGATGATGATGATGATGATGATGATGAT 900
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Db 1006 TATAATTAATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 1050

RESULT 3
AX427704 792 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 3 from Patent WO0233107.
DEFINITION AX427704
ACCESSION AX427704.1 GI:21537816
VERSION
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Bkaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
1 Nelam, A., Atkinson, H. J., McPherson, M. J. and Thomas, C. J. R.
AUTHORS Plant cell death system
TITLE Patent: WO 0233107-A 3 25-APR-2002;
JOURNAL CAMBRIDGE ADVANCED TECH (GB)
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misc_feature complement(436..462)
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variation 612
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681..686
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misc_feature 790..792
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Best Local Similarity 92.9%; Pred. No. 2.1e-173;
Matches 787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 73 ATAAATACGATCACCTTGAATGCTGAAATGSCACATTAACAATATGCACTTATG 132
Db 4 ATAAATACGATCACCTTGAATGCTGAAATGSCACATTAACAATATGCACTTATG 63
Qy 133 GAATCTCTGTGTAATCAAGCGAAAGATCAAACTAAATGCTATGCAATGCTA 192
Db 64 GAATCTCTGTGTAATCAAGCGAAAGATCAAACTAAATGCTATGCAATGCTA 123
Qy 193 CCGATATCTAATTCAGACCCCTTAAGTACTTATGTTAAGTCCCAAGTGCACCACTTAAA 252
Db 124 CCGATATCTAATTCAGACCCCTTAAGTACTTATGTTAAGTCCCAAGTGCACCACTTAAA 183
Qy 253 ACCATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 312
Db 184 ACCATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 243
Qy 313 AATGCAATAGTGTGTAATCAATATTAATGATTAACAAGCACGAAACGACATGAT 372
Db 244 AATGCAATAGTGTGTAATCAATATTAATGATTAACAAGCACGAAACGACATGAT 303
Qy 373 GTGAGAAATCTCTTGTCTCAAGTCTAAGTTCGTGTGTGTGTGTGTGTGTGTGTGT 432
Db 304 GTGAGAAATCTCTTGTCTCAAGTCTAAGTTCGTGTGTGTGTGTGTGTGTGTGTGT 363
Qy 433 AGCTTAATATCGACATGAGAAAGAGAGATTAATCAAGAAATCAAGTCCAAATG 492
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Qy 493 GGAATTCAAATCTCAGCAGTGAATTTGAAAAATCTCTGAGTGAATTCATTCCTGTA 552
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Qy 553 AAAAAGGAGGCTTTTCTTCTAAGTGTGATGATGATGATGATGATGATGATGATGAT 612
Db 484 AAAAAGGAGGCTTTTCTTCTAAGTGTGATGATGATGATGATGATGATGATGATGAT 543
Qy 613 AAGTACATGAGAACCAAGTCAAGATTAATTAATGAGATTCATCCGATCCGAAA 672
Db 544 AAGTACATGAGAACCAAGTCAAGATTAATTAATGAGATTCATCCGATCCGAAA 603
Qy 673 GTAATTAATTTGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACATGCCAAGAT 732
Db 604 GTAATTAATTTGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACATGCCAAGAT 663
Qy 733 GGGGCTTACCCAAACCACTTGAAGTGTGATGATGATGATGATGATGATGATGATGAT 792
Db 664 GGGGCTTACCCAAACCACTTGAAGTGTGATGATGATGATGATGATGATGATGATGAT 723
Qy 793 AGAGTGAATGAATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 852
Db 724 AGAGTGAATGAATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 783
Qy 853 ACAACTTA 860
Db 784 ACAACTTA 791

RESULT 4
AB071855 786 bp DNA linear PLN 19-MAR-2002
LOCUS Phytolacca americana paps2 gene for PAP-S2, partial cds.
DEFINITION AB071855
ACCESSION AB071855 GI:19570839
VERSION
KEYWORDS Phytolacca americana (American pokeweed)
SOURCE Phytolacca americana
ORGANISM Bukayocsa, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
AUTHORS Honjo,E. and Watanabe,K.
TITLE Cloning of genomic DNA encoding two types of pokeweed antiviral protein in seeds, PAP-S1 and PAP-S2, and functional comparison of their recombinant proteins with other PAP isoforms
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 786)
Watanabe,K. and Honjo,E.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2001) Keiichi Watanabe, Saga University, Department of Applied Biological Sciences, Honjo-machi, Saga city, Saga 840-8502, Japan (E-mail:wakei@cc.saga-u.ac.jp, Tel:81-952-28-8774, Fax:81-952-28-8774)
FEATURES
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Best Local Similarity 98.5%; Pred. No. 8e-169;
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DB 61 GATCTCTTGTATATCAAGGAAATCCAAAATAAATGCTATGCAATACCAATGCTA 120
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QY 253 ACCATTACCTAATTCGATGAGAGAAATTAATTAGTGATGGCTATTCGATCCCTTC 312
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DB 361 AGCTTATATCCGACCTTGGAAAAGAGAAAGAAATCAAGAAATCAAGTCCAATTG 420
QY 493 GGAATTCAAATACCTAGCAGTGCATTTGGAAAATCTCTGAGTTGATTCATTCCTGTA 552
DB 421 GGAATTCAAATACCTAGCAGTGCATTTGGAAAATCTCTGAGTTGATTCATTCCTGTA 480
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DB 481 AAAATCGAGGCTTTTTTTTCTACTGTGATCCATCAATGTTTCAAGAGCGAGCGATTC 540
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DB 661 GGGGCTTTTACCCAAACCTTGAGCTAGTGAATGCCAAGGTAAGGATGATGTTCTT 720
QY 793 AGAGTGATGAATCAATCGTATGATGAGCACTCCTTAAGTACGTTAATGGAACCTGAC 852
DB 721 AGAGTGATGAATCAATCGTATGATGAGCACTCCTTAAGTACGTTAATGGAACCTGAC 780
QY 853 ACAACT 858
DB 781 GCCACT 786

RESULT 5
AX427720 1092 bp DNA linear PAT 20-JUN-2002
LOCUS AX427720
DEFINITION Sequence 19 from Patent WO0233107.
ACCESSION AX427720
VERSION AX427720.1 GI:21537829
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 Neelam,A.; Atkinson,H.J.; Mcpherson,M.J. and Thomas,C.J.R.
AUTHORS
TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A 19 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES
source
1..1092
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PAP-S/Cystatin fusion"
1..29
misc_feature
/note="Binding site for primer PS1B"
variation
681..686
/note="Modified XbaI site"
misc_feature
complement(742..786)
/note="Binding site for primer PCS-PAPER"
misc_feature
766..806
/note="Binding site for primer PCS-Delta86F"
766..786
/note="TEV N1A protease cleavage site"
misc_feature
complement(1066..1092)
/note="Binding site for primer SYNPOTDelta86SR"
ORIGIN
Query Match 80.6%; Score 761.4; DB 6; Length 1092;
Best Local Similarity 99.9%; Pred. No. 1.4e-167;

Matches 762; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	73	ATAAATGATGACCTTGTGAAATGCGCAATTAACAAATATGCACTTATG	132
Db	4	ATAAATGATGACCTTGTGAAATGCGCAATTAACAAATATGCACTTATG	63
Qy	133	GAATCTCTGTATCAAGGAAAGATCCAAATTAAGCTATGCAATGCTA	192
Db	64	GAATCTCTGTATCAAGGAAAGATCCAAATTAAGCTATGCAATGCTA	123
Qy	193	CTGTATCTAATGAGACCCCTTAAGTACTTATGTTAGCTCAAGGTGCAACTTAA	252
Db	124	CTGTATCTAATGAGACCCCTTAAGTACTTATGTTAGCTCAAGGTGCAACTTAA	183
Qy	253	ACATTAACCTAATGCTGAGACGAATTAATGATGATGAGGCTATTCGATCCCTC	312
Db	184	ACATTAACCTAATGCTGAGACGAATTAATGATGATGAGGCTATTCGATCCCTC	243
Qy	313	AATGGCAATAGTGTCTTACATATATTAATGATATTAACAGACCGAAGCACTGAT	372
Db	244	AATGGCAATAGTGTCTTACATATATTAATGATATTAACAGACCGAAGCACTGAT	303
Qy	373	GTCGAGAAATCTCTTGTCTCAAGTTCTGCTGTGATGCAATGCTCACTTAACTA	432
Db	304	GTCGAGAAATCTCTTGTCTCAAGTTCTGCTGTGATGCAATGCTCACTTAACTA	363
Qy	433	AGCTTATATCGAATGAGAAAGAAAGAAAGTAATCAAGAAATCAAGTCAATG	492
Db	364	AGCTTATATCGAATGAGAAAGAAAGAAAGTAATCAAGAAATCAAGTCAATG	423
Qy	493	GGAATTCAAATCTCAGACAGTGAATGGAATAATCTGAGAGTTGATTCCTCTGA	552
Db	424	GGAATTCAAATCTCAGACAGTGAATGGAATAATCTGAGAGTTGATTCCTCTGA	483
Qy	553	AAAACTGAGGCTTTTCTTCTAATGTCATGCAATGCTTCAAGGCAAGGCGATTC	612
Db	484	AAAACTGAGGCTTTTCTTCTAATGTCATGCAATGCTTCAAGGCAAGGCGATTC	543
Qy	613	AAGTACATAGAGAACCAAGTCAAGCTAATTTTAATGAGATTCATCCCTGATCCAAA	672
Db	544	AAGTACATAGAGAACCAAGTCAAGCTAATTTTAATGAGATTCATCCCTGATCCAAA	603
Qy	673	GTAATTAATTTGAGAGAGAGTGGGCAAAATCTCTGAGCAATTCAAATGCGAAGAT	732
Db	604	GTAATTAATTTGAGAGAGAGTGGGCAAAATCTCTGAGCAATTCAAATGCGAAGAT	663
Qy	733	GGGGCTTTACCCCAACCACTTGAAGTATGATGATGCAAGGATCAAGTATGTTCTT	792
Db	664	GGGGCTTTACCCCAACCACTTGAAGTATGATGATGCAAGGATCAAGTATGTTCTT	723
Qy	793	AGAGTGAATGAAATCGATGATGATGAGCTCCTTAAATGACG	835
Db	724	AGAGTGAATGAAATCGATGATGATGAGCTCCTTAAATGACG	766
RESULT 6			
LOCUS	AY049785	1164 bp	mRNA
DEFINITION	Phytolacca acinosa anti-viral protein PAP (PAP) mRNA, complete cds.		
ACCESSION	AY049785		
VERSION	AY049785.1	GI:16356654	
KEYWORDS	Phytolacca acinosa (food pokeweed)		
SOURCE	Phytolacca acinosa		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.		
REFERENCE	Peng, X., Yuan, J. and Qiang, B.		
AUTHORS	Submitted (27-JUL-2001) Department of Biochemistry, Institute of Basic Medical Science, Chinese Academy of Medical Sciences, 5 Dong Dan San Tiao, Beijing 100005, P.R. China		
TITLE	JOURNAL		

FEATURES			
source			
Location/Qualifiers			
1..1164			
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/mol_type="mRNA"			
/db_xref="taxon:3528"			
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2..943			
/gene="PAP"			
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/protein_id="AL15442.1"			
/db_xref="GI:16356655"			
/translation="MKSMLVVTISVWLIPSTSMVNTIYNVSTTISKAYFLDN LNRADPSLICKVGIPLPVPNPVYVEIGSKKITTMLRPNNTLYMGVSDP DPKCRHIFSDISGERDVEITLLPKNRSRYSKINIDSRFTLESKAGYSRBY QLEIQILDSNIGIKISGVTSPTEKTEBFLVALQWSEARFPIGQVETNRRAN PNPKNLSESTWGIKISTAIHDANKVLPRLVLDVSGAKMIVLRVDIDIPVALINY VGSCCTVYQNAMPOLIMSTYNYMANIGLIEGF"			
ORIGIN			
Query Match 67.3%; Score 635.8; DB 15; Length 1164;			
Best Local Similarity 80.4%; Pred. No. 3,4e-138;			
Matches 758; Conservative 0; Mismatches 182; Indels 3; Gaps 1;			
Qy	6	GGTATGCTTGTATGTTGTGTCGTTAATAGGCTGCTATTCGACCACTTCAAC	65
Db	1	GATGAGTGCATCTGTGTGTCGTCGTCATGATGATGCTATTCCTGACCACTTCAAC	60
Qy	66	TTGTGTCATTAATAGATCACTTTGATGCTGGAATGCCACATTAACAAATATGCGAC	125
Db	61	TTGGGCTGTAAATACATATCATCTACATGTTGAGATGACACATTAAGCAATAGCGCAC	120
Qy	126	CTTTATGGAATCTCTTGTGATCAAGGAAAGATCCAAAATTAATGCTATGCGATAC	185
Db	121	TTTTCTGATTAATCTTGTATGAGGAAAGATCCAAAGTTTAAATGCTATGGAATAC	180
Qy	186	AATGCTACCTGATACCTAATTCGACCCCTAATGCTAATGCTAAGCTCCAGGTGCAA	245
Db	181	AATGTTGCCAATACCAATCCAAATCCAAAGTACGTTGAGCTCCAGGTTCAA	240
Qy	246	CCTAAACCATTAACATAATGCTGAGACCAATTAATTAATGCTATGCTATTCGA	305
Db	241	TAAATAACCATCACTAATGCTGAGACCAATTAATTAATGCTATGCTATTCGA	300
Qy	306	TCCCTTCATGGAATGATGCTGTTACATATTTAATGATTAACAACCGAAGC	365
Db	301	TCCCTTGAATCAATTAAGTGTGTTACATATCTTTAATGATTAATCAAGTACGTAACG	360
Qy	366	CACGTATGGAATACCTTTGCTCAAGTTGATGTCGCTGCTGCAATGTCANTTA	425
Db	361	CGAAGATGAGACCTATCTTTGCTCAAGTTGATGTCGCTGCTGCAATGTCANTTA	420
Qy	426	CTCAATAGCTTATTCGACCATGAGAAAGAAAGCAAGTAATCAAGAAATCAAGT	485
Db	421	CTATGATGATGATATTCACATTTGAATTAAGGAGGATTAATCAAGAGTCAAGT	480
Qy	486	CCAATGGGAATCAATTAATCTCAGAGTGAATGGAATAATCTCTGAGTTGATTCAT	545
Db	481	TCAACTGGGAATCAATTAATCTCAGAGTGAATGGAATAATCTCTGAGTTGATTCAT	540
Qy	546	CCCTGTAATAACGAGGCTTTTCTGATCGTATGATCCAAATGTTTCAAGGACG	605
Db	541	CACGAGAAACCGAAGCCGAATTCCTATCGTATGATCCAAATGTTTCAAGGACG	600
Qy	606	GCGATTCAGATACATAGAGAACCAATCAAGTAAATTTTAATAGACATTCACCTGA	665
Db	601	AAGATTCAGATACATAGAGAACCAATCAAGTAAATTTTAATAGACATTCACCTGA	660
Qy	666	TCCCAAGATTAATTAATTTGAGAGAGAGTGGGCAAAATCTCTGAGCAATTCACATGC	725
Db	661	TCCCAAGATTAATTAATTTGAGAGAGAGTGGGCAAAATCTCTGAGCAATTCACATGC	720

QY 726 CAAAGATGGGGCTTTTACCCAAACCACTTGAAGTATGGATGCCAAGATCAAGATGGAT 785
DB 721 CAAAGATGGGGCTTTTACCCAAACCTCGAGTATGGATGGAGTGGTCCAAAGTGGAT 780
QY 786 AGTTCTTAAGTGGATGAATCAATGCTGATGTGGCATCTCTTAAGTATGGATGAAC 845
DB 781 AGTTCTTAAGTGGATGAATCAAGCTGATGTGGCATCTCTTAAGTATGGATGAAC 840
QY 846 CTGTCCAGACAACTT---ACCAAAATGGCATGTTCTCTCAAGTTATATTTCTACTTATTA 902
DB 841 CTGTCCAGACAACTTATTAACCAAAATGGCATGTTCTCTCAAGTTATATGTCTACTTATTA 900
QY 903 TAAATATATGTCTAATCTTGTGATCTATTTGAAGATCTTAA 945
DB 901 TAAATATATGTCTAATCTTGTGATCTATTTGAAGATCTTGA 943

RESULT 7
A42103 1195 bp DNA 1linear PAT 05-MAR-1997
LOCUS A42103
DEFINITION Sequence 1 from Patent EP0637591.
ACCESSION A42103
VERSION A42103.1 GI:2297595
KEYWORDS
SOURCE Phytoleuca americana (American pokeweed)
ORGANISM

Phytoleuca americana (American pokeweed)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Myrtilloceae; Phytolacaceae; Phytolacaceae.
1 (bases 1 to 1195)
Moon, Y., Jeon, H., Choi, K., Lee, K. and Kim, M.

A novel expression vector for phytoleuca antiviral protein
Patent: EP 0637591-A 1 08-FEB-1995;
JINRO LIMITED (KR)

Other publication JP 662844 950914
Other publication JP 7067660 950314
Other publication CA 2102859 950103
Other publication AU 5064293 950119.
Location/Qualifiers
1. 1195
/organism="Phytoleuca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"

FEATURES
source

ORIGIN

Query Match 67.1%; Score 634; DB 6; Length 1195;
Best Local Similarity 80.1%; Pred. No. 8.9e-138;

Matches 758; Conservative 0; Mismatches 185; Indels 3; Gaps 1;

QY 3 GAAGTGATGCTTGTAGTGTGTGACGTTAATAGCGTGGCTGCTGACCAACTTC 62
DB 29 GAAGATGAAGTGCATGCTGTGTGACATATCATATAGCTCTATCTTGACCAACTTC 88
QY 63 AACTGTGCAATTAATACATGATCCTTTGATGTGGAAATGCCACATTAACAATATGC 122
DB 89 AACTGTGCGTGTGAATACATATCTTCAATGTGTGAAGTACACCACTTAAGCAATACGC 148
QY 123 CACTTTATGATGATCTCTGTATCAAGCAAGATCCAAACTAATATGCTATGCAT 182
DB 149 CACTTTTGTGATGATCTCTGTATCAAGCAAGATCCAAACTAATATGCTATGCAT 208
QY 183 ACCAATGCTACCTGATATTAATTCGACCCCTAAGTACTTATTTAGCTCCAAAGTGC 242
DB 209 ACCAATGCTGCCCAATACAAATTCAAATCCAAAGTACGTGTGTGAGCTCCAAAGTGC 268
QY 243 AAACCTAAACCAATTAACATATGCTGAGCAAAATTAATTAATGATGGCTATTC 302
DB 269 AAATATAAAACCAATCACTAATGTGTGAGCAAAATTAATGATGTGATGTGATTC 328
QY 303 TGAATCCCTTCAATGCAATAGTGTGATTAATATTAATTAATGATTAACAAGCAACG 362
DB 329 TGAATCCCTTGAACCAATTAATGTGTGATTAATCTTAATGATTAATCTCAAGTACTGA 388

QY 363 ACGCATGATGTGAGAAATATCTTTGTCTCAAGTCTAGTTCGTGTGTGCAATGTTCAT 422
DB 389 ACGCAAGATGTGAGATCTACTTTGTCCCAATGTCCAAATTCGTGTGTGATTAATAAT 448
QY 423 TAATCAATAGCTTTATTCACCATGAGAAAGAAAGCAAGATTAATCAAGAAATCA 482
DB 449 AAATCTGTATGTGATTCACCAATGGAATCAAAAGCGGGAGTAAATCAAGAAATCA 508
QY 483 AGTCAATGGGAATCAATATCACTGAGCATGATTTGGAAAAATCTCGAGTGTGATTC 542
DB 509 AGTCAATGGGAATCAATATCACTGAGCATGATTTGGAAAAATCTCGAGTGTGATTC 568
QY 543 ATTCCCTGAAAACTGAGGCTTTTCTACTGTAGTCCATCAATGCTTTCAGAGGC 602
DB 569 ATTCACTGAGAAAAAGGAGGCAATTCATATTGTGATGATCAATATGATTCAGAGGC 628
QY 603 AGCGCATTCAGTATCATGAGAACCAAGTCAAGATTAATTTAATAGACATTTCAACC 662
DB 629 AGCAAGATTCAGTATCATGAGAACCAAGTCAAGATTAATTTAATAGACATTTCAACC 688
QY 663 TGAATCCCAAGTAAATTTTGGAGGAGAGTGGGCAAAATCTCGAGCAATTCACAA 722
DB 689 TAATCCCAAGTAAATTTTGGAGGAGAGTGGGCAAAATCTCGAGCAATTCACAA 748
QY 723 TGCAGAAATGGGCTTTTACCCAAACCACTTGTAGTATGATGCCAAAGTACCAAGT 782
DB 749 TGCAGAAATGGGCTTTTACCCAAACCTTGTAGTATGATGCCAGTGTGCCAAGT 808
QY 783 GATATGTTCTTAAGTGTGAGAAATCAATGCTATGTGGCATCTCTTAAGTATGATG 842
DB 809 GATATGTTCTTAAGTGTGAGAAATCAAGCTGTATGATGATTTAACTTACCTGTG 868
QY 843 AACCTGTCCAGCAACTT---ACCAAAATGCCATGTTCTCTCAAGTTATATTTCTACTTA 899
DB 869 GAGCTGTCCAGCAACTTATTAACCAAAATGCCATGTTCTCTCAAGTTATATGTCTACTTA 928
QY 900 TTAATATTAATGTCTAATCTTGTGATCTATTTGAAGATCTTAA 945
DB 929 TTAATATTAATGTCTAATCTTGTGATCTATTTGAAGATCTTGA 974

RESULT 8
I43835 1195 bp DNA 1linear PAT 07-OCT-1997
LOCUS I43835
DEFINITION Sequence 1 from patent US 5633155.
ACCESSION I43835
VERSION I43835.1 GI:2468933
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1195)

Kim, M.-K., Lee, K.-H., Na, B.-K., Jeong, H.-S., Choi, K.-W., Moon, Y.-H.
and Jeon, H.-S.

Expression vector for phytoleuca antiviral protein and process for
preparing transgenic plant transformed therewith
Patent: US 5633155-A 1 27-MAY-1997;
Location/Qualifiers
1. 1195
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 67.1%; Score 634; DB 6; Length 1195;
Best Local Similarity 80.1%; Pred. No. 8.9e-138;

Matches 758; Conservative 0; Mismatches 185; Indels 3; Gaps 1;

QY 3 GAAGTGATGCTTGTAGTGTGTGACGTTAATAGCGTGGCTGCTGACCAACTTC 62
DB 29 GAAGATGAAGTGCATGCTGTGTGACATATCATATAGCTCTATCTTGACCAACTTC 88
QY 63 AACTGTGCAATTAATACATGATCCTTTGATGTGGAAATGCCACATTAACAATATGC 122

Db 89 AACTGGGCTGTGATACATCATCTACATGTTGGAGTACCACTTACCAATACGC 148
Qy 123 CACCTTATGGAATCTCTTGTATCAAGCAAGATCCAAATGCTAATGCGAT 182
Db 149 CACTTTCTGATGATCTTCTGTATGAGCAAGATCCAGTTTAAATGCTATGAT 208
Qy 183 ACCAATGCTACTGATACCTAATGACCCCTAAGTACTTATGTTAGTCCAGGTGC 242
Db 209 ACCAATGCTGCTCCATCAATATCAATCCAAAGTACGTGTTGTTAGTCCAGGTGC 268
Qy 243 AAACCTTAAAAACCTTACATTAATGCTGAGCAAGAAATTAATCTAATGCTGATGC 302
Db 269 AAATTAATAAACAATCACTTAATGCTGAGCAAGAAATTAATGCTGATGCTGATTC 328
Qy 303 TGATCCCTTCAATGATGATGCTGATCAATATTAATGATTAATCAACACCGA 362
Db 329 TGATCCCTTGAACCAATTAATGCTGATCAATCTTATGATTAATCTGATGATCA 388
Qy 363 ACAGCAATGATGAGATTAATCTTGTGCTCAAGTCTAATGCTGATGATGCTCAT 422
Db 389 ACAGCAATGATGAGATTAATCTTGTGCTCAAGTCTAATGCTGATGATGCTCAT 448
Qy 423 TAACTACAAATGCTTATATCCGACATGAGAAAGAAAGCAAGTAACTCAAGAAATCA 482
Db 449 AAATCTTGAATGATGATTAATCAATGATGATCAAAAGCGAGTAAATCAAGAAATCA 508
Qy 483 AGTCAATGAGGAAATCAATTAATCTCAGAGTCAATGAGAAATCTCTGAGTGAATTC 542
Db 509 AGTCAATGAGGAAATCAATTAATCTCAGAGTCAATGAGAAATCTCTGAGTGAATTC 568
Qy 543 ATTCCCTGTAAAACTGAGGCTTTTCTAATGCTGATGCTCAATGCTGATGATGCTCAT 602
Db 569 ATTCACTGAGAAACCGAAGCGAATTCCTATGCTGATGCTCAATGCTGATGATGCTCAT 628
Qy 603 AGGCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 662
Db 629 AGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 688
Qy 663 TGAATCCAAAGTAAATTAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 722
Db 689 TAAATCCAAAGTAAATTAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 748
Qy 723 TGCAGAAATGAGGCTTACCAACCACTTGAATGATGATGATGATGATGATGATGATGATG 782
Db 749 TGCAGAAATGAGGCTTACCAACCACTTGAATGATGATGATGATGATGATGATGATGATG 808
Qy 783 GATAGTCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 842
Db 809 GATAGTCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 868
Qy 843 AACCTGTCAGCAACT--ACCAATGCGCATGTTCTCAAGTAAATTTTCTACTTA 899
Db 869 GAGCTGTCAGCAACTTAATTAACCAAAATGCGCATGTTCTCAAGTAAATTTTCTACTTA 928
Qy 900 TTATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 945
Db 929 TTATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 974

RESULT 9
155866
LOCUS 155866 1195 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 5648234.
ACCESSION 155866
VERSION 155866.1 GI:2476660
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1195)
AUTHORS Moon, Y.-H., Jeon, H.-S., Choi, K.-W., Lee, K.-H. and Kim, M.-K.
TITLES Expression vector for Phytolacca antiviral protein
JOURNAL Patent: US 5648234-A 1 15-JUL-1997;

FEATURES
source
Location/Qualifiers
1..1195
/organism="unknown"
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Query Match
Best Local Similarity 80.1%; Pred. No. 8,9e-138;
Matches 758; Conservative 0; Mismatches 185; Indels 3; Gaps 1;

Qy 3 GAAAGTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 62
Db 29 GAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 88
Qy 63 AACTTGGCCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 122
Db 89 AACTTGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 148
Qy 123 CACCTTATGGAATCTCTGATATCAAGCAAGATCCAAATGCTAATGCGAT 182
Db 149 CACTTTCTGATGATCTTGTATGAGCAAGATCCAAATGCTAATGCGAT 208
Qy 183 ACCAATGCTACTGATACCTAATGACCCCTAAGTACTTATGTTAGTCCAGGTGC 242
Db 209 ACCAATGCTGCTCCATCAATATCAATCCAAAGTACGTGTTGATGCTCCAGGTGC 268
Qy 243 AAACCTTAAAAACCTTACATTAATGCTGAGCAAGAAATTAATCTAATGCTGATGC 302
Db 269 AAATTAATAAACAATCACTTAATGCTGAGCAAGAAATTAATGCTGATGCTGATTC 328
Qy 303 TGATCCCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 362
Db 329 TGATCCCTTGAACCAATTAATGCTGATCAATCTTATGATTAATCTGATGATCA 388
Qy 363 ACAGCAATGATGAGATTAATCTTGTGCTCAAGTCTAATGCTGATGATGCTCAT 422
Db 389 ACAGCAATGATGAGATTAATCTTGTGCTCAAGTCTAATGCTGATGATGCTCAT 448
Qy 423 TAACTACAAATGCTTATATCCGACATGAGAAAGAAAGCAAGTAACTCAAGAAATCA 482
Db 449 AAATCTTGAATGATGATTAATCAATGATGATCAAAAGCGAGTAAATCAAGAAATCA 508
Qy 483 AGTCAATGAGGAAATCAATTAATCTCAGAGTCAATGAGAAATCTCTGAGTGAATTC 542
Db 509 AGTCAATGAGGAAATCAATTAATCTCAGAGTCAATGAGAAATCTCTGAGTGAATTC 568
Qy 543 ATTCCCTGTAAAACTGAGGCTTTTCTAATGCTGATGCTCAATGCTGATGATGCTCAT 602
Db 569 ATTCACTGAGAAACCGAAGCGAATTCCTATGCTGATGCTCAATGCTGATGATGCTCAT 628
Qy 603 AGGCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 662
Db 629 AGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 688
Qy 663 TGAATCCAAAGTAAATTAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 722
Db 689 TAAATCCAAAGTAAATTAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 748
Qy 723 TGCAGAAATGAGGCTTACCAACCACTTGAATGATGATGATGATGATGATGATGATGATG 782
Db 749 TGCAGAAATGAGGCTTACCAACCACTTGAATGATGATGATGATGATGATGATGATGATG 808
Qy 783 GATAGTCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 842
Db 809 GATAGTCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 868
Qy 843 AACCTGTCAGCAACT--ACCAATGCGCATGTTCTCAAGTAAATTTTCTACTTA 899
Db 869 GAGCTGTCAGCAACTTAATTAACCAAAATGCGCATGTTCTCAAGTAAATTTTCTACTTA 928
Qy 900 TTATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 945
Db 929 TTATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 974

RESULT 10
AR009535
LOCUS AR009535 1379 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 1 from patent US 5756322.
ACCESSION AR009535
VERSION AR009535.1 GI:3968340
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1379)
AUTHORS Tumer,N.E.
TITLE Poxweed antiviral protein mutants
JOURNAL Patent: US 5756322-A 1 26-MAY-1998;
FEATURES
source location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 66.9%; Score 632.4; DB 6; Length 1379;
Best Local Similarity 80.0%; Pred. No. 2e-137;
Matches 757; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

QY 3 GAAGTGATGCTGTGATGTTGGTGAAGTTAATAGCGTGGCTGATTGCTGACCAACTTC 62
DB 221 GAAAGATGAAGTGCATCTTGTTGGTGAATATCAATATGCTGATCTTGGACCAACTTC 280
QY 63 AACTGTGCCAATAATACGATCACTTTGATGCTGAATGCAACCAATTAACAATATGC 122
DB 281 AACTGGGCTGTGAATACATCATCTACAAATGTTGGAAGTACCACTTGAACAATACGC 340
QY 123 CACCTTATGGAATCTCTTGATATCAAGGAAAGTCCAAACTAAATGCTATGCGAT 182
DB 341 CACTTTTCGAATGATCTTGATATGAAGGAAAGTCCAAAGTTTAAAGCTATGGAAT 400
QY 183 ACCAATGCTACCTGATATCTAATTCGACCCCTAAGTACTTATTTGTTAAGCTCCAGGTGC 242
DB 401 ACCAATGCTGCCAATTAACAATTAACAATTCAAAGTACGTGTTGGAGTCCAGGTTTC 460
QY 243 AAACCTTAATAACCATTAACATAATGCTGAGACGAATAACTTATACGTGATGCTATTC 302
DB 461 AAATAAAAAAACCATCACTAATGCTGAGACGAACAATTTGTATGATGATGGTTATTC 520
QY 303 TGATCCCTTCATAGGGAATAGTGTGTTACCATATATTAATGATATTAACAACCGCA 362
DB 521 TGATCCCTTTGAAACCAATTAATGTGTTACCATATCTTAAATGATATCTCAGGTATCGA 580
QY 363 ACGCATGATGAGGAATATCTTTGCTCAAGTTCTAGTTCTCGTGTGCAATGTCCAT 422
DB 581 ACGCCAAAGATGAGACATCTCTTGGCCAAATGCGCAATTCCTGTTAGTAAAAACAT 640
QY 423 TAACTAACAATAGCTTATATCCGACCATGAAAAAGAAAGCAAGTAATCAAGAAATCA 482
DB 641 AAACCTTTGATGATGATATCCAAATGGAATCAAAAAGCGAGTAAATCAAGAGTCA 700
QY 483 AGTCAATTTGGGAATTAATCAATCAAGCATGCACTTTGGAAAAATCTCTGGAATTTATTC 542
DB 701 GGTCCAACTGGGAATTAATCAATCAAGTAATATTTGGAAGATTTCTGGAGTGTATTC 760
QY 543 ATTCCCTGTAAAAACGAGGCTTTTCTTCACTGTGAGCATCAATGGTTTCAGAGGC 602
DB 761 ATTCACTGAGAAAACGAGGCGCAATTCATTTGTTGACCATCAATGTTATCAAGGC 820
QY 603 ACGGCAATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTAAATAGAGCAATTCACCC 662
DB 821 ACGAAGATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTAAAGAGCAATTCACCC 880
QY 663 TGATCCCAAGTAAATTAATTTGAGAGGAAGTGGGCAAAATCTCTGAGGCAATTCACCA 722
DB 881 TAACTCAATAGCTTATATTCGACCATGGAAGAAAGCAAGTAATTCAGCAATTCATGA 940

QY 723 TGCCAGAATGGGGCTTTTACCCAAACCACTTGAAGTATGCAAGTACCAAGT 782
DB 941 TGCCAGAATGGAGTTTACCCAAACCTTCAGAGTATGAGTATCCAGTGGTCCAAAGT 1000
QY 783 GATAGTTCTTAAGTATGATGAATCAATCATGTATGTGCACTCTTAAAGTACCTTAATGG 842
DB 1001 GATAGTGTGAGTGTGATGAATCAAGCCTGATGTAGCATCTTAACTACCTGTGGG 1060
QY 843 AACCTGTGAGCAACTT---ACCAAAATGCAATGTTCTGCAAGTATATTTCTACTTA 899
DB 1061 GAGCTGTGAGCAACTTATTAACCAAAATGCAATGTTCTGCACTTATATGTCTACTTA 1120
QY 900 TTATAATTAATGCTTAATCTGTTGATCTAATTTGAAGATTTCTAA 945
DB 1121 TTATAATTAATGCTTAATCTGTTGATCTAATTTGAAGATTTCTGA 1166

RESULT 11
AR136704
LOCUS AR136704 1379 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 1 from patent US 6137030.
ACCESSION AR136704
VERSION AR136704.1 GI:14477376
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1379)
AUTHORS Tumer,N.E.
TITLE Pap mutants that exhibit anti-viral and/or anti-fungal activity in plants
JOURNAL Patent: US 6137030-A 1 24-OCT-2000;
FEATURES
source location/Qualifiers
1..1379
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 66.9%; Score 632.4; DB 6; Length 1379;
Best Local Similarity 80.0%; Pred. No. 2e-137;
Matches 757; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

QY 3 GAAGTGATGCTGTGATGTTGGTGAAGTTAATAGCGTGGCTGATTGCTGACCAACTTC 62
DB 221 GAAAGATGAAGTGCATCTTGTTGGTGAATATCAATATGCTGATCTTGGACCAACTTC 280
QY 63 AACTGTGCCAATAATACGATCACTTTGATGCTGGAATGCAACCATTAACAATATGC 122
DB 281 AACTGGGCTGTGAATACATCATCTACAAATGTTGGAAGTACACCAATTAACAATACGC 340
QY 123 CACCTTATGGAATCTCTTGATATCAAGGAAAGTCCAAACTAATGCTATGCGAT 182
DB 341 CACTTTTCGAATGATCTTGATATGAAGGAAAGTCCAAAGTTTAAATGCTATGGAAT 400
QY 183 ACCAATGCTACCTGATATCTAATTCGACCCCTAAGTACTTATTTGTTAAGCTCCAGGTGC 242
DB 401 ACCAATGCTGCCAATTAACAATTAACAATTCAAAGTACGTGTTGGAGTCCAGGTTTC 460
QY 243 AAACCTTAATAACCATTAACATAATGCTGAGACGAATAACTTATACGTGATGCTATTC 302
DB 461 AAATAAAAAAACCATCACTAATGCTGAGACGAACAATTTGTATGATGGTTATTC 520
QY 303 TGATCCCTTCATAGGGAATAGTGTGTTACCATATATTAATGATATTAACAACCGCA 362
DB 521 TGATCCCTTTGAAACCAATTAATGTGTTACCATATCTTAAATGATATCTCAGGTATCGA 580
QY 363 ACGCATGATGAGGAATATCTTTGCTCAAGTTCTAGTTCTCGTGTGCAATGTCCAT 422
DB 581 ACGCCAAAGATGAGACATCTCTTGGCCAAATGCGCAATTCCTGTTAGTAAAAACAT 640
QY 423 TAACTAACAATAGCTTATATTCGACCATGGAAGAAAGCAAGTAATTCAGAAATCA 482

Db 641 AAATTGATAGTCATATCCAACTGGAAATCAAAAGCGGAGTAAATCAAGATCA 700
Qy 483 AGTCAATTTGGGAATTCAAATCTGAGAGTGAATGGAATCTCTGAGTGAATTC 542
Db 701 GGTCACTGGGAATTCAAATCTGAGAGTGAATGGAATCTCTGAGTGAATTC 760
Qy 543 ATTCCCTTAAATTCGAGGCTTTTCTCTGAGTGAATGGAATCTCTGAGTGAATTC 602
Db 761 ATTCACTGAGAAACCGAAGCGGATTCCTATGTTAGCCATGAGATGATCAGAGC 820
Qy 603 AGCGGATTCAGATCAATGAGAACCAAGTCAAGCTTAATTTAATGAGATTCATCC 662
Db 821 AGCAAGATTCAGATCAATGAGAACCAAGTCAAGCTTAATTTAATGAGATTCATCC 880
Qy 663 TGATCCCAAGTAAATTAATTTGAGAGAGAGTGGGCGAAATCTCTGAGGCAATTCACA 722
Db 881 TAAATCCCAAGTAAATTAATTTGAGAGAGAGTGGGCGAAATCTCTGAGGCAATTCACA 940
Qy 723 TGCCAGAAATGGGCTTTACCCAAACCACTGAGCTAGTGAATGCAAGGATCCAGATG 782
Db 941 TGCCAGAAATGGGCTTTACCCAAACCACTGAGCTAGTGAATGCAAGGATCCAGATG 1000
Qy 783 GATAGTTTGAAGTGAATGAAATCAATGATGATGCACTCTTAAGTACGTTAATG 842
Db 1001 GATAGTTTGAAGTGAATGAAATCAATGATGATGCACTCTTAAGTACGTTAATG 1060
Qy 843 AACCTGTGAGCAACTT---ACCAAAATGCGATGTTCTGCAAGTAAATTTCTACTTA 899
Db 1061 GAGCTGTGAGCAACTTAAATCAAAATGCGATGTTCTCTCACTTAATTAATGTTACTTA 1120
Qy 900 TTATTAATTAATGTTCTTAATCTTGTGATCTAATTTGAGAGATTCCTAA 945
Db 1121 TTATTAATTAATGTTCTTAATCTTGTGATCTAATTTGAGAGATTCCTAA 1166

RESULT 12
AX427731 1379 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 30 from Patent WO0233107.
DEFINITION AX427731
ACCESSION AX427731.1 GI:21537838
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
1 Neelam, A., Atkinson, H.J., McPherson, M.J. and Thomas, C.J.R.
AUTHORS Plant cell death system
TITLE Patent: WO 0233107-A 30 25-Apr-2002;
JOURNAL CAMBRIDGE ADVANCED TECH (GB)
FEATURES
Source
1. .1379
/organism="Phytolacca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"

ORIGIN
Query Match 66.9%; Score 632.4; DB 6; Length 1379;
Best Local Similarity 80.0%; Pred. No. 2e-137;
Matches 757; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

Qy 3 GAAGTATGCTTGTAGTGTGAGCTTAATACCGTGGCTCAATGCTGACCAATTC 62
Db 221 GAATATGAAGTGAATGCTTGTGAGCAATTAATGAGTGGCTCAATTCGACCAACTTC 280
Qy 63 AACTGTGCAATTAATGATCACTTGTGATGCTGAGAAATGCGACCAATTAATATATG 122
Db 281 AACTGTGCTGTGATCAATCACTTACATATGTTGAGAGTACCAACATTAATATATG 340
Qy 123 CACCTTAATGAAATCTTGTGATCAAGCAAAAGATCAAAATTAATGCTATGCGAT 182

Db 341 CACTTTCTGATGATCTTGTGATGAGCGAAAGATCCAAATTTAAATGCTATGAT 400
Qy 183 ACCATGTTACTGATTAATTAATGAGCCCTTAAGTACTTAATGTTAAGTCTCAAGTGC 242
Db 401 ACCAATGCTGCCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 460
Qy 243 AAACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 302
Db 461 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 520
Qy 303 TGATCCCTTCAATGAGCAATTAATGATGCTTACCAATTAATTAATTAATTAATTAATTA 362
Db 521 TGATCCCTTCAATGAGCAATTAATGATGCTTACCAATTAATTAATTAATTAATTAATTA 580
Qy 363 ACGCAATGATGAGAAATCTCTTGTGATGATGATGATGATGATGATGATGATGATGAT 422
Db 581 ACGCAATGATGAGAAATCTCTTGTGATGATGATGATGATGATGATGATGATGATGAT 640
Qy 423 TAACTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 482
Db 641 AAATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 700
Qy 483 AGTCAATTTGGAATTCAAATTAATGATGATGATGATGATGATGATGATGATGATGAT 542
Db 701 GGTCAATGGAATTCAAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 760
Qy 543 ATTCCCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 602
Db 761 ATTCACTGAGAAACCGAAGCGGATTCCTAATGATGATGATGATGATGATGATGATGAT 820
Qy 603 AGCGGATTCAGATCAATGAGAACCAAGTCAAGCTTAATTTAATGAGATTCATCC 662
Db 821 AGCAAGATTCAGATCAATGAGAACCAAGTCAAGCTTAATTTAATGAGATTCATCC 880
Qy 663 TGATCCCAAGTAAATTAATTTGAGAGAGAGTGGGCGAAATCTCTGAGGCAATTCACA 722
Db 881 TAAATCCCAAGTAAATTAATTTGAGAGAGAGTGGGCGAAATCTCTGAGGCAATTCACA 940
Qy 723 TGCCAGAAATGGGCTTTACCCAAACCACTGAGCTAGTGAATGCAAGGATCCAGATG 782
Db 941 TGCCAGAAATGGGCTTTACCCAAACCACTGAGCTAGTGAATGCAAGGATCCAGATG 1000
Qy 783 GATAGTTTGAAGTGAATGAAATCAATGATGATGCACTCTTAAGTACGTTAATG 842
Db 1001 GATAGTTTGAAGTGAATGAAATCAATGATGATGCACTCTTAAGTACGTTAATG 1060
Qy 843 AACCTGTGAGCAACTT---ACCAAAATGCGATGTTCTGCAAGTAAATTTCTACTTA 899
Db 1061 GAGCTGTGAGCAACTTAAATCAAAATGCGATGTTCTCTCACTTAATTAATGTTACTTA 1120
Qy 900 TTATTAATTAATGTTCTTAATCTTGTGATCTAATTTGAGAGATTCCTAA 945
Db 1121 TTATTAATTAATGTTCTTAATCTTGTGATCTAATTTGAGAGATTCCTAA 1166

RESULT 13
AY572976 942 bp mRNA linear PLN 05-APR-2004
LOCUS AY572976
DEFINITION Phytolacca americana antiviral protein (PAP) mRNA, complete cds.
ACCESSION AY572976
VERSION AY572976.1 GI:45826466
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
1 Xiao, Z.A. and Jiang, Y.
AUTHORS A gene encoding the pokeweed antiviral protein in the leaf of
TITLE Phytolacca americana
JOURNAL unpublished
REFERENCE 2 (bases 1 to 942)

AUTHORS Xiao, Z.A.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2004) College of Life Sciences, Beijing Normal University, No. 19 Xijiekouwai Street, Haidian District, Beijing 100875, China

FEATURES Location/Qualifiers

Source

1. .942
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 /mol_type="mRNA"

gene

CDS

1. .942
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 LRNEADPSLKYGIPLPNTNPKVLEQSNKRTITLRLRNLLVWGSDPF
 ETNKKRYHIENDISGERQDEETLLCPNARSRYKINIPDSRPPTLESKGVSRQV
 QLG1QILDNSNIGKISGVMSFTEKTEAFELVALIOWSEARPKYIEHQVTNFRAN
 PNRKVNLOETWKISIPAIHDANKGVLPKLEIVDASGAKMIVLRVDEIKPDVALINY
 VGSSCCTTNQNMFPQLINSTYNNVMNLGDLPEEG"

ORIGIN

Query Match 66.9%; Score 632.2; DB 15; Length 942;
 Best Local Similarity 80.2%; Pred. No. 2.5e-137;
 Matches 755; Conservative 0; Mismatches 183; Indels 3; Gaps 1;

8 TGAATCTGTGATGTTGGTGAAGCTTAATAGCGTCTCATTTGTCACCACTTCAACTT 67
 2 TGAAGGTGATGCTTGTGTGACATATCAATATGCTCATTTGTCACCACTTCAACTT 61
 68 GTGCATTAATATGACACCTTGTGATGCTGGAATGCGACATTAACAATATGCGACCT 127
 62 GGGCTGTGATATCAATCATTTCAATATGTTGAAAGTACACCATTAAGCAATAGCCACTT 121
 128 TTATGGAATCTCTTGTATCAAGCGAAGATCCAAATCAAAATGCTATGCAATCAAA 187
 122 TTCTGATGATCTTGTGATGAAAGCGAAGATCAAGTTTAAATGCTATGAAATCAAA 181
 188 TGTACTCTGATATTAATTTGCAACCCCTTAAGTACTTATTTAGTTCAGAGTCAAAAC 247
 182 TGTGCGCCATATCAATATCAAAATCAAAAGTATGTTGAGTCCCAAGTTCAAAATA 241
 248 TAAAAACATTAACCTATGATGCAAGCAATTAATTAATGATGATTAACAAGCAAGCA 307
 242 AAAAAACATCACTATATGCTAGACGAAACAAATTTGATGATGAGGTTATTTGATC 301
 308 CCTTCATGGAATTAAGTGTCTTACCATATATTTAATGATTAACAAGCAAGCAAGCA 367
 302 CCTTGAACCAATTAATATGCTTACCATATCTTAAATGATCTCAAGTACGAAGGCC 361
 368 CTGATGTGAGAACTACTCTTGTCTCAAGTTCTAGTTCTGCTGTTGCAATCTCAATTA 427
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 428 ACAATAGTTAATTCGACCATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGTCC 487
 422 TTGATAGTGTATTCACCACTTGAATCAAAAGCGGAGTAAATCAAGATCTCAAGTCC 481
 488 AATTGGAATTCGAATTAAGTCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCC 547
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 548 CTGTAAATTCGAGGCTTTTCTTCTAGTGTATGATCAATGCTTCAAGGCAAGGCC 607
 542 CTGAGAAACCGAAGCGAATTCCTATGTGTAGCCATCAAAATGATCAAGAGCGAGCA 601
 608 GATTCAAGTATAGAGCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCC 667
 602 GATTCAAGTATAGAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCC 661

QY 668 CCAAGTATTAATTTGAGAGAGAGGGGCAAAATCTCTGAGCAATTCACAAATGCCA 727
 DB 662 CCAAGTATTAATTTGAGAGAGAGGGGCAAAATCTCTGAGCAATTCACAAATGCCA 721
 QY 728 AGAATGGGCTTTACCAACCACTTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 787
 DB 722 AGAATGGGCTTTACCAACCACTTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 781
 QY 788 TTCTGAGAGTATGAAATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 847
 DB 782 TGTGAGAGTATGAAATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 841
 QY 848 GTGAGCAACTT--ACCAAAATGATGATGATGATGATGATGATGATGATGATGATGAT 904
 DB 842 GTGAGCAACTTATTAACCAAAATGATGATGATGATGATGATGATGATGATGATGATGAT 901
 QY 905 ATTAATGCTTAATCTTGTGATCTATTTGAAGATCTTAA 945
 DB 902 ATTAATGCTTAATCTTGTGATCTATTTGAAGATCTTGA 942

RESULT 14

AF533515 1114 bp mRNA linear PLN 01-AUG-2005
 LOCUS Phytolacca oclandria anti-viral protein (pap) mRNA, partial cds.
 DEFINITION AF533515
 ACCESSION AF533515
 VERSION AF533515.1 GI:33329822

SOURCE

Phytolacca oclandria
 Phytolacca oclandria

Bukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.

1 (bases 1 to 1114)
 Lin, J.S. and McNally, K.P.

Submitted (29-JUL-2002) Reproductive Technologies, AgResearch
 Wallaceville, Ward Street, Upper Hut, Wellington, New Zealand

FEATURES Location/Qualifiers

source

1. 1114
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 /mol_type="mRNA"

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<1..920
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ORIGIN

Query Match 66.9%; Score 632.2; DB 15; Length 1114;
 Best Local Similarity 81.4%; Pred. No. 2.4e-137;
 Matches 746; Conservative 0; Mismatches 168; Indels 3; Gaps 1;

QY 32 TAATAGCGTGTCTATGCTGCAACCACTTCAATTTGCAATTAATAGATCACTTTG 91
 DB 4 TATCACTATAGGCTCATTTCTTGCAACCACTTCAATTTGCGGCGTGAATCAATCATCTTACA 63
 QY 92 ATGCTGGAATGCAACCATTAACAATATGCAACCTTATGAAATCTCTTGGTAATCAAG 151
 DB 64 ATGTTGAAGTACCAACATTAACAACCACTTCTCTGATGATCTTCTGTAATGAAG 123

Qy	152	CGAAGATCCAAA	CTAAATGCTATGCGATACCAATGCTACCTGATCTAATTCGACC	211
Db	124	CGAAGATCCAAA	TTTAAATGCTATGGAATACCAATGCTGCTCCCAATCAATCCAGATC	183
Qy	212	CTAAGTCTTATG	TTTGAAGTCCAAAGTGCAGAACTTAAACCTTAACTTACCTATGCTGA	271
Db	184	CAAGTACGTTG	TGGTGAAGTCCAAAGTGCAGAACTTAAACCTTAACTTACCTATGCTGA	243
Qy	272	GACCAATTAAT	CTTACGTTGAGGCTATTCCTGATCCCTTCAGTACCAATTAAGTGTGTT	331
Db	244	GACCAATTAAT	CTTACGTTGAGGCTATTCCTGATCCCTTCAGTACCAATTAAGTGTGTT	303
Qy	332	ACCAATATTTA	TGATATTAACAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG	391
Db	304	ACCAATATTTA	TGATATTAACAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG	363
Qy	392	CAATTTCTAGT	CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	451
Db	364	CAATTTCTAGT	CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	423
Qy	452	AAAGAAAGCAG	AGTAACTCAAGAAATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG	511
Db	424	AAAGAAAGCAG	AGTAACTCAAGAAATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG	483
Qy	512	GTCACATTTGA	AAAAATCTCTGAGTTCATTCCTCTGTAATAAATGAGGCTTTTCTTC	571
Db	484	GTCACATTTGA	AAAAATCTCTGAGTTCATTCCTCTGTAATAAATGAGGCTTTTCTTC	543
Qy	572	TACTGTGATCA	TCAATGCTTTCAGAGCGAGCGAGCTTCAAGTACATGAGAACCAAG	631
Db	544	TACTGTGATCA	TCAATGCTTTCAGAGCGAGCGAGCTTCAAGTACATGAGAACCAAG	603
Qy	632	TCAAGCTAAT	TTTAAATGAGCATTCACCTGATCCCAAGTAATTAATTTGAGAGGA	691
Db	604	TCAAGCTAAT	TTTAAATGAGCATTCACCTGATCCCAAGTAATTAATTTGAGAGGA	663
Qy	692	AGTGGGCAAA	ATCTGAGGCAATTCACATGCGCAAGATGAGGCTTTCACCAACAC	751
Db	664	AGTGGGCAAA	ATCTGAGGCAATTCACATGCGCAAGATGAGGCTTTCACCAACAC	723
Qy	752	TTGAGCTAGT	AGATGCCAAGGTACCAAGTGCATGTTCTTGAAGTGCATGATCAATC	811
Db	724	TTGAGCTAGT	AGATGCCAAGGTACCAAGTGCATGTTCTTGAAGTGCATGATCAATC	783
Qy	812	GTCATGTCG	CACTTAAAGCTTAAATGAGCACTGTCAGCAACTT---ACCAAAATG	868
Db	784	GTCATGTCG	CACTTAAAGCTTAAATGAGCACTGTCAGCAACTTAAATGAGCAACTT	843
Qy	869	CCATGTCCTC	CAAGTATTAATTTCTTATTAATTAATTAATTAATTAATTAATTAATTAAT	928
Db	844	CCATGTCCTC	CAAGTATTAATTTCTTATTAATTAATTAATTAATTAATTAATTAATTAAT	903
Qy	929	TAATTTGAG	GAATTTCTAA 945	
Db	904	TAATTTGAG	GAATTTCTGA 920	

RESULT 15

PAPAP	LOCUS	PAPAP	1164 bp	mRNA	linear	PLN 18-NOV-1991
DEFINITION	P. americana PAP gene for anti-viral protein.					
ACCESSION	X55383					
VERSION	X55383.1 GI:20421					
KEYWORDS	antiviral protein; cell wall protein; PAP gene; ribosome					
SOURCE	Phytolacca americana (American pokeweed)					
ORGANISM	Phytolacca americana					
REFERENCE	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolacaceae; Phytolacca.					
REFERENCE	1 (bases 1 to 1164)					
AUTHORS	Lin, Q., Chen, Z. C., Antoniw, J. F. and White, R. F.					
TITLE	Isolation and characterization of a cDNA clone encoding the					

JOURNAL	anti-viral protein from Phytolacca americana
PUBMED	Plant Mol. Biol. 17 (4), 609-614 (1991)
REFERENCE	1912488
AUTHORS	2 (bases 1 to 1164)
TITLE	Antoniw, J. F.
JOURNAL	Submitted (05-NOV-1990) Antoniw J.F., AFRC Inst of Arable Crops Research, Dept. of Plant Pathology, Rothamsted Experimental Station, Harpenden, Hert, AL5 2JQ, UK
FEATURES	Location/Qualifiers
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	/db_xref="taxon:3527"
	/tissue_type="leaf"
	/dev_stage="vegetative"
gene	1. 1164
	/gene="PAP"
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	/product="anti-viral protein"
	/protein_id="CAA39054.1"
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ORIGIN

Query Match	66.8%; Score 631; DB 15; Length 1164;
Best Local Similarity	80.1%; Pred. No. 4.5e-137;
Matches	755; Conservative 0; Mismatches 185; Indels 3; Gaps 1;
Qy	6 GGTGATGCTTGTAGTGTGTGATGCTTAAATGCTGCTCAATGCTGCACTTCAAC 65
Db	1 GATGAATGCAATGTTGTGATGCAATATGCTGCTCAATGCTGCACTTCAAC 60
Qy	66 TTGTCATTAATACGATCACTTGTATGCTGGAATGCGACCAATTAACAATATGCGAC 125
Db	61 TTGGGCTGTAAATCAATCATCTTACATGTTGGAAGTACCACTTACGAATATGCGAC 120
Qy	126 CTTTATGAAATCTCTTGATATCAAGCAAGATCCAAAATAATGCTATGCGATACC 185
Db	121 TTTTCTGAATGATCTTGATATGAGCAAGATCCAAATGTTAAATGCTATGGAATACC 180
Qy	186 AATGCTACCTGATCTAATTCGACCCCTAAGTACTTATGTTAAGTCCAGGTGCAA 245
Db	181 AATGCTGCCCAATTAACAATCAATCCAAATGCTGCTGTTGAGGCTCCAAAGTTGCAA 240
Qy	246 CTTAAAAACATTAACATTAATGCTGAGCAAGAAATTAATTAAGTATGAGGCTATTCGA 305
Db	241 TAAAAAACATTAACATTAATGCTGAGCAAGAAATTAATTAAGTATGAGGCTATTCGA 300
Qy	306 TCCCTTCATGCAATAGTGTGTTACATATATTAATTAATTAATTAATTAATTAATTAAT 365
Db	301 TCCCTTTGAACAATTAATGTTGTTACATATCTTTAATGATATCTGAGTCTGAACG 360
Qy	366 CACTGATGGAAGATATCTTTTGTCTCAAGTTCTAGTTCTGCTGTTGCAATATTCATTA 425
Db	361 CCAAGATGTAAGACTACTTTTGCCCAATGCAATTCGCTGTTAGTAAAAACAATAA 420
Qy	426 CTACAAATGCTTATCCGACATGAGAAAGCAAGATTAACCTCAAGAAATCAAGT 485
Db	421 CTTTGATATGCTATTCACATTTGAAATCAAAAGCGAGTAAATCAAGAGTCAAGT 480
Qy	486 CCAATTTGGAATTCAAATTAATCTGACAGTGCATTTGGAATAATCTCTGAGTTGATTCAT 545
Db	481 CCAATTTGGAATTCAAATTAATCTGACAGTGCATTTGGAATAATCTCTGAGTTGATTCAT 540

QY 546 CCTGTAAAACTGAGGCTTTTCTACTGTAGCCATCCAAATGTTTCAGAGGAGC 605
Db 541 CACTGAGAAAAACGAGGCCGAAATTCATGTGTAGCCATCAAAATGTTATCAGAGGAGC 600
QY 606 GCGATTCAGTACTATGAGAACCAAGTCAAGACTAATTTAATGAGCAATTCACCTGA 665
Db 601 AGATTCAAGTACATGAGAAATCAGGAAACTAATTTAACAAGACATTCAACCTTA 660
QY 666 TCCCAAGTAAATTAATTTGAGAGAAAGTGGGCAAAATCTGAGGCAATTCACAAATG 725
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QY 726 CAAGAATGGGCTTTAACCCAAACCACTTGAAGTATGATGCAAAAGTACCAAGTGA 785
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QY 786 AGTCTTAAGTGTGAATCAATGCTGATGTGGCACTCCTTAAGTACGTTAATGGAAC 845
Db 781 AGTGTGAGAGTGTGAATCAAGCTGATGTGACACTCTTAAGTACGTTAATGTTGAG 840
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Db 841 CTGTGAGACAACTTATAACCAAAATGCAATGTTCTGTCAAGTTATAATTTCTACTATTA 900
QY 903 TAATTATATGTCTAATCTTGTGATCTAATTTGAAGATTCTAA 945
Db 901 TAATTATATGTCTAATCTTGTGATCTAATTTGAAGATTCTGA 943

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OM nucleic - nucleic search, using sw model

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Title: US-09-978-274A-1

Perfect score: 945

Sequence: 1 atgaagtgatgcttctgagc.....atctattgaagattcttaa 945

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	945	100.0	945	6 AAD42715	Aad42715 Pokeweed
2	786.4	83.2	792	6 AAD42716	Aad42716 Pokeweed
3	761.4	80.6	1092	6 AAD42729	Aad42729 Pokeweed
4	634.2	67.1	1164	11 ADM74765	Adm74765 HIV-1 inh
5	632.4	66.9	1378	12 ADG76061	Adg76061 American
6	632.4	66.9	1379	3 AAZ5197	Aaz5197 Wild-type
7	632.4	66.9	1379	3 AAZ59220	Aaz59220 Pokeweed
8	632.4	66.9	1379	6 AAD42738	Aad42738 Pokeweed
9	632.4	66.9	1379	10 ADI05787	Adi05787 DNA encod
10	630.8	66.8	1195	2 AAO56672	Aao56672 Sequence
11	630.8	66.8	1195	4 AAC87929	Aac87929 P. ameriec
12	629.2	66.6	1137	6 AAO81457	Aao81457 Phytolacc
13	629.2	66.6	1378	6 AAD42739	Aad42739 Pokeweed
14	629.2	66.6	1379	3 AAZ59221	Aaz59221 Variant p
15	624.2	66.1	2472	2 AAO43967	Aao43967 Pokeweed
16	597.4	62.3	1164	11 ADM74751	Adm74751 HIV-1 inh
17	588.6	62.1	882	2 AAT95556	Aat95556 Phytolacc
18	586.4	62.1	2369	2 AAT95557	Aat95557 Phytolacc
19	586.4	62.1	2369	2 ABA95543	Aba95543 Phytolacc

20	543.8	57.5	918	2 AAO64893	Aao64893 Antiviral
21	543.8	57.5	918	2 AAT04782	Aat04782 DNA pJWC2
22	459	48.6	465	6 AAD42717	Aad42717 Pokeweed
23	329	34.8	333	6 AAD42718	Aad42718 Pokeweed
24	110.8	11.7	934	3 AAZ45198	Aaz45198 Wild-type
25	110.8	11.7	934	6 AAD42740	Aad42740 Pokeweed
26	97.8	10.3	600	2 ABA96716	Aba96716 Cloning v
27	97.8	10.3	603	2 ABA96547	Aba96547 Cloning v
28	96	10.2	864	1 AAN91504	Aan91504 DNA of ri
29	88.4	9.4	804	2 AAO53895	Aao53895 Saporin c
30	88.4	9.4	804	2 AAO53896	Aao53896 Saporin c
31	88.4	9.4	804	2 AAO53385	Aao53385 Saporin c
32	88.4	9.4	804	2 AAO53384	Aao53384 Saporin c
33	88.4	9.4	804	2 AAO99041	Aao99041 M13mp18-G
34	88.4	9.4	804	2 AAO99042	Aao99042 M13mp18-G
35	88.4	9.4	804	2 AAT17962	Aat17962 Saporin c
36	88.4	9.4	804	2 AAT17963	Aat17963 Saporin c
37	88.4	9.4	804	2 AAT17964	Aat17964 Saporin c
38	88.4	9.4	804	3 AAA12861	Aaa12861 Saporin D
39	88.4	9.4	804	3 AAA12862	Aaa12862 Saporin D
40	88.4	9.4	804	9 ACDE7204	Acde7204 Common 80
41	88.4	9.4	804	9 ACDE7205	Acde7205 Common 80
42	88.4	9.4	804	10 ADC34588	Adc34588 Common 80
43	88.4	9.4	804	10 ADC34589	Adc34589 Common 80
44	88.4	9.4	804	10 ADH92013	Adh92013 DNA encod
45	88.4	9.4	804	10 ADH92012	Adh92012 DNA encod

ALIGNMENTS

RESULT 1	
AAAD42715	
ID	AAAD42715 standard; DNA; 945 BP.
XX	AAAD42715;
AC	
XX	
DT	15-NOV-2002 (first entry)
XX	
DE	Pokeweed pro-PAP-S protein encoding DNA.
XX	
KW	Neurotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KM	gene; ds.
XX	
OS	Phytolacca americana.
PH	
PH	Key
FT	Location/Qualifiers
FT	CDS
FT	1..945
FT	/*tag= a
FT	/product= "Pro-PAP-S protein"
FT	1..24
FT	/*tag= b
FT	/bound_moiety= "Primer PPS1BP"
FT	complement (735..776)
FT	/*tag= c
FT	/bound_moiety= "Primer PSXDR"
FT	736..777
FT	/*tag= d
FT	/bound_moiety= "Primer PSXDF"
FT	750..759
FT	/*tag= e
FT	/note= "Sequence replacing removed XbaI site"
FT	complement (922..945)
FT	/*tag= f
FT	/bound_moiety= "Primer PPS2BR"
XX	
XX	MO200233107-A2.
XX	
XX	25-APR-2002.
XX	
XX	15-OCT-2001; 2001MO-GB004593.
XX	
XX	14-OCT-2000; 2000GB-00025217.

XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
 PA Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;
 PI WPI; 2002-489891/52.
 DR P-PSDB; AAE25918.

XX Inducing necrotic effect in specific cells of plant by transforming plant
 PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
 PT which acts in response to application of specific stimulus to plant.

XX Claim 24; Page 73-74; 87pp; English.

XX The invention relates to a method of inducing a necrotic effect in
 CC specific cells of a plant. The method involves transforming the plant
 CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
 CC PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
 CC in response to the application of a specific stimulus to the plant so as
 CC to facilitate expression of the pokeweed antiviral protein in specific
 CC cells of the plant. The method is useful for inducing a necrotic effect
 CC in specific cells of a plant. The present sequence is pokeweed pro-PAP-S
 CC protein encoding DNA

XX Sequence 945 BP; 307 A; 187 C; 180 G; 271 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 945; DB 6; Length 945;

XX Best Local Similarity 100.0%; Pred. No. 3.4e-254;

XX Matches 945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGGTGATGCTTGTAGTGTGTCGTCATTAATGCGTGCATTTGCTGCACCACT 60

DB 1 ATGAAGGTGATGCTTGTAGTGTGTCGTCATTAATGCGTGCATTTGCTGCACCACT 60

QY 61 TCAACTTGGCCCTAATATAGATCACCCTTGATGCTGGAATGCCACCTAATCAATAT 120

DB 61 TCAACTTGGCCCTAATATAGATCACCCTTGATGCTGGAATGCCACCTAATCAATAT 120

QY 121 GCCACCTTATGATCTCTTGTGATCAAGGAAAGATCCAAACTAATGCTATGGC 180

DB 121 GCCACCTTATGATCTCTTGTGATCAAGGAAAGATCCAAACTAATGCTATGGC 180

QY 181 ATACCAATGCTACCTGATACCTAATTCGACCCCTTAAGTACTTATGCTCAAGGT 240

DB 181 ATACCAATGCTACCTGATACCTAATTCGACCCCTTAAGTACTTATGCTCAAGGT 240

QY 241 GCAAACTTAAAAACCTTACACCTAATGCTGAGCGAAATTAATACGATGGGCTAT 300

DB 241 GCAAACTTAAAAACCTTACACCTAATGCTGAGCGAAATTAATACGATGGGCTAT 300

QY 301 TCGATCCCTTCAATGGAATAGTGTGCTTACCATATATTTAATGATATTAACAAGCACC 360

DB 301 TCGATCCCTTCAATGGAATAGTGTGCTTACCATATATTTAATGATATTAACAAGCACC 360

QY 361 GAAAGCAGTATGATGGAATATCTTTGCTCAAGTTCTAGTTCTCGTGTGCAATGTCC 420

DB 361 GAAAGCAGTATGATGGAATATCTTTGCTCAAGTTCTAGTTCTCGTGTGCAATGTCC 420

QY 421 ATTAATCAATATGCTTATATTCGACCAATGGAAGAAAGAAAGCAATGTAATCAAGAAAT 480

DB 421 ATTAATCAATATGCTTATATTCGACCAATGGAAGAAAGAAAGCAATGTAATCAAGAAAT 480

QY 481 CAAGTCCATTTGGGAATTCAGAGTCAAGTGAATTTGGAATAATCTCTGAGATTGAT 540

DB 481 CAAGTCCATTTGGGAATTCAGAGTCAAGTGAATTTGGAATAATCTCTGAGATTGAT 540

QY 541 TCAATTCCTGTAAAACTGAGGCTTTTCTAATGTCGTAACCAATGATGTTTCAGAG 600

DB 541 TCAATTCCTGTAAAACTGAGGCTTTTCTAATGTCGTAACCAATGATGTTTCAGAG 600

QY 601 GCAGCCGATTCAGATACATAGAAACCAAGTCAAGACTAATTTTATAGACATTCTAC 660

DB 601 GCAGCCGATTCAGATACATAGAAACCAAGTCAAGACTAATTTTATAGACATTCTAC 660

QY 661 CCGATCCCAAGTAATTAATTTGAGAGAAAGTGGGCAAAATCTCTGAGCAATTCAC 720
 DB 661 CCGATCCCAAGTAATTAATTTGAGAGAAAGTGGGCAAAATCTCTGAGCAATTCAC 720
 QY 721 AATGCCAAGATGGGGCTTTACCCAAACCACTTGAAGTATGATGCCAAGGTACCAAG 780
 DB 721 AATGCCAAGATGGGGCTTTACCCAAACCACTTGAAGTATGATGCCAAGGTACCAAG 780
 QY 781 TGGATAGTCTTAGAGTGAATCAATCGATGTGCACTCTCTAAGTACGTTAAT 840
 DB 781 TGGATAGTCTTAGAGTGAATCAATCGATGTGCACTCTCTAAGTACGTTAAT 840
 QY 841 GGAACCTGTCAGACACTTACCAAAATGCGATGCTCTCAAGTTAATTTCTACTTAT 900
 DB 841 GGAACCTGTCAGACACTTACCAAAATGCGATGCTCTCAAGTTAATTTCTACTTAT 900
 QY 901 TATTAATTAATGCTTAATCTTGGTATCTAATTTGAAGATTCTAA 945
 DB 901 TATTAATTAATGCTTAATCTTGGTATCTAATTTGAAGATTCTAA 945

RESULT 2

ID AAD42716 standard; DNA; 792 BP.

XX AAD42716;

XX 15-NOV-2002 (first entry)

XX Pokeweed mature PAP-S protein encoding DNA.

XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;

XX gene; ds.

XX Phytoacca americana.

XX Key Location/Qualifiers

FT CDS 1..792 /tag= a

FT /product= "Mature PAP-S protein"

FT primer_bind 1..29 /tag= b

FT /bound_molecly= "Primer PS1BF"

FT primer_bind /tag= c

FT /bound_molecly= "Primer PS1SR"

FT primer_bind /tag= d

FT /bound_molecly= "Primer PS2BF"

FT misc_feature 681..686 /tag= e

FT /note= "Sequence replacing removed XbaI site"

FT primer_bind /tag= f

FT /bound_molecly= "Primer PS2SR"

PN MO200233107-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-GB004593.

XX 14-OCT-2000; 2000GB-00025217.

XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.

XX Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;

XX WPI; 2002-489891/52.

XX P-PSDB; AAE25918.

XX Inducing necrotic effect in specific cells of plant by transforming plant

PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT which acts in response to application of specific stimulus to plant.
PS Claim 2; Page 76; 87pp; English.

CC The invention relates to a method of inducing a necrotic effect in
CC specific cells of a plant. The method involves transforming the plant
CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
CC in response to the application of a specific stimulus to the plant so as
CC to facilitate expression of the pokeweed antiviral protein in specific
CC cells of the plant. The method is useful for inducing a necrotic effect
CC in specific cells of a plant. The present sequence is pokeweed mature PAP
CC -S protein encoding DNA

XX Sequence 792 BP; 268 A; 161 C; 151 G; 212 T; 0 U; 0 Other;

Query Match 83.2%; Score 786.4; DB 6; Length 792;
Best Local Similarity 99.9%; Pred. No. 8.9e-210;

Matches 787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 73 ATAAATCGATCAGCTTGTGATGCGAATATGCCATTTAACTATATGCACTTTATG 132
DB 4 ATAAATCGATCAGCTTGTGATGCGAATATGCCATTTAACTATATGCACTTTATG 63
QY 133 GAATCTCTGATATCAAGCGAAGATCCAAATCTAAATGCTATGCGATACCAATGCTA 192
DB 64 GAATCTCTGATATCAAGCGAAGATCCAAATCTAAATGCTATGCGATACCAATGCTA 123
QY 193 CCGATATCTAATTCGACCCCTTAAGTACTTATGCTTAAAGCTCAAGGTGCAACCTTAA 252
DB 124 CCGATATCTAATTCGACCCCTTAAGTACTTATGCTTAAAGCTCAAGGTGCAACCTTAA 183
QY 253 ACCATTAACCTAATTCGCGAAGCGAATTAATCTAATGCTATGCGATACCAATGCTA 312
DB 184 ACCATTAACCTAATTCGCGAAGCGAATTAATCTAATGCTATGCGATACCAATGCTA 243
QY 313 AATGCGAATAGTGTGCTTACATATATTTAATGATTTAACAACGACGAAAGCACTGAT 372
DB 244 AATGCGAATAGTGTGCTTACATATTTAATGATTTAACAACGACGAAAGCACTGAT 303
QY 373 GTGAGAAATACCTTTGCTCAAGTCTAGTCTGTGTGCAATGTCATTAATCAAT 432
DB 304 GTGAGAAATACCTTTGCTCAAGTCTAGTCTGTGTGCAATGTCATTAATCAAT 363
QY 433 AGCTTATATCCGACGATGGAAGAAAGCAAGTAACTCAAGAAATCAAGTCAATG 492
DB 364 AGCTTATATCCGACGATGGAAGAAAGCAAGTAACTCAAGAAATCAAGTCAATG 423
QY 493 GGAATTCAAATACCTCAGCAGTCACTGGAATAATCTCTGAGTTGATTAATCCCTGTA 552
DB 424 GGAATTCAAATACCTCAGCAGTCACTGGAATAATCTCTGAGTTGATTAATCCCTGTA 483
QY 553 AAAAAGTGAAGCTTTTCTTACTGTGTAGCCATCAAAATGTTTCAAGAGCGACGATTC 612
DB 484 AAAAAGTGAAGCTTTTCTTACTGTGTAGCCATCAAAATGTTTCAAGAGCGACGATTC 543
QY 613 AAGTACATAGAAACCAAGTCAAGATTAATTTAATGAGCATTTACCTGATCCAAA 672
DB 544 AAGTACATAGAAACCAAGTCAAGATTAATTTAATGAGCATTTACCTGATCCAAA 603
QY 673 GTAATTAATTTGAGGAGGAGGCAAAATCTCTAGGCAATTCACANTGCCAAAT 732
DB 604 GTAATTAATTTGAGGAGGAGGCAAAATCTCTAGGCAATTCACANTGCCAAAT 663
QY 733 GGGGCTTTTACCACCAACCACTTGAAGTATGATGCCAAAGTACCAAGTGAATGTTCT 792
DB 664 GGGGCTTTTACCACCAACCACTTGAAGTATGATGCCAAAGTACCAAGTGAATGTTCT 723
QY 793 AAGTGAATGAATTCATGCTGATGTGGCACTCTTAAAGTACGTTAATGGAACCTGTGAG 852
DB 724 AAGTGAATGAATTCATGCTGATGTGGCACTCTTAAAGTACGTTAATGGAACCTGTGAG 783
```

QY 853 ACAACTTA 860
DB 784 ACAACTTA 791

RESULT 3
AAD42729
ID AAD42729 standard; DNA; 1092 BP.

AC AAD42729;

DT 29-AUG-2003 (revised)
DT 15-NOV-2002 (first entry)

DE Pokeweed PAP-S/TEV PCS/rice cystatin delta D86 fusion DNA.

XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KW chimeric; rice; cystatin delta D86; N1a protease cleavage site; PCS; ds.

OS Phytotheca americana.

OS Oryza sativa.

OS Tobacco; Etch virus.

OS Chimeric.

OS Key

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

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FT primer_bind

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FT primer_bind

FT primer_bind

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FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

CC and Tobacco Etch virus (TEV) N1A protease cleavage site (PCS). (Updated
 CC on 29-AUG-2003 to standardise OS field)
 XX
 XX Sequence 1092 BP; 369 A; 195 C; 222 G; 306 T; 0 U; 0 Other;

Query Match 80.6%; Score 761.4; DB 6; Length 1092;
 Best Local Similarity 99.9%; Pred. No. 1e-202;
 Matches 762; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 73 ATAAATACGATCACTTGGATGCTGAAATGCCACATTAACAAATATGACCTTATG 132
 |||||
 DB 4 ATAAATACGATCACTTGGATGCTGAAATGCCACATTAACAAATATGACCTTATG 63
 |||||
 QY 133 GAATCTCTTGGTATCAAGGAAAGATCCAAAATTAATGCTATGCGATACCAATGCTA 192
 |||||
 DB 64 GAATCTCTTGGTATCAAGGAAAGATCCAAAATTAATGCTATGCGATACCAATGCTA 123
 |||||
 QY 193 CCGTATATCAATTCGACCCCTTAAGTACTTATGTTAGCTCCAAAGTGCAACTTAA 252
 |||||
 DB 124 CCGTATATCAATTCGACCCCTTAAGTACTTATGTTAGCTCCAAAGTGCAACTTAA 183
 |||||
 QY 253 ACCATTACACTTAATGCTGAGACGAAATACCTTAAGTGAAGGGCTATTCGATCCCTTC 312
 |||||
 DB 184 ACCATTACACTTAATGCTGAGACGAAATACCTTAAGTGAAGGGCTATTCGATCCCTTC 243
 |||||
 QY 313 AATGGCAATAGTGTGCTTACATATATTTAATGATATTAACAAGCACCGACACTGAT 372
 |||||
 DB 244 AATGGCAATAGTGTGCTTACATATATTTAATGATATTAACAAGCACCGACACTGAT 303
 |||||
 QY 373 GTCGAGAAATCTCTTGGCTCAAGTTCAGTTCGTGCTGCTGCTGCTGCTGCTGCTGCT 432
 |||||
 DB 304 GTCGAGAAATCTCTTGGCTCAAGTTCAGTTCGTGCTGCTGCTGCTGCTGCTGCTGCT 363
 |||||
 QY 433 AGCTTATATCCGACCATGAAAAAGAAAGAGAAATCAAGAATCAAGTCCAAATG 492
 |||||
 DB 364 AGCTTATATCCGACCATGAAAAAGAAAGAGAAATCAAGAATCAAGTCCAAATG 423
 |||||
 QY 493 GGAATTCAAATCTCAGCAGTGAATTGAAAAATCTCTGAGTGAATTCCTCCCTGA 552
 |||||
 DB 424 GGAATTCAAATCTCAGCAGTGAATTGAAAAATCTCTGAGTGAATTCCTCCCTGA 483
 |||||
 QY 553 AAAACGAGGCTTTTTTCTACCTGCTGACCATCCAAATGTTTCAAGGCGAGCCATTC 612
 |||||
 DB 484 AAAACGAGGCTTTTTTCTACCTGCTGACCATCCAAATGTTTCAAGGCGAGCCATTC 543
 |||||
 QY 613 AAGTACATAGAGAACCAAGTCAAGACTAATTTTAAATGAGCAATTCACCTGATCCCAA 672
 |||||
 DB 544 AAGTACATAGAGAACCAAGTCAAGACTAATTTTAAATGAGCAATTCACCTGATCCCAA 603
 |||||
 QY 673 GTAATTAATTTGGAGAGAAAGTGGGGCAAAATCTCTGAGGCAATTCACAATGCCAAGAT 732
 |||||
 DB 604 GTAATTAATTTGGAGAGAAAGTGGGGCAAAATCTCTGAGGCAATTCACAATGCCAAGAT 663
 |||||
 QY 733 GGGGCTTTACCCCAACCACTTGAGCTAGTGGATGCCAAAGTACCAAGTGAATGTTCTT 792
 |||||
 DB 664 GGGGCTTTACCCCAACCACTTGAGCTAGTGGATGCCAAAGTGAATGTTCTT 723
 |||||
 QY 793 AGAGTGAATGAATCAATGCTGATGTGGCACTCTCTTAAGTACG 835
 |||||
 DB 724 AGAGTGAATGAATCAATGCTGATGTGGCACTCTCTTAAGTACG 766
 |||||

RESULT 4
 ADM74765
 ID ADM74765 standard; cDNA; 1164 BP.
 XX
 AC ADM74765;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE HIV-1 inhibition activity related Tat cDNA.
 XX
 KW human immunodeficiency virus; HIV-1; tumour; plant;

KW Chinese phytoleuca leaf; trans-acting activation factor; Tat; mutant;
 KW gene; ss.
 XX
 OS Human immunodeficiency virus 1.
 XX
 FH Key Location/Qualifiers
 FT CDS 2..943
 FT /*tag= a
 FT /product= "Tat HIV-1 protein"

PN CN1400220-A.
 XX
 PD 05-MAR-2003.
 XX
 PF 02-AUG-2001; 2001CN-00123911.
 XX
 PR 02-AUG-2001; 2001CN-00123911.
 XX
 PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
 XX
 PI Peng X, Bai L, Yin B;
 XX
 DR WPI; 2003-469263/45.
 DR P-PSDB; ADM74766.
 XX
 PT Two kinds of cDNA with activity capable of extensively inhibiting HIV and
 PT its expression, separation and purification method in protokaryon.
 XX
 PS Example 9; Page 11-12; 17bp; Chinese.
 XX
 CC The present invention relates to two kinds of cDNA which can inhibit
 CC human immunodeficiency virus (HIV-1) activity, including separation clone
 CC of two kinds of cDNA, external mutation, fusion expression in prokaryons
 CC and application of the cDNA in preparation of preparation for curing the
 CC virus and tumours. One of the described cDNAs is obtained by separation
 CC and cloned from a plant Chinese phytoleuca leaf, and one from the trans-
 CC acting activation factor (Tat) mutant coded by human immunodeficiency
 CC virus HIV-1 gene. This polynucleotide sequence represents the Tat cDNA
 CC used in the HIV-1 inhibition activity of the invention.
 XX
 SQ Sequence 1164 BP; 403 A; 203 C; 218 G; 340 T; 0 U; 0 Other;

Query Match 67.1%; Score 634.2; DB 11; Length 1164;
 Best Local Similarity 80.3%; Pred. No. 4.6e-167;
 Matches 757; Conservative 0; Mismatches 183; Indels 3; Gaps 1;

QY 6 GGTGATGCTTGTATGCTGTGATCGTAAATAGGTGGCTCATGTCGACCAACTTCAAC 65
 |||||
 DB 1 GATGAAGTCGATGCTTGTGATCGTAAATAGGTGGCTCATGTCGACCAACTTCAAC 60
 |||||
 QY 66 TTGTGCAATTAATACGATCACTTGTATGCTGGAATGCAACCATTAACAAATATGCAAC 125
 |||||
 DB 61 TTGTGCAATTAATACGATCACTTGTATGCTGGAATGCAACCATTAACAAATATGCAAC 120
 |||||
 QY 126 CTTTATGGAATCTCTTGTATCAACGGAAGATCCAAAATTAATGCTATGGCAATTC 185
 |||||
 DB 121 TTTTGTGGAATCTCTTGTATCAACGGAAGATCCAAAATTAATGCTATGGCAATTC 180
 |||||
 QY 186 AATGCTACTGGAATCAATTTCCAGCCCTTAAGTACTTATGTTGTTAACTCCAAAGTGCA 245
 |||||
 DB 181 AATGCTACTGGAATCAATTTCCAGCCCTTAAGTACTTATGTTGTTAACTCCAAAGTGCA 240
 |||||
 QY 246 CTTAAAAACCATTAACATATGCTGAGAGCAAAATTAATACGATGAGGCTATTCGA 305
 |||||
 DB 241 TAAABAAAACCATTAACATATGCTGAGAGCAAAATTAATACGATGAGGCTATTCGA 300
 |||||
 QY 306 TCCCTTCAATGSCAATAGTGTGTTACCAATATTTAATGATATTAACAAGCAACGAGC 365
 |||||
 DB 301 TCCCTTGTATACCAATAGTGTGTTACCAATATTTAATGATATTAACAAGTACTGAGC 360
 |||||
 QY 366 CACTGATGAGGAATACCTTGTGCAAGTCTATTCCTCGTGTGCAATGTCCATTA 425
 |||||
 DB 361 CCAAGATGTAGAGACTACTCTTGTGCCCCAAATCCCAATCTCGTGTAGTAAACATTA 420
 |||||

QY CTACATAGCTTATATCCGACCATGAGAAAAGAAAGCAAGTAAACTCAAGAAATCAAGT 485
DB CTATGATAGTCGATATCCACATCTTGGAATCAAAAGCGGAGTAAATCAAGAGTCAAGT 480
QY CCAATGGGAATCAAAATCTCAGCAGTGAATTTGAAAATCTCTGAGTTGATTCAT 545
DB TCAACTGGGAATCAAAATCTCAGCAGTGAATTTGAAAATCTCTGAGTTGATTCAT 540
QY CCCGTGAAAATCAAGCTTTTCTTCTAGTGTGAGTCAATTCGTTCAAGGAGC 605
DB CACTGAGAAAACCGAAGCCGAATTCCTAGTGTGAGTCAATTCGTTCAAGGAGC 600
QY GCGATTCAGTATAGAGAAACCAAGTCAAGTCAATTTATATAGATTCATTCCTGA 665
DB AAGATTCAGTATAGAGAAACCAAGTCAAGTCAATTTATATAGATTCATTCCTGA 660
QY TCCCAAGTATATATTTGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCAGAAATGC 725
DB TCCCAAGTATATATTTGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCAGAAATGC 720
QY CAGAAATGGGCTTTACCCAAACCACTTGAGTGTGATGCGCAAGTACCAAGTGCAT 785
DB CAGAAATGGGCTTTACCCAAACCACTTGAGTGTGATGCGCAAGTACCAAGTGCAT 780
QY AGTCTTGAAGTGTGATGATCAATCGATGATGCGCACTCTTAAAGTACGTTATGGAAC 845
DB AGTCTTGAAGTGTGATGATCAATCGATGATGCGCACTCTTAAAGTACGTTATGGAAC 840
QY CTGTGACAACTT---ACCAAAATGCGATGTTCTCTCAAGTAAATTTCTACTATTA 902
DB CTGTGACAACTT---ACCAAAATGCGATGTTCTCTCAAGTAAATTTCTACTATTA 900
QY TAAATTAATGCTTAATCTTGTGATCTAATTTGAAAGATTCGA 945
DB TAAATTAATGCTTAATCTTGTGATCTAATTTGAAAGATTCGA 943

RESULT 5
ADG76061
ID ADG76061 standard; DNA; 1378 BP.
AC ADG76061;
XX
DT 11-MAR-2004 (first entry)
DE American pokeweed antiviral protein (PAP) DNA SegID 1.
XX
KM gene; ds; pokeweed antiviral protein; PAP; HIV-1; anti-HIV; antiviral;
KM nucleoside analogue inhibitor; viral protease inhibitor; viral infection;
KM american pokeweed; retroviral.
XX
OS Phytolacca americana.
XX
PN MO2003106479-A2.
XX
PD 24-DEC-2003.
XX
PE 17-JUN-2003; 2003MO-US019141.
XX
PR 17-JUN-2002; 2002US-0389649P.
XX
PA (PARK-) PARKER HUGHES INST.
XX
PI Uckun FM;
XX
DR WPI; 2004-082156/08.
XX
PT P-PSDB; ADG76064.
XX
PT Novel modified pokeweed antiviral protein useful for inhibiting viral
PT replication, for inducing deprivation of viral RNA, or for treating
XX viral infection in subject.

PS Example 2; SEQ ID NO 1; 62bp; English.
XX
CC This invention relates to novel modified pokeweed antiviral proteins
CC (PAPs). Specifically, it refers to modifications relative to wild-type
CC PAP that confer increased activity towards viral RNA, particularly
CC retroviral RNA such as HIV-1 and drug resistant HIV-1. Furthermore,
CC modified PAP also exhibits decreased activity towards ribosomal RNA
CC relative to wild-type PAP. The present invention describes a molecular
CC model of PAP-HIV RNA interactions that have been used for the rational
CC redesign of PAP mutants with potent anti-HIV activity, where
CC modifications have been introduced in regions other than the active site.
CC Accordingly, these mutants represent antiviral agents that can work as
CC nucleoside analogue inhibitors of reverse transcriptase, as well as viral
CC protease inhibitors that can be used for treating viral infections. As
CC such, they are useful for inhibiting viral replication and for
CC depleting viral RNA. This polynucleotide sequence is the DNA encoding
CC the wild type american pokeweed antiviral protein (PAP) of the invention.
XX
SQ Sequence 1378 BP; 487 A; 234 C; 268 G; 389 T; 0 U; 0 Other;

Query Match 66.9%; Score 632.4; DB 12; Length 1378;
Best Local Similarity 80.0%; Pred. No. 1.6e-166;
Matches 757; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

QY 3 GAAGTATGCTTGTAGTGTGAGCACTTAATAGCGGTGCTATTGCTGACCAACTTC 62
DB GAAGTATGCTTGTAGTGTGAGCACTTAATAGCGGTGCTATTGCTGACCAACTTC 279
QY 63 AACTTGTCCATTAATACATCACTTGTGATGCGCAAAATCACTTAATTAATATGC 122
DB AACTTGTCCATTAATACATCACTTGTGATGCGCAAAATCACTTAATTAATATGC 339
QY 280 AACTTGTCCATTAATACATCACTTGTGATGCGCAAAATCACTTAATTAATATGC 182
DB AACTTGTCCATTAATACATCACTTGTGATGCGCAAAATCACTTAATTAATATGC 399
QY 123 CACCTTATGGAATCTCTGTATCAAGGAAATCCAAATTAATGCTATGCGAT 182
DB CACCTTATGGAATCTCTGTATCAAGGAAATCCAAATTAATGCTATGCGAT 399
QY 340 CACTTTCGAAAGATCTCTGTATGAGGAAAGATCCAAATTAATGCTATGCGAT 182
DB CACTTTCGAAAGATCTCTGTATGAGGAAAGATCCAAATTAATGCTATGCGAT 399
QY 183 ACCAATGCTACGATGATTAATTCGACCCCTAAGTCTTAATGCTATGCTATGCGAT 242
DB ACCAATGCTACGATGATTAATTCGACCCCTAAGTCTTAATGCTATGCTATGCGAT 459
QY 400 ACCAATGCTACGATGATTAATTCGACCCCTAAGTCTTAATGCTATGCTATGCGAT 459
DB ACCAATGCTACGATGATTAATTCGACCCCTAAGTCTTAATGCTATGCTATGCGAT 519
QY 243 AAACCTTAATTAATACATCACTTGTGATGCGCAAAATCACTTAATTAATATGC 302
DB AAACCTTAATTAATACATCACTTGTGATGCGCAAAATCACTTAATTAATATGC 519
QY 460 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 519
DB AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 519
QY 303 TGAATCCTTAATGAGCAATAGTGTGTTACCAATTAATTAATTAATTAATTAAT 362
DB TGAATCCTTAATGAGCAATAGTGTGTTACCAATTAATTAATTAATTAATTAAT 579
QY 520 TGAATCCTTAATGAGCAATAGTGTGTTACCAATTAATTAATTAATTAATTAAT 579
DB TGAATCCTTAATGAGCAATAGTGTGTTACCAATTAATTAATTAATTAATTAAT 579
QY 363 AGCAGTATGAGGAGATCTCTTGTGATGCGCAATGCTATGCTATGCTATGCGAT 422
DB AGCAGTATGAGGAGATCTCTTGTGATGCGCAATGCTATGCTATGCTATGCGAT 639
QY 580 AGCAGTATGAGGAGATCTCTTGTGATGCGCAATGCTATGCTATGCTATGCGAT 639
DB AGCAGTATGAGGAGATCTCTTGTGATGCGCAATGCTATGCTATGCTATGCGAT 639
QY 423 TAACTCAATAGCTTATATCCGACCATGAGAAAAGCAAGTAACTCAAGAAATCA 482
DB TAACTCAATAGCTTATATCCGACCATGAGAAAAGCAAGTAACTCAAGAAATCA 699
QY 640 AAATCTTGAATAGTCAATCAATCAATGGAATCAAAAGGAGTAAATCAAGAAATCA 699
DB AAATCTTGAATAGTCAATCAATCAATGGAATCAAAAGGAGTAAATCAAGAAATCA 699
QY 483 AGTCCAAATGGGAATCAATTAATCTCAGCAGTGAATTTGAAAATCTCTGAGTTGATTC 542
DB AGTCCAAATGGGAATCAATTAATCTCAGCAGTGAATTTGAAAATCTCTGAGTTGATTC 759
QY 700 GGTCCAACTGGGAATCAATTAATCTCAGCAGTGAATTTGAAAATCTCTGAGTTGATTC 759
DB GGTCCAACTGGGAATCAATTAATCTCAGCAGTGAATTTGAAAATCTCTGAGTTGATTC 759
QY 543 ATTCCGTGAAAATCAAGGCTTTTCTTCTAGTGTGAGTCAATTCGTTCAAGGAGC 602
DB ATTCCGTGAAAATCAAGGCTTTTCTTCTAGTGTGAGTCAATTCGTTCAAGGAGC 819
QY 760 ATTCCGTGAAAATCAAGGCTTTTCTTCTAGTGTGAGTCAATTCGTTCAAGGAGC 819
DB ATTCCGTGAAAATCAAGGCTTTTCTTCTAGTGTGAGTCAATTCGTTCAAGGAGC 819
QY 603 AGCGAATTCAGTATAGAGAAACCAAGTCAAGTCAATTTATATAGAGATTCATCC 662
DB AGCGAATTCAGTATAGAGAAACCAAGTCAAGTCAATTTATATAGAGATTCATCC 879
QY 820 AGCAAGTTCAGTATAGAGAAACCAAGTCAAGTCAATTTATATAGAGATTCATCC 879
DB AGCAAGTTCAGTATAGAGAAACCAAGTCAAGTCAATTTATATAGAGATTCATCC 879
QY 663 TGAATCCCAAGTATTAATTTGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCAGAA 722
DB TGAATCCCAAGTATTAATTTGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCAGAA 939
QY 880 TAAATCCCAAGTATTAATTTGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCAGAA 939
DB TAAATCCCAAGTATTAATTTGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCAGAA 939
QY 723 TGCCAAAGATGGGGCTTACCCAAACCACTTGAAGTATGAGATGCCAAAGTACCAAGT 782

```
DB 940 TGCAGAAATGAGATTACCCAAACCTCTGAGCTGAGATGCCAGTGTGCCAAGTG 999
QY 783 GATAGTTCTTAGATGATGAATCAGTGCAGCTCCTTAAGTACCTTAATG 842
DB 1000 GATAGTGTGAGATGATGAATCAGTGCAGCTCCTTAAGTACCTTAATG 1059
QY 843 AACCTGTGACAACTT---ACCAAAATGCGATGTTCTCAAGTTAAATTTCTACTTA 899
DB 1060 GAGCTGTGACAACTTATTAACCAAAATGCGATGTTCTCAAGTTAAATTTCTACTTA 1119
QY 900 TTTATTAATTAATGCTTAATCTTGTGATCTTAATTTGAAGATTCTAA 945
DB 1120 TTTAATTAATGCTTAATCTTGTGATCTTAATTTGAAGATTCTGA 1165

RESULT 6
AA245197
ID AA245197 standard; DNA; 1379 BP.
AC AA245197;
XX
DT 29-FEB-2000 (first entry)
DE Wild-type pokeweed antiviral protein (PAP) nucleotide sequence.
XX
KM Pokeweed antiviral protein; PAP; PAP II; antifungal; transgenic plant;
KM ribosome inhibiting protein; RIP; cereal crop; viral resistance; PVX;
KM potato virus X; cucumber mosaic virus; CMV; SS;
KM tomato yellow leaf curl virus.
XX
OS Phytolacca americana.
XX
FH Key Location/Qualifiers
FT CDS 225..1166
FT FT /*tag= a
FT FT /product= "PAP"
FT FT /note= "Pokeweed antiviral protein"

MO960843-AI.
XX
PD 02-DEC-1999.
XX
PF 21-MAY-1999; 99MO-US01301.
XX
PR 22-MAY-1998; 98US-0086374P.
XX
PA (RUTP ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI Turner NE, Wang P;
XX
DR MPI; 2000-062555/05.
XX
DR P-PSDB; AAYS8025.
XX
PT New antiviral DNA useful for generating transgenic plants resistant to
PT viruses and/or fungi.
XX
PS Example; Page 4-5; 43pp; English.
XX
XX This is the Pokeweed antiviral protein (PAP) nucleotide sequence. PAP is
CC a type I ribosome-inhibiting protein (RIP) found in the cell walls of
CC Phytolacca americana (pokeweed). It is a single polypeptide chain that
CC catalytically removes a specific adenine residue from a highly conserved
CC stem-loop structure in the 28S rRNA of eukaryotic ribosomes. The pokeweed
CC antiviral protein II (PAP II) protein confers antiviral and or antifungal
CC activities to plants. A DNA molecule encoding a PAP II protein with an
CC intact catalytic active site amino acid residue (E172) is useful for
CC generating transgenic plants. PAP II DNA is useful for generating a
CC transgenic plants (especially cereal crops) through transforming a
CC prooplast or introducing the DNA directly into a plant part prior to
CC regeneration. Cells and seeds which exhibit anti-viral and/or anti-fungal
CC activity thus have increased resistance to viruses and/or fungi. Viruses
CC include potato virus X (PVX), cucumber mosaic virus (CMV), and tomato
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CC yellow leaf curl virus, and fungi include Pythium, Phytophthora,
CC Sclerotinia and Aspergillus. PAP II proteins also confer resistance to
CC other plants pests including insects, bacteria and nematodes. PAP II DNA
CC is also useful for identifying a PAP II protein having reduced
CC cytotoxicity. PAP II has a reduced cytotoxicity compared to PAP, so
CC unlike PAP transgenic plants which are stunted and sterile, PAP II
CC transgenic plants have a normal and fertile phenotype
XX
SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
Query Match 66.9%; Score 632.4; DB 3; Length 1379;
Best Local Similarity 80.0%; Pred. No. 1,6e-166;
Matches 757; Conservative 0; Mismatches 186; Indels 3; Gaps 1;
QY 3 GAAGTGAATGCTTGTATGTTGGTGAAGTTAATAGGAGGCTGATGTCGACCAATTC 62
DB 221 GAAAGATGAATGCTGATGTTGGTGAAGTTAATAGGAGGCTGATGTCGACCAATTC 280
QY 63 AACTGTGCGATTAATAGATGATGATGATGATGATGATGATGATGATGATGATGAT 122
DB 281 AACTGTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 340
QY 123 GACCTTTAATGAAATCTTCTGATATCAAGGAAAGTCCAAAATTAATGCTATGCGAT 182
DB 341 CACTTTTCGAATGAAATCTTCTGATATCAAGGAAAGTCCAAAATTAATGCTATGCGAT 400
QY 183 ACCAATGCTACCTGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATG 242
DB 401 ACCAATGCTACCTGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATG 460
QY 243 AAACCTTAAACCATTAATCAATTAATGATGATGATGATGATGATGATGATGATGATGATG 302
DB 461 AAATTAATAAAACCATTAATCAATTAATGATGATGATGATGATGATGATGATGATGATGATG 520
QY 303 TGATCCCTTCAATGCGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 362
DB 521 TGATCCCTTCAATGCGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 580
QY 363 AGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 422
DB 581 AGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 640
QY 423 TAACTCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 482
DB 641 AAACCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 700
QY 483 AGTCCAAATGCGATTAATCAATTAATGATGATGATGATGATGATGATGATGATGATGATG 542
DB 701 GGTCCAAATGCGATTAATCAATTAATGATGATGATGATGATGATGATGATGATGATGATG 760
QY 543 ATCCCTGTAATAAATGAGGCTTTTCTGATGATGATGATGATGATGATGATGATGATGATG 602
DB 761 ATCCCTGTAATAAATGAGGCTTTTCTGATGATGATGATGATGATGATGATGATGATGATG 820
QY 603 AGGCGATTAATCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 662
DB 821 AGGCGATTAATCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 880
QY 663 TGATCCCAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 722
DB 881 TGATCCCAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 940
QY 723 TGCAGAAATGAGGCTTTTACCCAAACCTGATGATGATGATGATGATGATGATGATGATGATG 782
DB 941 TGCAGAAATGAGGCTTTTACCCAAACCTGATGATGATGATGATGATGATGATGATGATGATG 1000
QY 783 GATAGTTCTTAGATGATGAATCAGTGCAGCTCCTTAAGTACCTTAATG 842
DB 1001 GATAGTGTGAGATGATGAATCAGTGCAGCTCCTTAAGTACCTTAATG 1060
QY 843 AACCTGTGACAACTT---ACCAAAATGCGATGTTCTCAAGTTAAATTTCTACTTA 899
DB 1061 GAGCTGTGACAACTTATTAACCAAAATGCGATGTTCTCAAGTTAAATTTCTACTTA 1120
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CC spectrum of plant pests e.g. viruses and fungi. This polynucleotide
CC sequence represents the DNA encoding the wild-type pokeweed antiviral
CC protein of the invention.

Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Query Match	66.9%	Score 632.4;	DB 10;	Length 1379;
Best Local Similarity	80.0%;	Pred. No. 1.6e-166;		
Matches 757; Conservative	0;	Mismatches 186;	Indels 3;	Gaps 1;

QY	3	GAAGTGAATGCTTGATAGTTGGTGTGAACCTTTAATACCGTGGCTCATTTGCTGACCAACTTC	62
Db	221	GAATATGAAGTCGATGCTTGTGTGTGACAAATATATATATGCTCATTTCTTGACCAACTTC	280
QY	63	AACTGTGCCATAAATATACATCACCTTGTATGCTGGAATATGCCACCATTTACAAATATGC	122
Db	281	AACTTGGGCTGTGAATATCAATCATCATATGTTGGAAGTACACCAATTAGAAATATAGC	340
QY	123	CACCTTTATGGAATCTCTTCTGTATCAAGCCGAAGATCCAAACTTAAATGTATATGCAT	182
Db	341	CACCTTCTGTATGATCTTCTGTAAAGACGGAAGATCCAGTTTAAATGTATATGAT	400
QY	183	ACCAATGCTACCTGTATCTAATTTGCAACCCCTAAGATCTTATGTGTTAAGTCCAAAGTGC	242
Db	401	ACCAATGTGCCCCAATACAAATACAAATCCAAAGTACGTGTGGTTGAGCTCCAAAGTTC	460
QY	243	AAACTTAAAAACATTAACATTAATGCTGAGAGGAATTAATTAATCTGATGCGTATATTC	302
Db	461	AAATTAATAAAAAACATCACACTTAATGCTGAGAGGAACAATTTGATGTGATGGGTTATTC	520
QY	303	TGATTCCTTCAATGGCAATTAAGTGTCTTACATATATTTAATGATATTAACAAGACCGA	362
Db	521	TGATTCCTTGAACAACAAATTAATGTCTTACCATATCTTATATGATATCTCAGATACGA	580
QY	363	ACGACATGATGNGAGAAATACCTTTGTCACAGTTCTATGTTCTGAGTGTGCAATGCCAT	422
Db	581	ACGCCAAGATGTAGAGACTACTCTTTGGCCAAATCCAAATTCCTGTGTAGTAAAAACAT	640
QY	423	TAACTACAAATAGCTTATATTCGACCATGGAAGAAAGACAGAAATTAATCAAGAAATCA	482
Db	641	AAACTTTGATATGTGATATTCACAACATTTGGAATCAAAACGGGAGTAAATCAAGAAATCA	700
QY	483	AGTCCAAATGGGAATTCAAATATCTCAGAGTGAATTG3AAAATCTCTGAGTTGATTC	542
Db	701	GGTCCAACTGGGAATTCAAATATCTCAGAGTGAATTTG3AAAAGATTTCTGAGTGTATTC	760
QY	543	ATTCCTGTAAAACTGAGGCTTTTTTCTACTGTTACCAATCCAAATGCTTTCAGAGGC	602
Db	761	ATTCATGAGAAAACCGAAGCCGAATTCCTATTTGTATCCAAATCAAAATGATATCGAAGGC	820
QY	603	AGCCGATTCAGATCATAGAGAACCAAGTCAAGACTAATTTTATATAGCATTTTACCC	662
Db	821	AGCAAGATTCAGATCATAGAGAAATCAGGTGAAAATCTAATTTTAAACAGACATTCACCC	880
QY	663	TGATCCCAAGTAATTAATTTTGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACAA	722
Db	881	TAAATCCCAAGTAATTAATTTTGCAAGAGACATGGGGTAAGATTTCAACAGCAATTCAGA	940
QY	723	TGCCAAGAAATGGGGCTTTAACCCAAACCACTTGAAGTATGATGTCGAAAGGTATCCAAATG	782
Db	941	TGCCAAGAAATGAGATTTTAACCCAAACCTCTGAGCTATGTGATGTCAGATGGGCCAAATG	1000
QY	783	GATAGTTCTTATAGATGATGAATCAATCTGTGATGTGGCACTCCTTAATAGTACGTAATG	842
Db	1001	GATAGTTCTTATAGATGATGAATCAATCAACCTGATATGACATCTTAAACTATGTTGGTGG	1066
QY	843	AACTGTGACAACTT--ACCAAAATGCAATGTTCTCTCAAGTTATTAATTTTACTTAA	899
Db	1061	GAGCTGTGACAACTTATTAACCAAAATGCAATGTTCTCTCAACTTAATATATGTTACTTAA	1120
QY	900	TTATATATATATATATCTTATCTTGTGATCTATTTGAAGAATTTCTAA	945
Db	1121	TTATATATATATATATCTTGTGATCTATTTGAAGAATTTCTAA	1166

RESULT 10

AAQ56672
ID AAQ56672 standard; cDNA; 1195 BP

AC AAQ56672;

DT 16-OCT-2003 (revised)

DT 04-SEP-1994 (first entry)

DB Sequence of Phytolacca anti

KW Antiviral protein; PAP; virus-resistance; transgenic

Phytolacca americana; L.

Key	Location/Qualifiers
22	
FH	

CBS	33 : 2/4
F1	/*tag= a
FT	

PN EP585554-A1.

PD 09-MAR-1994

30-JUN-1993; 93EP-00110445.

PR 16-AUG-1992; 92KR-00014895.

PA (JINR-) JIN RO LTD.

PI Kim M, Lee K, Na B, Jeong H, Choi K, Moon Y, Jeon H;

DR WPI; 1994-076002/10.

XX
XX
E-1000, 11/10/10

transgenic virus-resistant plants and for producing the antiviral agent.

PS Disclosure; Fig 1; 15pp; English.

CC To isolate PAP gene, total cellular mRNA was purified from leaves of

CC The PAP gene was selected by immunoscreening employing anti-PAP antibody

sequence of the PAP genomes was determined. (Updated on 25-MAR-2003 to

XX

SQ Sequence 1195 BP; 420 A; 201 C; 230 G; 344 T; 0 U; 0 Other;

Query Match	66.8%;	Score 630.8;	DB 2;	Length 1195;
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	Matches	756;	Conservative	0;	Mismatches	187;	Indels	3;	Gaps	1;
Qy	3	GAAGTGAATGCTTGTAGTGTGTGAGCTTAATAGCGTGGCTCATTTGCTGCACCAATCTC	62							
Db	29	GAAGTGAATGCGATGCTTGTGTGTGTGCAAAATATCATATGCTCATTTTGCACCAACTTC	88							
Qy	63	AACCTTGTGCCATAATACGATCACCTTTGATGCTGGAATGCCACCTTAACAATATGC	122							
Db	89	AACCTGGGCTGTGAATCAATCATCTCAATGTTGGAAGTACACCACTTACCAATATGCG	148							
Qy	123	CACCTTATGGAATCTCTTGSTATTCAGCGAAAGATCCAAAATCTAAAATGCTATGGCAT	182							
Db	149	CACCTTTCTGAATGATCTTCTGTAATGAGCGAAAGATCCAGTTTAAAATCTATGGAAAT	208							
Qy	183	ACCATGTCTACTGATCTAATTCGACCCCTAAGTACTTATTTGTTAAGTCCAAAGTGC	242							
Db	209	ACCATGTGCTGCCAATACAAATACAAATCCAAAGTACGTGTGGTTGAGCTCCAAAGGTTTC	268							
Qy	243	AAACCTAAAAACCTTACCTAATGCTGAGACGAATTACTTATACGTGATGGGCTATTC	302							

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Db 269 AAAAAAAAAACATCACTAAATGCTGAGACGAAACAATTTGTATGTATGCGTTATTC 328
QY 303 TGATCCCTTCATATGSCAATATAGTCTGTACCATATATTATATGATATTAACAACCGA 362
Db 329 TGATCCCTTCATATGSCAATATAGTCTGTACCATATATTATGATATTAACAACCGA 388
QY 363 AGCGACTGATGTGAGAAATCTCTTGTCTCAAGTTCTAGTTCTGTGTGTCATATGTCAT 422
Db 389 ACCGCAAGATGTAGAGCTACTCTTGTGCGCAAAATGCAAAATTCGTGTGATAAAAAT 448
QY 423 TAACTCAATATGCTTATATCCGACATGAGAAAAAGAAAGAAAGTAACTCAAGAAATCA 482
Db 449 AAATCTTGATATGTCATATCAATTCATTTGATCAAAAGCGAGATAAATCAAGAAATCA 508
QY 483 AGTCAATGTGGAATTCATTAATCTCAGCAGTGAATTTGAAATCTCTGAGTTGATTC 542
Db 509 AGTCAATGTGGAATTCATTAATCTCAGCAGTGAATTTGAAATCTCTGAGTTGATTC 568
QY 543 ATTCCCTGTAAAACTGAGGCTTTTCTTCTATCTGTATGCAATCCAAATGCTTCAAGGC 602
Db 569 ATTCACGTGAGAAAAACGAAACCGAAATTCCTATTTGTATGCAATCAATGCTATCAGAGC 628
QY 603 AGCGCAATTCATATGATAGAGAAACGAGTCAAGTCAATTTTAAATAGACATTTTACC 662
Db 629 AGCAAGATTCATATGATAGAGAAACGAGTCAAGTCAATTTTAAATAGACATTTTACC 688
QY 663 TGAATCCCAAGTATTAATTTGAGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACA 722
Db 689 TATCCCAAGTATTAATTTGAGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACA 748
QY 723 TGCAGAAATGGGGCTTTTACCCAAACCACTTGAAGTATGATGACCAAGTACCAAGT 782
Db 749 TGCAGAAATGGGGCTTTTACCCAAACCTCTGAGATGATGATGACCAAGTACCAAGT 808
QY 783 GATAGTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 842
Db 809 GATAGTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 868
QY 843 AACCTGTCAACAATCT--ACCAAAATGCAATGTTCTCTCAAGTATTAATTTCTACTTA 899
Db 869 GAGCTGTCAACAATCTTAATTAACCAAAATGCAATGTTCTCTCAAGTATTAATTTCTACTTA 928
QY 900 TTTATATTTATATGATCTTATTTGTTGATCTTATTTGAAAGATTTCTAA 945
Db 929 TTTATATTTATATGATCTTATTTGTTGATCTTATTTGAAAGATTTCTGA 974

RESULT 11
AAC87929
ID AAC87929 standard; DNA; 1379 BP.
XX
AC AAC87929;
XX
DT 06-MAR-2001 (first entry)
XX
DE P. americana pokeweed antiviral protein encoding DNA SEQ ID NO:1.
XX
KW Phytoactin americana; pokeweed; pokeweed antiviral protein; PAP; cancer;
KW bioherbicide; fusion protein; immunomodulator; mutant; cytotoxic;
KW anti-HIV; human immunodeficiency virus; AIDS; leukemia; lymphoma;
KW brain tumour; neuroblastoma; soft tissue sarcoma; osteosarcoma; ss.
XX
OS Phytoactin americana.
XX
FH Key Location/Qualifiers
FT CDS 225..1166
FT /tag= a
FT /product= "pokeweed antiviral protein (PAP)"
XX
PN US6146628-A.
XX
PD 14-NOV-2000.
XX
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PF 11-JUL-1995; 95US-00501253.
XX
PR 11-JUL-1995; 95US-00501253.
XX
PA (MINU) UNIV MINNESOTA & RUTGERS.
PA (UINR-) UNIV STATE NEW JERSEY.
XX
PI Uckun FM, Turner NE;
XX
DR WPI; 2001-040422/05.
XX
DR P-PSDB; AAB36500.
XX
PT Immunocytogenetics useful for treating cancer and acquired immunodeficiency
PT syndrome, comprises mutant pokeweed anti-viral protein and a targeting
XX
XX
PS Disclosure; Col 47-50; 32pp; English.
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The present invention describes a fusion protein or an immunocytogenetics (1), comprising mutant Pokeweed Anti-viral Protein (PAP) having an amino acid substitution at residue 75, 97 or 176 of native PAP and a targeting moiety that binds a cell surface receptor. (1) can have cytotoxic and anti-HIV activities, and is an inhibitor of cellular RNA or protein synthesis. (1) is useful for treating AIDS and cancers including leukemia, lymphoma, a brain tumour, neuroblastoma, osteosarcoma, soft tissue sarcoma, breast, prostate, ovarian, testicular, melanoma, lung, or colon cancer. Immunocytogenetics prepared using PAP mutants exhibit an improved therapeutic index over immunocytogenetics containing either wild-type PAP or variant PAP. The present sequence encodes the wild-type PAP, which is given in the exemplification of the present invention

Sequence 1379 BP; 488 A; 234 C; 268 G; 389 T; 0 U; 0 Other;

Query Match 66.8%; Score 630.8; DB 4; Length 1379;
Best Local Similarity 79.9%; Pred. No. 4,4e-166;
Matches 756; Conservative 0; Mismatches 187; Indels 3; Gaps 1;

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QY 3 GAGGTGATGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 62
Db 221 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 280
QY 63 AACTGTGCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 122
Db 281 AACTGTGCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 340
QY 123 CACTTTTCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 182
Db 341 CACTTTTCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 400
QY 183 ACCAATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 242
Db 401 ACCAATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 460
QY 243 AAATCTTAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 302
Db 461 AAATCTTAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 520
QY 303 TGATCCCTTCATATGSCAATATAGTCTGTACCATATATTATGATATTAACAACCGA 362
Db 521 TGATCCCTTCATATGSCAATATAGTCTGTACCATATATTATGATATTAACAACCGA 580
QY 363 AGCGACTGATGTGAGAAATCTCTTGTCTCAAGTTCTAGTTCTGTGTGTCATATGTCAT 422
Db 581 AGCGCAAGATGTAGAGACTACTCTTGTGCGCAAAATGCAAAATTCGTGTAGTAAACAT 640
QY 423 TAACTCAATATGCTTATATCCGACATGAGAAAAAGAAAGAAAGTAACTCAAGAAATCA 482
Db 641 AAATCTTGATATGTCATATCAATTCATTTGATCAAAAGCGAGATAAATCAAGAAATCA 700
QY 483 AGTCAATGTGGAATTCATTAATCTCAGCAGTGAATTTGAAATCTCTGAGTTGATTC 542
Db 701 AGTCAATGTGGAATTCATTAATCTCAGCAGTGAATTTGAAATCTCTGAGTTGATTC 760
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QY 543 ATTCCCTGTAAGAACTGAGGCTTTTCTACTAGTACCCATCCAAATGGTTTCAGAGGC 602
 DB 761 ATTCACTGAGAAACCCAGCCGAATTCCTATTGTGACCATACAAATGGTATCAGAGGC 820
 QY 603 AGCGCGATTCAAGTACATAGAGAAACAAGTCAAGACTTAATTTAATAGAGATTCTACCC 662
 DB 821 AGCGAGATTCAAGTACATAGAGAAACAAGTCAAGACTTAATTTAATAGAGATTCTACCC 880
 QY 663 TGATCCCAAGTAATTAATTTGGAGGAGAAAGTGGGCGAAATCTCTAGGCAATTCACAA 722
 DB 881 TAATCCCAAGTAATTAATTTGGAGGAGAAAGTGGGCGAAATCTCTAGGCAATTCACAA 940
 QY 723 TGCCCAAGATGGGCGCTTACCCAAACCACTGAGTATGAGTATCCAAAGTACCAATG 782
 DB 941 TGCCCAAGATGGGCGCTTACCCAAACCTGAGTATGAGTATCCAAAGTATCCAAATG 1000
 QY 783 GATAGTTCTTAAAGTATGATGAATCAATCGTATGAGTATGAGTATGAGTATGAGTATG 842
 DB 1001 GATAGTTCTTAAAGTATGATGAATCAATCGTATGAGTATGAGTATGAGTATGAGTATG 1060
 QY 843 AACCTGTCAGCAACTT--ACCAAAATGGCAATGTCCTCAAGTATTAATTTCTACTTA 899
 DB 1061 GAGCTGTCAGCAACTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1120
 QY 900 TTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 945
 DB 1121 TTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1166

RESULT 12

AAQ81457
 ID AAQ81457 standard; cDNA; 1195 BP.

AC AAQ81457;

XX 16-OCT-2003 (revised)
 DT 25-AUG-1995 (first entry)

XX Phytoleuca antiviral protein (PAP) cDNA.

XX Antiviral protein; vector pMJ12; KCM 10037; PAP; BB.

XX Phytoleuca americana; L.

XX AU9350642-A.

XX 19-JAN-1995.

XX 11-NOV-1993; 93AU-00050642.

XX 02-JUL-1993; 93KR-00012360.

XX (JINR-) JIN RO LTD.

XX Lee K, Choi K, Jeon H, Kim M, Moon Y;

XX WPI; 1995-067518/10.

PT Recombinant vector for producing Phytoleuca anti-viral protein - and
 PT transformed E. coli useful for making immunconjugates for treatment of
 PT AIDS.

XX Claim 1; Fig 1; 27pp; English.

CC Total cellular mRNA from leaves of *P. americana* was used to produce a
 CC cDNA library and this screened with anti-PAP antibody raised in rabbits
 CC against purified PAP. Inserts were isolated from 2 clones and sequenced
 CC to identify a 1195 ORF (AAQ81457) that encodes a 313 AA PAP including a
 CC 22 AA signal peptide. The mature PAP gene was subjected to PCR
 CC amplification using primers AAQ81458 and AAQ81459. The amplification
 CC product was cut with Hind III and inserted into the commercial FLAG (RTM)
 CC vector cut with the same enzyme to form pMJ12. pMJ12 is deposited with
 CC the Korean Collection of Culture and Microorganism (KCCM), an

CC International Depository Authority, on June 30 1993, ad deposition No.
 CC KCM 10037, and claimed. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 1195 BP; 420 A; 203 C; 229 G; 343 T; 0 U; 0 Other;

XX Query Match 66.6%; Score 629.2; DB 2; Length 1195;

XX Best Local Similarity 79.8%; Pred. No. 1.2e-165;

XX Matches 755; Conservative 0; Mismatches 188; Indels 3; Gaps 1;

QY 3 GAGGTGATGCTTGTATGTTGTGTGACGTTAATAGCTGCTCATCTGCACTTC 62
 DB 29 GAGGTGATGCTTGTATGTTGTGTGACGTTAATAGCTGCTCATCTGCACTTC 88
 QY 63 AACTGTGCAATTAATTCAGTACCTTGTATGAGGAAATCCAACTTAATATATG 122
 DB 89 AACTGTGCAATTAATTCAGTACCTTGTATGAGGAAATCCAACTTAATATATG 148
 QY 123 CACCTTATGAAATCTTGTATGATCAAGGAAATCCAACTTAATATATG 182
 DB 149 CACCTTATGAAATCTTGTATGATCAAGGAAATCCAACTTAATATATG 208
 QY 183 ACCAATGCTACCTGATCTAATTCAGCCCTTAAGTATTTGTTAAGCTCCAGTGC 242
 DB 209 ACCAATGCTACCTGATCTAATTCAGCCCTTAAGTATTTGTTAAGCTCCAGTGC 268
 QY 243 AAACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 302
 DB 269 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 328
 QY 303 TGATCCCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 362
 DB 329 TGATCCCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 388
 QY 363 AGCGAATGATGAGATATCTTGTCTCAAGTTCTAGTTCTGTGTGATGTCAT 422
 DB 389 AGCGAATGATGAGATATCTTGTCTCAAGTTCTAGTTCTGTGTGATGTCAT 448
 QY 423 TAACTCAATGATGATATCCGACATGAGAAAGAAAGAAAGTAACTCAAGAAATCA 482
 DB 449 AAATCTTGAATGATGATATCAATGATGAGATCAAGGAGTAAATCAAGAAATCA 508
 QY 483 AGTCAATGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 542
 DB 509 AGTCAATGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 568
 QY 543 ATTCCCTGTAAGAACTGAGGCTTTTCTACTGTGATGATCAATGATTCAGAGGC 602
 DB 569 ATTCACTGAGAAACCGAAGCCGAATTCCTATTGTATGATCAATGATTCAGAGGC 628
 QY 603 AGCGGATTCAGTATGATGAGAAACCAAGTCAAGTCAATTAATTAATTAATTAATTA 662
 DB 629 AGCGGATTCAGTATGATGAGAAACCGAATTCCTATTGTATGATCAATGATTCAGAGGC 688
 QY 663 TGATCCCAAGTAATTAATTTGAGGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACAA 722
 DB 689 TAATCCCAAGTAATTAATTTGAGGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACAA 748
 QY 723 TGCCCAAGATGGGCGCTTACCCAAACCACTTGAAGTATGATGATGATGATGATGATG 782
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 QY 783 GATAGTTCTTAAAGTATGATGAATCAATGATGATGATGATGATGATGATGATGATG 842
 DB 809 GATAGTTCTTAAAGTATGATGAATCAATGATGATGATGATGATGATGATGATGATG 868
 QY 843 AACCTGTCAGCAACTT--ACCAAAATGGCAATGTCCTCAAGTATTAATTTCTACTTA 899
 DB 869 GAGCTGTCAGCAACTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 928
 QY 900 TTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 945
 DB 929 TTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 974

PI Kaniewski WK, Tumer NB, Lodge JK;
 XX WPI; 2000-126326/11.
 XX
 XX Production of transgenic potato plants or tubers expressing pokeweed
 PT antiviral protein which are resistant to potato virus X or Y.
 XX
 XX Claim 7; Fig 5; 30pp; English.
 XX
 CC This is the coding sequence for a variant spring leaf form of the
 CC pokeweed antiviral protein (PAP) which is used to generate transgenic
 CC potato plants. PAP is able to confer resistance to infection by potato
 CC virus X (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in
 CC the potato plant or tuber expressing PAP'. PAP' varies from PAP
 CC (AA59220) by mutations 120R and Y49H
 CC
 SQ Sequence 1379 BP; 489 A; 234 C; 269 G; 387 T; 0 U; 0 Other;
 Query Match 66.6%; Score 629.2; DB 3; Length 1379;
 Best Local Similarity 79.8%; Pred. No. 1.2e-165;
 Matches 755; Conservative 0; Mismatches 188; Indels 3; Gaps 1;
 QY 3 GAAGTGTATGCTTGTAGTGTGAGCTTAAATGCGTGTCTGTCGACCACTTC 62
 DB 221 GAAGATTAAGTCAATGCTGTGGAGCAATATGCTCAATTCCTGACCACTTC 280
 QY 63 AACTTGTGCAATTAATGATCACTTGTGAAATGCGCACTTAACAATATGC 122
 DB 281 AACTTGTGCTGTGATCAATCAATGTTGAAATGCGCACTTAACAATATGC 340
 QY 123 CACCTTTATGAAATCTCTGTATCAAGCAAAATGCAAAATGCAATATGTCAT 182
 DB 341 CACTTTGCAATGATCTTGTATGAAAGCAAAATGCAAAATGCAATATGTCAT 400
 QY 183 ACCAATGCTATGATCTTATGACCCCTTAATGCTTATGCTTAAAGTCCAGTGC 242
 DB 401 ACCAATGCTATGATCTTATGACCCCTTAATGCTTATGCTTAAAGTCCAGTGC 460
 QY 243 AAACCTTAATAACCTTATGATGAGCAAAATGCAAAATGCAAAATGCAATATG 302
 DB 461 AAATTAATAATAACCTTATGATGAGCAAAATGCAAAATGCAAAATGCAATATG 520
 QY 303 TGAATCCCTTCAATGCAATATGCTTATGCAATATGCAATATGCAATATGCA 362
 DB 521 TGAATCCCTTCAATGCAATATGCTTATGCAATATGCAATATGCAATATGCA 580
 QY 363 AGCGCATGATGAGCAATATGCTTATGCAATATGCAATATGCAATATGCAAT 422
 DB 581 AGCGCATGATGAGCAATATGCTTATGCAATATGCAATATGCAATATGCAAT 640
 QY 423 TAATCAATATGCTTATGCAATATGCAATATGCAATATGCAATATGCAATATG 482
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 QY 483 AGTCAATGAGCAATATGCAATATGCAATATGCAATATGCAATATGCAATATG 542
 DB 701 GGTCAATGAGCAATATGCAATATGCAATATGCAATATGCAATATGCAATATG 760
 QY 543 ATTCCCTGTAAATGAGGCTTTTGTATGCAATATGCAATATGCAATATGCA 602
 DB 761 ATTCACTGTAAATGAGGCTTTTGTATGCAATATGCAATATGCAATATGCA 820
 QY 603 AGGCGATTAAGTATGAGCAATATGCAATATGCAATATGCAATATGCAATATG 662
 DB 821 AGGCGATTAAGTATGAGCAATATGCAATATGCAATATGCAATATGCAATATG 880
 QY 663 TGAATCCCAATATGAGCAATATGCAATATGCAATATGCAATATGCAATATG 722
 DB 881 TAATCCCAATATGAGCAATATGCAATATGCAATATGCAATATGCAATATG 940
 QY 723 TGCAGAAATGAGGCTTTTATGCAATATGCAATATGCAATATGCAATATGCA 782
 DB 941 TGCAGAAATGAGGCTTTTATGCAATATGCAATATGCAATATGCAATATGCA 1000

QY 783 GATAGTCTTATGAGTGAATGAATCAATCGATGAGCACTCCTTAAGTACGTTAAG 842
 DB 1001 GATAGTCTTATGAGTGAATGAATCAATCGATGAGCACTCCTTAAGTACGTTAAG 1060
 QY 843 AACCTGTACAGCACTT---ACCAAAATGCAATGCTTCAAGTATTAATTTCTACTTA 899
 DB 1061 GAGCTGTACAGCACTTATTAACCAAAATGCAATGCTTCTCACTTAATTAATGCTACTTA 1120
 QY 900 TTATTAATTAATGCTTATGCTTGTGATCTTATTTGAAGATTTCA 945
 DB 1121 TTATTAATTAATGCTTATGCTTGTGATCTTATTTGAAGATTTCA 1166
 RESULT 15
 AAQ43967
 ID AAQ43967 standard; DNA; 2472 BP.
 XX
 AC AAQ43967;
 XX
 DT 09-NOV-1993 (first entry)
 XX
 DE Pokeweed antiviral protein.
 XX
 KW Pokeweed; ricin; protein synthesis inhibitor; cancer;
 KM polymerase chain reaction; PCR; ss.
 XX
 OS Phytolacca americana.
 XX
 FH Key
 FT CAAT_signal
 FT CAAT_signal
 FT CAAT_signal
 FT TATA_signal
 FT sig_peptide
 FT sig_peptide
 FT mat_peptide
 FT mat_peptide
 FT polyA_signal
 FT polyA_signal
 PN JP05137580-A.
 XX
 XX 01-JUN-1993.
 XX
 XX 20-NOV-1991; 91UP-00329672.
 XX
 XX 20-NOV-1991; 91UP-00329672.
 XX
 XX (NISB) JAPAN TOBACCO INC.
 XX
 DR WPI; 1993-211306/26.
 DR P-PSDB; AAR37345.
 XX
 PT New pokeweed antiviral protein (PAP) with similar activity to ricin -
 PT used to treat cancer and as an agricultural chemical.
 XX
 PS Claim 2; Page 11-13; 14pp; Japanese.
 XX
 CC PAP has a similar activity to ricin, i.e. inhibits protein synthesis. The
 CC protein may be obtained all year round by recombinant DNA techniques. PAP
 CC can be used partic. against cancer and as an agricultural chemical. Total
 CC mRNA, is extracted from the seeds, leaves and roots of pokeweed and used
 CC to prepare cDNA using PCR. The resultant cDNA is used to prepare two DNA
 CC fractions, which are introduced into a cloning vector EMBL3 and then into
 CC host B.coli PLK-17 (P2) to produce PAP
 XX
 SQ Sequence 2472 BP; 864 A; 375 C; 463 G; 770 T; 0 U; 0 Other;
 Query Match 66.1%; Score 624.2; DB 2; Length 2472;

Best Local Similarity 82.2%; Pred. No. 3.9e-164; Matches 780; Conservative 0; Mismatches 158; Indels 11; Gaps 5;

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QY 1 ATGAAGTATGCTGTAGTGTGTGACGCTTAATAGCCGTGCTCATTTGCTGCACCACT 60
Db 1014 ATGAAGTATGCTGTAGTGTGTGACGCTTAATAGCCGTGCTCATTTGCTGCACCACT 1073
QY 61 TCACCTTGTGCCATAAATAGATCACCTTTGATGCTGAAATGCCACATTAACTAATAT 120
Db 1074 TCACCTTGTGCCATAAATAGATCACCTTTGATGCTGAAATGCCACATTAACTAATAT 1133
QY 121 GCCACCTTATGGAATCTCTGCTAATCAAGCGAAGATCCAAACTTAAATGCTATGCG 180
Db 1134 GCCACCTTATGGAATCTCTGCTAATCAAGCGAAGATCCAAACTTAAATGCTATGCG 1193
QY 181 ATACCAATGCTACTGATTAATTCGACCCCTAAGTACTTAATTTGTTAAGTCCAAGT 240
Db 1194 ATACCAATGCTACTGATTAATTCGACCCCTAAGTACTTAATTTGTTAAGTCCAAGT 1253
QY 241 GCMAACTTAAAAACCTTACCTAATGCTGAGACGAATTAATTATACGTATGCGCTAT 300
Db 1254 TCMAAGTTTAAAAACCTTACCTAATGCTGAGACGAATTAATTATACGTATGCGCTAT 1313
QY 301 TCTGATCCCTTCAATGGCAATAGTGTGCTTACCATATATTTAATGATATTACA---AGC 357
Db 1314 GCTGACACTATATATGCG---AAGTGTCTTATCATATATTTAAGATATCTCAAAATACT 1370
QY 358 ACCGAACGCACTGATGTGAGAAATACTCTTTGCTCAAGTTCTGATTCGTTGCAATG 417
Db 1371 ACTGAACGAATGATGTGATGATCTCTTTGCTCAAGTTCTGATTCGTTGCAATG 1430
QY 418 TCCTATTAACTCAATAGCTTATATCCGACCATGAAAAAGAACAGAGTAATCTCAAG 477
Db 1431 AACATTAACTCAATAGCTTATATCCGACCATGAAAAAGAACAGAGTAATCTCAAG 1487
QY 478 AATCAAGTCCAAATTTGGGAATTCGAATATCTCAGAGGACATTTGGAATATCTCGAGTT 537
Db 1488 AATCAAGTCCAAATTTGGGAATTCGAATATCTCAGAGGACATTTGGAATATCTCGAGTT 1547
QY 538 GATTCATTCCTGTAAAACTGAGGCTTTTCTACTGTGAGCCATCCCAATGTTTCA 597
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QY 598 GAGGACGCGGATTCAGATACATAGAGAACCAAGTCAAGCTAATTTTAATAGAGCATTC 657
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Db 1668 TACCCGTGATCCCAAGTATTTAATTTGGAGAGAAATGGGGCAAAATCTTGAGGCAATT 1727
QY 718 CACAATGCCAAGAAATGGGCTTTTACCAACCACTTGAGTGTGATGTCGCAAAAGGTACC 777
Db 1728 CACAATGCCAAGAAATGGGCTTTTACCAACCACTTGAGTGTGATGTCGCAAAAGGTACC 1787
QY 778 AAGTGATAGTCTTAGAGTGAATGAATCAATCGTATGTGCACTCCTTAAGTACGTT 837
Db 1788 AAGTGATAGTCTTAGAGTGAATGAATCAATCGTATGTGCACTCCTTAAGTACGTT 1847
QY 838 AATGGAACCTGTCAAGCACTTAACCAATGCAATGCTTCTCAAGTATTAATTTCTACT 897
Db 1848 AATGGAACCTGTCAAGCACTTAACCAATGCAATGCTTCTCTC-ACCTAATATGCTACT 1906
QY 898 TATTATTAATTATATGCTAATCTTGCTGA-TCTATTTGAAGATTTCTAA 945
Db 1907 TATTATTAATTATATGCTAATCTTGCTGA-TCTATTTGAAGATTTCTAA 1955
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Job time : 571.609 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:25:18 ; Search time 4476.73 Seconds
(without alignments)
9876.364 Million cell updates/sec

Title: US-09-978-274A-1

Perfect score: 945

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Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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EST.*
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5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*
10: gb_est10.*
11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	87	9.2	993	2	BE035039
C 2	80.6	8.5	816	2	BE035038
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4	62.2	6.6	498	5	BQ588134
5	61.6	6.5	829	7	CN7882289
6	59	6.2	649	6	CA838757
7	59	6.2	649	6	CA838757
8	59	6.2	661	6	CA835330
9	59	6.2	671	6	CA835330
10	59	6.2	689	6	CA835330
11	57.4	6.1	639	6	CA835330
12	57.4	6.1	639	6	CA835330
13	55.4	5.9	1038	2	BE035546
14	52.4	5.5	405	8	T24255
15	50.8	5.4	639	2	BE037217
16	47.2	5.0	837	1	AM053634
17	46.6	4.9	489	1	BE130330
18	45.4	4.8	267	1	AA856221
19	44.6	4.7	1021	2	BE036639
20	44.4	4.7	701	9	BE031330
21	43.6	4.6	919	10	CNS0296A
22	42.6	4.5	414	10	CG637661

C 23	42.4	4.5	561	9	AQ156306
C 24	42.4	4.5	1101	10	CNS0039G
25	41.8	4.4	717	9	BH974953
C 26	41.8	4.4	658	10	CZ857242
27	41.6	4.4	571	7	CO298356
C 28	41.1	4.3	788	10	CG690741
29	40.8	4.3	1001	10	CNS0078E
30	40.4	4.3	228	10	CG503780
31	40.4	4.3	307	4	AK190946
32	40.4	4.3	431	10	CG517501
33	40.4	4.3	525	6	CA548609
34	40.4	4.3	526	10	CL256443
35	40.4	4.3	557	1	AM230870
36	40.4	4.3	563	9	AO670952
37	40.4	4.3	575	5	BU743805
38	40.4	4.3	579	3	BU365833
39	40.4	4.3	616	5	BY729128
C 40	40.4	4.3	630	7	CO102355
41	40.4	4.3	635	1	AM323815
42	40.4	4.3	685	2	BG920190
43	40.4	4.3	810	6	CA751457
44	40.4	4.3	812	7	CV557169
45	40.4	4.3	813	5	BU961361

ALIGNMENTS

RESULT 1
BE035039/c 993 bp mRNA linear EST 07-JUN-2000
LOCUS
DEFINITION
NM02A03 MM Mesembryanthemum crystallinum cDNA 5' similar to
antiviral protein, mRNA sequence.

ACCESSION
BE035039
VERSION
BE035039.1 GI:8330048
KEYWORDS
SOURCE
ORGANISM
Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzooceae; Mesembryanthemum.

REFERENCE

AUTHORS

Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Saton, M.,
Ferreira, H., Kawasaki, S., McColough, A., Michalowski, C.B.,
Palacio, C., Scarpa, G., Wheeler, M. and Zepeda, G.R.

Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu

TITLE

JOURNAL

COMMENT

FEATURES

source

1..993
/organism="Mesembryanthemum crystallinum"
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/db_xref="taxon:3544"
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XhoI; Plants stressed 6 weeks in 500mM NaCl"

ORIGIN

Query Match 9.2%; Score 87; DB 2; Length 993;
Best local similarity 60.1%; Pred. No. 5.6e-12;

Matches 163; Conservative 0; Mismatches 105; Indels 3; Gaps 1;

DB 455 AGAAGCAGAGTAACTCAAGAAATCAAGTCAATTGGAGATTAACATCAAGCAGT 514
681 AGAAGCTGCGGTCAAGCAGAAACAGTATGATTGGGGCTTCAACTAGAGTTTG 622

QY 515 ACATGGAAAAATCTGTGAGTTGATTCATTCCTGTAAATACTGAGCTTTTCTTAC 574
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Db 621 CCATCGAGTGTATTAAGTAATAAAACGATCGATGGAAATCGAGCCAAATTTCTAC 562
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QY 575 TGTGATGATCCAAATGTTTTCAGAGCGAGCGGATTCAGATCATAGAACCAAGT-- 632
| | | | |
Db 561 TGAATGCGATCCAGATGTTTCAGAGCAGCAGGTTCCATTTATCGAGACTAGAGTGA 502
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QY 633 -CAAGACTAATTTAATAGAGCATTCACCTGATCCCAAGTAATTAATTTGGAGAGA 691
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Db 501 CCGAAAGTGGGTACATGTTCTTCCTCAACCCGATCCGAAGTGATTAATTCGGAGACA 442
| | | | |
QY 692 AGTGGGCAAAATCTGTGAGCAATTGACA 722
| | | | |
Db 441 ACTGGGGAAGATTTCGATGATGATTCATTA 411
| | | | |
RESULT 2 816 bp mRNA linear EST 07-JUN-2000
BE035038
LOCUS BE035038.1 MM Mesembryanthemum crystallinum cDNA 5' similar to
DEFINITION antifungal protein, mRNA sequence.
ACCESSION BE035038
VERSION BE035038.1 GI:8330047
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
COMMENT Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 816)
REFERENCE Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Baton, M.,
Ferreira, H., Kawasaki, S., McColough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
CONTACT: Michalowski, C.B.
UNIVERSITY OF ARIZONA
BIO SCIENCES WEST ROOM 513, TUCSON, AZ 85721, USA
TEL: 520-621-7982
FAX: 520-621-1697
EMAIL: cbm@u.arizona.edu.
LOCATION/Qualifiers
FEATURES
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/note="Vector: Bluescript SK+; Site 1: EcoRI; Site 2:
XhoI; Plants stressed 6 weeks in 500mM NaCl"

ORIGIN

Query Match 8.5%; Score 80.6; DB 2; Length 816;
Best Local Similarity 58.7%; Pred. No. 2.8e-10;
Matches 159; Conservative 0; Mismatches 109; Indels 3; Gaps 1;

QY 455 AGAAGCAGAAAGTAATCTCAAGAAATCAAGTCCAAATTTGGAAATCTCAAGCAGT 514
| | | | |
Db 680 AGAAGCCTGCGGTCAAGCAGAAACAGTAATGACGTGGGCTTGCTAAATAGAGTTG 621
| | | | |
QY 515 ACATGGAAAAATCTGTGAGTTGATTCATTCCTGTAAATACTGAGCTTTTCTTAC 574
| | | | |
Db 620 CCATCGAGTGTATTAAGTAATAAAACGATCGATGGAAATCGAGCCAAATTTCTAC 561
| | | | |
QY 575 TGTGATGATCCAAATGTTTTCAGAGCGAGCGGATTCAGATCATAGAACCAAGT-- 632
| | | | |
Db 560 TGAATGCGATCCAGATGTTTCAGAGCAGCAGGTTCCATTTATCGAGACTAGAGTGC 501
| | | | |
QY 633 -CAAGCTAATTTAATAGAGCATTCACCTGATCCCAAGTAATTAATTTGGAGAGA 691
| | | | |

Db 500 CCGAAAGTGGGTACATGTTCTGTCAAAACCCGATCCGAAGTGATTAATTCGAGAGACA 441
| | | | |
QY 692 AGTGGGCAAAATCTGTGAGCAATTGACA 722
| | | | |
Db 440 ACTGGGGAAGATTTCGATGATGATTCATTA 410
| | | | |

RESULT 3 1033 bp mRNA linear EST 07-JUN-2000
BE036541
LOCUS BE036541
DEFINITION ME01807 MP Mesembryanthemum crystallinum cDNA 5' similar to
antifungal protein, mRNA sequence.
ACCESSION BE036541
VERSION BE036541.1 GI:8331550
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
COMMENT Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 1033)
REFERENCE Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Baton, M.,
Ferreira, H., Kawasaki, S., McColough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
CONTACT: Michalowski, C.B.
UNIVERSITY OF ARIZONA
BIO SCIENCES WEST ROOM 513, TUCSON, AZ 85721, USA
TEL: 520-621-7982
FAX: 520-621-1697
EMAIL: cbm@u.arizona.edu
LOCATION/Qualifiers
FEATURES
source 1..1033
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/cissue_type="apical meristem and leaf primordia"
/dev_stage="6 weeks"
/clone_1lb="MP"
/note="3 d 500mM NaCl"

ORIGIN

Query Match 6.9%; Score 65.6; DB 2; Length 1033;
Best Local Similarity 55.1%; Pred. No. 3e-06;
Matches 150; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

QY 453 AAGAAAGCAGAAAGTAATCTCAAGAAATCAAGTCCAAATTTGGAAATCTCAAGCAG 512
| | | | |
Db 193 AGAAGAGCTGCAAGCAAGCGCCGAATTCATAGATGAGGGGTGAATTAATAGATT 252
| | | | |
QY 513 TGAATGGAAGAAATCTGTGAGTTGATTCATTCCTGTAAATACTGAGGCTTTTCT 572
| | | | |
Db 253 TGCATGAGTGGCTTTTGTGAAGACCGGATTAATGAGCGGTTAGCGCCAAATCTT 312
| | | | |
QY 573 ACTGTAGCCATTCAAATGTTTTCAGAGCGAGCGGATTCAGATCATAGAACCAAGT 632
| | | | |
Db 313 GCTGATGCTATACATAGTGTTCGAAAGCAGCAGGTTTAAATTAATTAAGTAAGT 372
| | | | |
QY 633 ---CAAGCTAATTTAATAGAGCATTCACCTGATCCCAAGTAATTAATTTGGAGGA 689
| | | | |
Db 373 GACCCAAAGTGGGTACATGTCGTTCAATCCGACCGGAAGTGTCTAGTTGAGAA 432
| | | | |
QY 690 GAAGTGGGCAAAATCTGTGAGCAATTGACA 721
| | | | |
Db 433 CAATGCGGGAAGATTTCGCAAGAGATTGATA 464
| | | | |

RESULT 4 498 bp mRNA linear EST 06-DEC-2002
BOS88134
LOCUS BOS88134
DEFINITION E012337-024-009-G14-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone

024-009-G14 5-PRIME, mRNA sequence.
ACCESSION BQ588134
VERSION BQ588134.1 GI:26117717
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 498)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stalld., Wruock,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 498 Std Error: 0.00
Plate: 9 row: G column: 14
Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers
1..498
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:184726"
/db_xref="taxon:161934"
/clone="024-009-G14"
/issue_type="leaf"
/lab_host="EMD10B"
/clone_1lb="MP1Z-ADIS-024-leaf"
/note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet. library provided by KWS Kleinwanzlebener Saatnuech AG Birbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polYA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Best project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 6.6%; Score 62.2; DB 5; Length 498;
Best local Similarity 56.7%; Pred. No. 2.1e-05;
Matches 140; Conservative 0; Mismatches 98; Indels 9; Gaps 1;
QY 83 TCACCTTGTATGCTGAAATGCCACATTAAACAATATGCACTTATGAAATCTCTTC 142
DB 169 TAACTTTTACCTTGAAGAGCTTCAAGACAAATATGSCACTTTCTTAAGAACTTAC 228
QY 143 GTATATACGGAAGATCCAAAATCTAAATGCTATGCGATACCAATGCTACTGATATCTA 202
DB 229 GCAACATATGAGGATTCAAAGCTATGATACGAAATTCCAATGCTCCCGCACCAT 288
QY 203 ATTGACCCCTAGTACTTATGTTAGTCAAGTCCAGTGCAAA-----CTTAAAA 253
DB 289 CAAACACGAAATATCTTTTATGCGAGCTTAAAGCTTAAAGAGCCGGTACTGACATTA 348
QY 254 CCATTACACTAATGCTGAGACGAATATCTATATGCTATGCGCTATTCATCCCTTCA 313
DB 349 CCATCACACTGCTGTAGCAAAATATGATATATGATGAGCTTTTACATGATCAAGTNG 408
QY 314 ATGGCA 320
DB 409 CAGGTAA 415

RESULT 5
LOCUS CN782289
DEFINITION EST00385 cgeed Chenopodium quinoa cDNA clone 802J22 5' similar to antiviral ribosome-inactivating protein CAP308 (Chenopodium album), mRNA sequence.
ACCESSION CN782289
VERSION CN782289.1 GI:47561753
KEYWORDS EST.
SOURCE Chenopodium quinoa (quinoa)
ORGANISM Chenopodium quinoa
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Chenopodium.
1 (bases 1 to 829)
AUTHORS Coles,N.D., Coleman,C.E., Christensen,S.A., Jellen,E.N., Stevens,M.R., Bonifacio,A., Rojas-Beltran,J.A., Fairbanks,D.U. and Maughan,P.J.
TITLE Development and use of an expressed sequenced tag library in quinoa (Chenopodium quinoa Willd.) for the discovery of single nucleotide polymorphisms
JOURNAL Plant Sci. 168 (2), 439-447 (2005)
COMMENT Contact: Coleman, Craig E.
Department of Plant and Animal Sciences
Brigham Young University
275 WIDB, Brigham Young University, Provo, UT 84602, USA
Tel: (801) 422-5145
Fax: (801) 422-0008
Email: craig.coleman@byu.edu
Plate: 02 row: J column: 22
Seq primer: M13 Forward
High quality sequence stop: 829.
Location/Qualifiers
1..829
/organism="Chenopodium quinoa"
/mol_type="mRNA"
/cultivar="Real"
/db_xref="taxon:63459"
/clone="S02J22"
/issue_type="Developing Seed"
/lab_host="XL-1 Blue"
/clone_1lb="cgeed"
/note="Vector: pTRIPLEX2; Site 1: SfiI; Site 2: SfiI; Developing Seed cDNA library from Chenopodium quinoa"

ORIGIN

Query Match 6.5%; Score 61.6; DB 7; Length 829;
Best local Similarity 51.2%; Pred. No. 3.4e-05;
Matches 291; Conservative 0; Mismatches 244; Indels 33; Gaps 5;
QY 99 AATGCCACATTAAACAATATGCGACCTTTATGAAATCTTCTGTAATCAAGCAAGA 158
DB 115 AAACCTACAGAAATATCTATTAACCTTTCTGAAAGTATACGACCAACTAAGA 174
QY 159 TCCAAACCTAAATGCTATGCGATACCAATGCTACTGATATCTAATTCACCCCTAAGTA 218
DB 175 TCCAAAGCTTATGATGAGGAATCCCAATGATCCGACCAACCAACCCAGATACATA 234
QY 219 CTTATTTGTTAGCTCCAAAGTCCAAACCTTAAAC-----CATTAAGTATGCT 269
DB 235 TCTTTTGTGACCTTGAATCTTAAAGATTAAGATGATATTCATTAACCTTGCTTT 294
QY 270 GAGAGAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 329
DB 295 AAGTGAAGACGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 354
QY 330 TTACATATATTTAATGATATTAACAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 389
DB 355 CCAATTTCTTTTCCAAATCTTAACATTGACCACTTGTATTAAGCAAGAA-----AGTTTTC 410
QY 390 CTCAAGTTCTAGTCTCGTGTGCAATGTCATTAATCAATTAAGCTTATATCCAGCAT 449

Db 411 CAGAACTCAGGTTTC-----ATAATATTAAGTATGGGAAAGTTACAGTCAAT 462
QY 450 GGAAGAAAGAGAGAGTAAGTCAAGAAATCAAGATCCAAATGGGAATTCAAATATCTG 509
Db 463 CGAAGCAATGCTGTGTAACAACCGATTAGT--TTCCGTTGGGGTTGATTAACCTTAA 519
QY 510 CAGTGCATTTGAAAAAATCTCTGAGTTGATTCATTCCTGTG-----AAATCTGA 560
Db 520 AACTTACATGAAAAAGTCTATGGGATGATCTAAGGCCAAAGATTATAGCAAACTGA 579
QY 561 GGGTTTTTTTCTACTGCTGAGCCATCCAAATGTTTCAGAGGACGCCGATTCAGTACAT 620
Db 580 AGCTCGTTCCTACATCATCGCATTCAAATGTTTGACAGAGCGCGATTCAGATCAAT 639
QY 621 AGAGAACCAAGTCAAGACTAATTTTAA 648
Db 640 CCGAGGAAGAGCTATGCTTACTACAAAT 667

RESULT 6
CA838757 649 bp mRNA linear EST 12-DEC-2002
LOCUS MCT020B02.167445 Ice plant Lambda Uni-Zap XR expression library, 5
DEFINITION days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
(5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT020B02 5,
mRNA sequence.

ACCESSION CA838757
VERSION CA838757.1 GI:26566522
KEYWORDS EST.

SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 649)
Cushman, J.C.

REFERENCE An expressed sequence tag database for the common ice plant,
AUTHORS Mesembryanthemum crystallinum
TITLE Unpublished (1997)

JOURNAL Contact: Cushman JC
COMMENT Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 020 row: B column: 02
Seq primer: T3 20mer

High quality sequence stop: 649.
Location/Qualifiers

FEATURES
source 1..649
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT020B02"
/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 6.2%; Score 59; DB 6; Length 649;
Best Local Similarity 53.8%; Pred. No. 0.00016;
Matches 147; Conservative 0; Mismatches 120; Indels 6; Gaps 1;

QY 453 AAAGAAAGCAGAGTAATCTCAAGAAATCAAGTCCAAATGGGAATTCAAATATCTCAGCAG 512
Db 87 AAGAAATGCTGAAACCAACGACGAGAGGCCATAGATTAGGGGTGAGTAATCTAGAGTT 146
QY 513 TGAATTTGAAAAAATCTCTGAGTTGATTCATTCCTGTAAAAACTAGGCTTTTTCCT 572
Db 147 TCGATTCGAGTGGTTTATGTGTAACATCGCAAGTCAAGAAATGAGGGCCAAATTCCT 206
QY 573 ACTGGATGCATCCAAATGCTTCAGAGCAGCGGATTCAGTACATAGAACCAACT 632
Db 207 GCTGATTCGATACAGATGCTTTCTGAGCAGCAAGTTCAAGTATTTGAGATGAGT 266
QY 633 CAAGCTAATTT-----TAATGAGCAATTCACCTGATCCCAAGTAATTAATTGGA 686
Db 267 GAACCAAGTGGGTTAGATTATGAAATCGTTCTTACCCGACCCGAAATGCTCTTTTGA 326
QY 687 GGAAGAAATGGGCAAAATCTCTGAGGCAATTCA 719
Db 327 GACCAATTTGGGGGAAGATTTCCGACGAGATTCA 359

RESULT 7
CA839330 649 bp mRNA linear EST 12-DEC-2002
LOCUS MCT026C11.171755 Ice plant Lambda Uni-Zap XR expression library, 5
DEFINITION days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
(5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT026C11 5,
mRNA sequence.

ACCESSION CA839330
VERSION CA839330.1 GI:26567095
KEYWORDS EST.

SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 649)
Cushman, J.C.

REFERENCE An expressed sequence tag database for the common ice plant,
AUTHORS Mesembryanthemum crystallinum
TITLE Unpublished (1997)

JOURNAL Contact: Cushman JC
COMMENT Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 026 row: C column: 11
Seq primer: T3 20mer

High quality sequence stop: 649.
Location/Qualifiers

FEATURES
source 1..649
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT026C11"
/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 6.2%; Score 59; DB 6; Length 649;
Best Local Similarity 53.8%; Pred. No. 0.00016;
Matches 147; Conservative 0; Mismatches 120; Indels 6; Gaps 1;

ORIGIN

Lambda UnizapXR vector and cDNA synthesis kit."

Query Match 6.2%; Score 59; DB 6; Length 671;
Best Local Similarity 53.8%; Pred. No. 0.00016;
Matches 147; Conservative 0; Mismatches 120; Indels 6; Gaps 1;

QY 453 AAGAAAGCAGAGTAATCAAGAAATCAAGTCCATTGGGAATTCAAATTAATCTACAGAC 512
DB 87 AGAGAAATGCTGCAACCAACGACGAGAGCATGATGAGGGGTGATTAATCAAGAGTT 146
QY 513 TGACATTGGAAAAATCTCTGAGATTGATTCATTCCTGTAAAACTGAGGCTTTTTCCT 572
DB 147 TGGATCGAGTCCGTTTATGTAGACATGACAGCAAGTCAGAGAAATGAGCCCAATTCCT 206
QY 573 ACTGTAGCCATCCAAATGTTTCAGAGGAGCGCATTCAGATACATAGAACCAAGT 632
DB 207 GCTGATTCGCATCAAGATGTTTCTGAGCAGCAGGTTCCAGATATTTGAGAGTAAAGT 266
QY 633 CAAGACTAATTT-----TAATAGACATTCCTACCTGATCCCAAGTAATTAATTGGA 686
DB 267 GAACCAAGTGCCTTAGATTATGATGATGTTCTTACCCGACCCGAAATGCTGCTTTTGA 326
QY 687 GGAAGAGTGGGCGCAAAATCTCTGAGGCAATTCA 719
DB 327 GACCAATTGGGGGAGAGATTTCGACAGAGATTCA 359

RESULT 10

CA833333

LOCUS 689 bp mRNA linear EST 12-DEC-2002
DEFINITION MCS021A09 151944 Ice plant Lambda Uni-Zap XR expression library, 5

days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS021A09 5, mRNA sequence.

ACCESSION CA833333
VERSION CA833333.1 GI:26561098

SOURCE Mesembryanthemum crystallinum (common iceplant)
KEYWORDS EST.

ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.

REFERENCE Cushman, J.C.

AUThORS An expressed sequence tag database for the common ice plant,
TITLe Mesembryanthemum crystallinum

JOURNAl Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

FEATURES

source

/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCS021A09"
/issue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase I (2 AM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-, Site_1:"

ORIGIN

EcoRI, Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UnizapXR vector and cDNA synthesis kit."

Query Match 6.2%; Score 59; DB 6; Length 689;
Best Local Similarity 53.8%; Pred. No. 0.00016;
Matches 147; Conservative 0; Mismatches 120; Indels 6; Gaps 1;

QY 453 AAGAAAGCAGAGTAATCAAGAAATCAAGTCCATTGGGAATTCAAATTAATCTACAGAC 512
DB 98 AGAGAAATGCTGCAACCAACGACGAGAGCATGATGAGGGGTGATTAATCAAGAGTT 157
QY 513 TGACATTGGAAAAATCTCTGAGATTGATTCATTCCTGTAAAACTGAGGCTTTTTCCT 572
DB 158 TGGATCGAGTCCGTTTATGTAGACATGACAAATCAGAGAAATGAGCCCAATTCCT 217
QY 573 ACTGTAGCCATCCAAATGTTTCAGAGGAGCGCATTCAGATACATAGAACCAAGT 632
DB 218 GCTGATTCGCATCAAGATGTTTCTGAGCAGCAGGTTCCAGATATTTGAGAGTAAAGT 277
QY 633 CAAGACTAATTT-----TAATAGACATTCCTACCTGATCCCAAGTAATTAATTGGA 686
DB 278 GAACCAAGTGCCTTAGATTATGATGATGTTCTTACCCGACCCGAAATGCTGCTTTTGA 337
QY 687 GGAAGAGTGGGCGCAAAATCTCTGAGGCAATTCA 719
DB 338 GACCAATTGGGGGAGAGATTTCGACAGAGATTCA 370

RESULT 11

CA833383

LOCUS 689 bp mRNA linear EST 12-DEC-2002
DEFINITION MCS021F04 152044 Ice plant Lambda Uni-Zap XR expression library, 5

days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS021F04 5, mRNA sequence.

ACCESSION CA833383
VERSION CA833383.1 GI:26561148

SOURCE Mesembryanthemum crystallinum (common iceplant)
KEYWORDS EST.

ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.

REFERENCE Cushman, J.C.

AUThORS An expressed sequence tag database for the common ice plant,
TITLe Mesembryanthemum crystallinum

JOURNAl Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

FEATURES

source

/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCS021F04"
/issue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid

metabolism, phase I (2 AM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 6.2%; Score 59; DB 6; Length 689;
Best Local Similarity 53.8%; Pred. No. 0.0016;
Matches 147; Conservative 0; Mismatches 120; Indels 6; Gaps 1;

QY 453 AAAGAAAGCAGAACTGAAGTCAAGTCCAAATTCGAATTCAGACAG 512
DB 98 AGAAGATGCTGCAACCAACGACGAGCCATAGAGTGGGGTGAATTAACAGATT 157
QY 513 TGACATTGGAAAAATCTCTGAGATTGATTCCCTGTAATAAATGAGGCTTTTCT 572
DB 158 TGGCATGAGTCGGGTTATGTTAGATGACATGACATGACAGAAATGAGCCAAATTCCT 217
QY 573 ACTGTGAGCCATCCAAATGTTTCAAGGACGCGGATTCAGATACATAGAAACCAAGT 632
DB 218 GCTGATGCGCATACAGATGTTTCTGAAGCAGCAAGTTCAAGTATATGAGAGTAAGT 277
QY 633 CAAGACTAATTT-----TAATAGCATTTCTACCTGATCCCAAGTAATTAATTGA 686
DB 278 GAACCAAGTCGTTAGATTGATGATCGTTCTTACCCGACCCGAAATGCTGCTTTTGA 337
QY 687 GGAGAGTGGGGGCAAAATCTCTGAGGCAATTC 719
DB 338 GACCAATTGGGGGAAGATTTCGACAGAGATTCA 370

RESULT 12

CA835855 639 bp mRNA linear EST 12-DEC-2002
LOCUS CA835855
DEFINITION MCS004612.161218 Ice plant Lambda Uni-Zap XR expression library, 5
days 0.5 M NaCl treatment; Crassulacean acid metabolism, phase I (2
AM). Mesembryanthemum crystallinum cDNA clone MCS004612 5, mRNA
sequence.

ACCESSION CA835855
VERSION CA835855.1
KEYWORDS GI:26563620
SOURCE EST.
ORGANISM Mesembryanthemum crystallinum (common iceplant)

Mesembryanthemum crystallinum
Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 639)
Cushman, J.C.
An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
Unpublished (1997)

JOURNAL

COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 004 row: G column: 12
Seq primer: T3 20mer
High quality sequence stop: 639.

FEATURES

source 1. 639
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCS004612"
/tissue_type="leaf"
/dev_stage="five-oid"

/clone_1lb="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment; Crassulacean acid
metabolism, phase I (2 AM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 6.1%; Score 57.4; DB 6; Length 639;
Best Local Similarity 53.5%; Pred. No. 0.0043;
Matches 146; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

QY 453 AAAGAAAGCAGAACTGAAGTCAAGTCCAAATTCGAATTCAGACAG 512
DB 98 AGAAGATGCTGCAACCAACGACGAGCCATAGAGTGGGGTGAATTAACAGATT 157
QY 513 TGACATTGGAAAAATCTCTGAGATTGATTCCCTGTAATAAATGAGGCTTTTCT 572
DB 158 TGGCATGAGTCGGGTTATGTTAGATGACATGACATGACAGAAATGAGCCAAATTCCT 217
QY 573 ACTGTGAGCCATCCAAATGTTTCAAGGACGCGGATTCAGATACATAGAAACCAAGT 632
DB 218 GCTGATGCGCATACAGATGTTTCTGAAGCAGCAAGTTCAAGTATATGAGAGTAAGT 277
QY 633 CAAGACTAATTT-----TAATAGCATTTCTACCTGATCCCAAGTAATTAATTGA 686
DB 278 GAACCAAGTCGTTAGATTGATGATCGTTCTTACCCGACCCGAAATGCTGCTTTTGA 337
QY 687 GGAGAGTGGGGGCAAAATCTCTGAGGCAATTC 719
DB 338 GACCAATTGGGGGAAGATTTCGACAGAGATTCA 370

RESULT 13

BE033546 1038 bp mRNA linear EST 07-JUN-2000
LOCUS BE033546
DEFINITION MF03A09 MF Mesembryanthemum crystallinum cDNA 5' similar to
ribosome-inactivating protein, mRNA sequence.

ACCESSION BE033546
VERSION BE033546.1
KEYWORDS GI:8328555
SOURCE EST.
ORGANISM Mesembryanthemum crystallinum (common iceplant)

Mesembryanthemum crystallinum
Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 1038)
Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Baton, M.,
Ferreira, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M., and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)

JOURNAL

COMMENT Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu
An open reading frame exists.
Location/Qualifiers

FEATURES

source 1. 1038
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/tissue_type="Root"
/dev_stage="5-6 weeks old"
/clone_1lb="MF"
/note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN

Query Match 5.9%; Score 55.4; DB 2; Length 1038;

Best Local Similarity 52.7%; Pred. No. 0.0016;
Matches 144; Conservative 0; Mismatches 126; Indels 3; Gaps 1;

QY 453 AAGAAAGCAGAAAGTAATCTCAAGAAATCAAGTCCAAATGGGAATTCAAAATACCTACAGAG 512
DB 286 AGAAGAGCTGCAAGAGAGCCGAAATGCAATGAGTTAGGGGTGAATTAATAGAGCTT 345
QY 513 TGACATTTGAAAATCTCTGAGATTGATTCATTCCTGTAAATACTAGAGCTTTTCTCT 572
DB 346 CGGATGAGATCGGTTTGGTAAAGAACCGGATTAATGGGAGGTTGAGGCCAAATCTT 405
QY 573 ACTGTAGCATCCAAATGTTTCAAGAGAGCCGCAATTCAGATCAATAGAAACCAAGT 632
DB 406 GCTGATTTGCTTAACAGATGTTCTCTGAGAGCAGACGGTTTAAGTTTAAAGTAAGT 465
QY 633 CA--AGACTAATTTTATAGACATCTACCTGTATCCCAAGTAATTAATTTGAGAGA 689
DB 466 GACCCAAAGTGTCTACATGCTTTTCAAAACCCGAAAGTGTGAGTTGGTGT 525
QY 690 GAAGTGGGCAAAATCTCTGAGGCAATTCACAA 722
DB 526 CAATGGGTGAACATTTTCCATGAGACTCATAA 558

RESULT 14

LOCUS T24255 405 bp mRNA linear EST 28-JUL-1995
DEFINITION crie1345 lambdaZAPST Ricinus communis cDNA clone pcrs1345, mRNA
sequence.

ACCESSION T24255
VERSION T24255.1 GI:669074

KEYWORDS

SOURCE

ORGANISM

Ricinus communis (castor bean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae;
Acalyphaeae; Ricinus.
1 (bases 1 to 405)

REFERENCE
AUTHORS vandeloo, F.J., Turner, S. and Somerville, C.
TITLE Expressed sequence tags from developing castor seeds
JOURNAL Plant Physiol. 109, 1141-1150 (1995)
COMMENT Contact: Somerville CR
Carnegie Institution
Carnegie Institution, 290 Panama St., Stanford, CA 94305
Tel: 4153251521
Email: crs@andrew.stanford.edu
Seq primer: T3

FEATURES

source

1. .405
Location/Qualifiers

/organism="Ricinus communis"
/mol_type="mRNA"
/strain="Baker 296"
/db_xref="taxon:3988"
/clone_1="pcrs1345"
/clone_1b="lambdaZAPST"
/note="Vector: lambdaZAPIT; Site 1: EcoRI; Site 2: XhoI;
Poly(A) + RNA was purified from developing stage III to
stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760,
1982) endosperm plus embryo of immature castor fruits.
cDNA was synthesized and cloned into lambdaZAPIT according
to the instructions of the manufacturer (Stratagene);
synthesis was primed from the poly(A) tail, and cloned
directionally into XhoI (3') and EcoRI (5') sites. In few
cases, sequence data indicated that this directionality
was reversed. Partial cDNA clones predominate."

ORIGIN

Query Match 5.5%; Score 52.4; DB 8; Length 405;
Best Local Similarity 59.2%; Pred. No. 0.0084;
Matches 125; Conservative 0; Mismatches 79; Indels 7; Gaps 2;

QY 555 AACTGAGGCTTTTCTTCTGATGCAATCAATGTTTCAAGAGCAGCGGATTCAA 614

DB 82 AACCTGGCTCGTTCCTTTATGTTTGATCCAAATGATTCAGAGCAGACAGATTCCA 141

QY 615 GTACATAGAAACCAAGTCAAGCTAATTTT-----AATAGCATTTCACTGATTC 668

DB 142 GTTCAATTTGAGGAGAAATGCGCAGAAATTAAGTACACCGAAGATCTGACACCAATCC 201

QY 669 CAAGTAAATTAATTTGGAGAGAGTGGGCAAAATCTCTGAGCAATTCACA-ATGCCA 727

DB 202 TAGCGTATTAATCACTTNNAGAAATGTTGGGAGACCTTCCACTGCAATTCAGAGCTCTA 261

QY 728 AGAATGGGCTTTACCCAAACCACTTGAGCT 758

DB 262 ACCAAGGAGCCTTTGCTAGTCANTTCAACT 292

RESULT 15

LOCUS

BE037217 639 bp mRNA linear EST 07-JUN-2000

DEFINITION MP18B02 MP Mesembryanthemum crystallinum cDNA 5' similar to
ribosome-inactivating protein/antiviral protein, mRNA sequence.

ACCESSION BE037217
VERSION BE037217.1 GI:8332233

KEYWORDS

SOURCE

ORGANISM

Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Rozaceae; Mesembryanthemum.
1 (bases 1 to 639)

REFERENCE
AUTHORS Bohner, H.U., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
Ferreira, H., Kawasaki, S., McColough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
TITLE Functional Genomics of Plant Stress Tolerance
JOURNAL Unpublished (2000)
COMMENT Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu

FEATURES

source

1. .639
Location/Qualifiers

/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/ribuse_type="apical meristem and leaf primordia"
/dev_stage="6 weeks"
/clone_1b="MP"
/note="3 d 500mM NaCl"

ORIGIN

Query Match 5.4%; Score 50.8; DB 2; Length 639;
Best Local Similarity 61.2%; Pred. No. 0.025;
Matches 104; Conservative 0; Mismatches 57; Indels 9; Gaps 1;

QY 463 GAAGTAACTCAAGAAATCAAGTCAATTTGGGAATTCATCAATCTCGAGTCAATTCGA 522

DB 308 GAGAGCTAAGGAGAAAGAGATCGCAATTTAGTATTTAGTAAATAGTTTCAATAA 367

QY 523 AAAATCTGAGATTGATTCATTCCTGTAATAAATGAGGCTTTTCTTACTGTAGCC 582

DB 368 AACAGC-----GATTAATGATGAAAGATGAGGCTAATTTCTTCTAGTTGGG 418

QY 583 ATCCAAATGTTTCAAGAGCAGCGGATTCAGATCAATGATGAGAACCAAGT 632

DB 419 ATTCAATGTTTGTGAGGCTGACGCTTCTTACATTCAGAGAAAGGT 468

Search completed: April 9, 2006, 04:11:00
Job time : 4477.73 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2006, 09:19:56 ; Search time 328.047 Seconds
(without alignments)
5120.590 Million cell updates/sec

Title: US-09-978-274A-1

Perfect score: 945
Sequence: 1 atgaagtcgtactgtgtg.....atctattgaagattctaa 945

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	634	67.1	1195	2 US-08-373-858-1	Sequence 1, Appl1
2	634	67.1	1195	2 US-08-342-7868-1	Sequence 1, Appl1
3	632.4	66.9	1379	2 US-08-500-611-1	Sequence 1, Appl1
4	632.4	66.9	1379	2 US-08-500-694-1	Sequence 1, Appl1
5	632.4	66.9	1379	3 US-07-865-169-1	Sequence 1, Appl1
6	632.4	66.9	1379	3 US-09-005-273-1	Sequence 1, Appl1
7	632.4	66.9	1379	6 PCT-US95-11546-1	Sequence 1, Appl1
8	630.8	66.8	1379	3 US-08-501-253A-1	Sequence 1, Appl1
9	629.2	66.6	1379	3 US-07-865-169-2	Sequence 2, Appl1
10	629.2	66.6	1379	3 US-09-005-273-3	Sequence 3, Appl1
11	543.8	57.5	918	2 US-08-318-636-1	Sequence 1, Appl1
12	543.8	57.5	918	2 US-08-319-622A-1	Sequence 1, Appl1
13	543.8	57.5	918	2 US-08-471-564-1	Sequence 1, Appl1
14	543.8	57.5	918	2 US-08-356-161-6	Sequence 6, Appl1
15	88.4	9.4	804	2 US-08-356-161-7	Sequence 7, Appl1
16	88.4	9.4	804	3 US-08-718-904-22	Sequence 22, Appl1
17	88.4	9.4	804	3 US-08-718-904-23	Sequence 23, Appl1
18	88.4	9.4	804	3 US-09-449-249-22	Sequence 22, Appl1
19	88.4	9.4	804	3 US-09-449-249-23	Sequence 23, Appl1
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22	88.4	9.4	804	6 PCT-US95-10973A-6	Sequence 6, Appl1
23	88.4	9.4	804	6 PCT-US95-10973A-7	Sequence 7, Appl1
24	88.2	9.3	774	6 PCT-US91-05766-1	Sequence 1, Appl1

25	82	8.7	804	2 US-08-356-161-4	Sequence 4, Appl1
26	82	8.7	804	3 US-08-718-904-20	Sequence 20, Appl1
27	82	8.7	804	3 US-09-449-249-20	Sequence 20, Appl1
28	82	8.7	804	6 PCT-US93-05702-4	Sequence 4, Appl1
29	82	8.7	804	6 PCT-US95-10973A-4	Sequence 4, Appl1
30	80.4	8.5	804	2 US-08-356-161-3	Sequence 3, Appl1
31	80.4	8.5	804	2 US-08-356-161-5	Sequence 5, Appl1
32	80.4	8.5	804	3 US-08-718-904-19	Sequence 19, Appl1
33	80.4	8.5	804	3 US-08-718-904-21	Sequence 21, Appl1
34	80.4	8.5	804	3 US-09-449-249-19	Sequence 19, Appl1
35	80.4	8.5	804	3 US-09-449-249-21	Sequence 21, Appl1
36	80.4	8.5	804	6 PCT-US93-05702-3	Sequence 3, Appl1
37	80.4	8.5	804	6 PCT-US93-05702-5	Sequence 5, Appl1
38	80.4	8.5	804	6 PCT-US95-10973A-3	Sequence 3, Appl1
39	80.4	8.5	804	6 PCT-US95-10973A-5	Sequence 5, Appl1
40	79.6	8.4	1233	3 US-08-718-904-80	Sequence 80, Appl1
41	79.6	8.4	1233	3 US-09-449-249-80	Sequence 80, Appl1
42	73	7.7	813	2 US-07-901-707-11	Sequence 59, Appl1
43	73	7.7	813	2 US-07-901-707-57	Sequence 57, Appl1
44	73	7.7	813	2 US-07-988-430-11	Sequence 11, Appl1
45	73	7.7	813	2 US-07-988-430-11	Sequence 11, Appl1

ALIGNMENTS

RESULT 1
US-08-373-858-1
; Sequence 1, Application US/08373858
; Patent No. 5633155
; GENERAL INFORMATION:
; APPLICANT: Kim, Man-Keun
; APPLICANT: Lee, Kwan-Ho
; APPLICANT: Na, Byoung-Kook
; APPLICANT: Jeong, Han-Seung
; APPLICANT: Choi, Kyu-Whan
; APPLICANT: Moon, Young-Ho
; APPLICANT: Jeon, Hong-Seob
; TITLE OF INVENTION: Expression Vector for Phytoacta
; TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Darby & Darby
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,858
; FILING DATE: 18-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0136/17986-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7770
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Phytolacca americana*
 TISSUE TYPE: Leaf
 US-08-373-858-1

Query Match 67.1%; Score 634; DB 2; Length 1195;
 Best Local Similarity 80.1%; Pred. No. 1,3e-168;
 Matches 758; Conservative 0; Mismatches 185; Indels 3; Gaps 1;

3 GAAGGTGATGCTTGTAGTGTGAGAGCTTAATAGCTGCTCATTTGCTGACCACTTC 62
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 29 GAAGATGAAGTCAGATGCTGTGTGAGAAATATCAATATGCTCATTTCTGACCACTTC 88
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 63 AACTGTGCGATTAATACATACCTTTGATGCTGAAATGCGACCATTAACAATATGC 122
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 89 AACTTGGGCTGTATATCATCATCTATCAATGTTGGAAATGACCATTTGCAAAATGCG 148
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 123 CACCTTTATGGAATCTTTGATATCAAGGAAAGATCCAAACTAAATGCTATGCGAT 182
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 149 CACTTTTCTGAATGATCTTGTATATGAAAGAAAGATCCAAAGTTTAAATGCTATGGAAT 208
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 183 ACCAATGCTACCTGATATCTAATTCGACCCCTAAGTACTTATGCTTACCTCCAGGTGC 242
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 209 ACCAATGCTGCGCAATATCAATATCAATCCAAAGTACGTGTGAGCTCCAAAGGTTC 268
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 243 AAACCTTAAACCATTAACATTAATGCTGAGACGAAATTAATCTTACGTATGAGGCTATTC 302
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 303 TGATCCCTTCATATGCAATATAGTGTGCTTACATATATTTAATGATATTAACAACACCGA 352
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 363 AGCGCATGATGTGGAATATCTCTTGTCTCAATTTCTAGTTCCTGCTTGCATATGTCAT 422
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 423 TAACTCAATAGCTTATATCCGACATGAGAAAGAAAGCAAGATTAATCAAGAAATCA 482
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 449 AAACCTTGAATGCTATATCAATCAATTTGAAATCAAAAGCGGAGTAAATCAAGAAATCA 508
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 483 AGTCCCAATTTGGGAATTCAAATTAATCAAGAGTGAATTTGAAAAATCTCTGAGGTTGATTC 542
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 509 AGTCCCAATCTGGGAATTCAAATTAATCAAGATTAATTTGAAAAATTTCTGAGAGTGAATTC 568
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 543 ATTCCCTGTAATAAGAGGCTTTTCTTCTATCTGTATAGCCATCCAAATGTTTCAAGAGGC 602
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 569 ATTCTGTAAGAAACCGAAAGCGCAATTCCTATTTGATGACCAATATGATCAAGAGGC 628
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 603 AGCGCATTCAGATATAGAGAAACCAAGTCAAGATTAATTTAATAGAGCATTTCTACCC 662
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 629 AGCAAGATTCAGATATAGAGAAATCAAGTGAAGAAATTAATTTAACAAGAGCATTTCAACC 688
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 663 TGATCCCAAGTATTAATTTGAGAGGAAGAGGCGCAAAATCTGAGGCAATTCACAA 722
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 689 TATATCCCAAGTATTAATTTGAGAGGACATGGGGTAAAGATTTCACAGCAATTCATGA 748
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 723 TGCGAAGATGAGGCTTTTACCCAAACCATGAGCTATAGTGAAGCCAAAGGTACCAAGTG 782
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 749 TGCGAAGATGAGGCTTTTACCCAAACCTTCGAGCTATAGTGAAGCCAAAGGTACCAAGTG 808
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 783 GATAGTCTTGAAGTGAATCAATCAATGCTGATGAGCACTCTTAACTACAGTGTGAG 842
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 843 AACTGTGCGATTAATACATACCTTTGATGCTGAAATGCGACCATTAACAATATGCG 899
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 869 AACTGCGCTGTGATATCAATCAATGCTGATGAGCACTCTTAACTACAGTGTGAG 928
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 900 TTAATATTAATGATCTTGTATGATCTATTTGAAGATTCCTAA 945
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Db 929 TTAATATTAATGATCTTGTATGATCTATTTGAAGATTCCTGA 974

RESULT 2

US-08-342-786B-1
 Sequence 1, Application US/08342786B

Patent No. 5648234

GENERAL INFORMATION:

APPLICANT: Moon, Young-Ho

APPLICANT: Jeon, Hong-Seob

APPLICANT: Choi, Kyu-Whan

APPLICANT: Lee, Kwan-Ho

APPLICANT: Kim, Man-Keun

TITLE OF INVENTION: A No. 5648234e1 Expression Vector for *Phytolacca*

TITLE OF INVENTION: Antiviral Protein

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dady & Dady

STREET: 805 Third Ave.

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/342,786B

FILING DATE: 21-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/147,024

FILING DATE: 01-NOV-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, S. Peter

REGISTRATION NUMBER: 25,351

REFERENCE/DOCKET NUMBER: 0136/08862-US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)527-7700

TELEFAX: (212)753-6237

TELEX: 236687

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1195 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: *Phytolacca americana* L.

IMMEDIATE SOURCE:

CLONE: PAP

US-08-342-786B-1

Query Match 67.1%; Score 634; DB 2; Length 1195;

Best Local Similarity 80.1%; Pred. No. 1,3e-168;

Matches 758; Conservative 0; Mismatches 185; Indels 3; Gaps 1;

3 GAAGGTGATGCTTGTAGTGTGAGAGCTTAATAGCTGCTCATTTGCTGACCACTTC 62
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 29 GAAGATGAAGTCAGATGCTGTGTGAGAAATATCAATATGCTCATTTCTGACCACTTC 88
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 63 AACTGTGCGATTAATACATACCTTTGATGCTGAAATGCGACCATTAACAATATGCG 122
 |||||
 89 AACTGCGCTGTGATATCAATCAATGCTGATGAGCACTCTTAACTACAGTGTGAG 148
 |||||
 123 CACCTTTATGGAATCTTTGATATCAAGGAAAGATCCAAACTAAATGCTATGCGAT 182
 |||||
 149 CACTTTTCTGAATGATCTTGTATATGAAAGAAAGATCCAAAGTTTAAATGCTATGGAAT 208
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Oy	133	ACCAATGCTACCTGTAATCTAATTCGACCCTTAAGTACTTAATGGTTAAGCTCCAAAGTGC	242
Db	209	ACCAATGCTGCCCAATTAACAAATCCAAAGTACGTGTGGTGAAGCTCCAAAGTTC	268
Oy	243	AAACCTAAAAACCATTAACACTAATGTCTGAGACGAAATTAACCTTAACGTATGGGCTATTC	302
Db	269	AAATTAATAAAACCATCAACTAATGTCTGAGACGAAACAAATTTGTATGTATGGTTATTC	328
Oy	303	TGATCCCTTCAAATGGCAATPAGTGTCTTACCATATATTTAATATGATTTACAAAGACCGA	362
Db	329	TGATCCCTTGAACCAATTAATGTGTCTTACCATATCTTTAAATGATATCTCAAGTACTGA	388
Oy	363	ACGCACTGATGTGGGAATATCTTTGTCTCAAGTTCTAGTTCGTCTGTTGCCAATGTCAT	422
Db	389	ACGCCAAGATGTAGAGACTACTCTTTGGCCAAATGCCAATTTCTGTGTATGTAATAAATCAT	448
Oy	423	TAACTACATATAGCTTATATCCGACCATGTGMAAAGAAAGCAGAAGTAAACTCAAGAAATCA	482
Db	449	AAACTTTGATGTATCGATATCCAAATTTGGAAATCAAAAGGGGAGTAAATTCAGAAAGTCA	508
Oy	483	AGTCCAAATTTGGGAATTCAAATTAATCTGACGAGTGCATTGGAAAAATCTGTGAAGTTGATTC	542
Db	509	AGTCCAAATTTGGGAATTCAAATTAATCTGACAGTATATATTTGMAAAATTTCTGAGATGATGC	568
Oy	543	ATTCCCTGTAAAAACGTAGGCTTTTTCCTTACCTGTAGGCATCCAAATGGTTTCAAGAGC	602
Db	569	ATTCACTGAGAAAACCGAAGCCGAATTCCTATTGTGAGCCATACAAATGGTATCAAGAGC	628
Oy	603	AGCGGATTCAGATCATAGAGAACCAAGTCAAGATTAATTTTAATAGACATTTCAACC	662
Db	629	AGCAAGATTCAGATCATAGAGATCAGGTGAAAATCTAATTTTACAGAGCATTTCAACC	688
Oy	663	TGATCCCAAGTAAATTAATTTGGAGAGAAATGTGGGCAAAATCTCTGAGCAATTCACAA	722
Db	689	TAAATCCCAAGTAAATTAATTTGGAGAGACATGGGGTAAAGATTTCAACAGCAATTCATGA	748
Oy	723	TGCCAAGATGTGGGCTTATCCCAACCATGTAGCTAGTGGATGGCCAAAGGTACCAAGTG	782
Db	749	TGCCAAGATGTGGGCTTATCCCAACCTCTCGAGCTAGTGGATGGCCAGTGTGCCAAGTG	808
Oy	783	GATAGTCTTAGAGTGGATGAATCAATCGTATGTGGCACTCTTAAGTACCTTAATG	842
Db	809	GATAGTCTTAGAGTGGATGAATCAAGCTGATGTAGCACTTTAAACTACGTTGTGTG	868
Oy	843	AACTGTGAGACACTT--ACCAAAATGCCATGTTCTCTCAAGTAAATTTCTACTTA	899
Db	869	GAGCTGTCAAGCAACTTAATACCAAAATGCCATGTTCTCTCAACTTAATATGTCTACTTA	928
Oy	900	TTATATTAATATATGCTCAATCTTGGTGAATGTAATTTGAAGATTTCTAA	945
Db	929	TTATATTAATATATGCTTAATCTTGGTGAATGTAATTTGAAGATTTCTGA	974

RESULT 3

US-08-500-611-1

; Sequence 1, Application us/08500611

; Patent No. 5756332

GENERAL INFORMATION:

APPLICANT: Tumer, Nilgun B.

TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik

STREET: 600 South Avenue West

CITY: Westfield

STATE: NJ

COUNTRY: USA

ZIP: 07090-1497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

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1      SOFTWARE: PatentIn Release #1.0, Version #1.25
2      CURRENT APPLICATION DATA:
3      APPLICATION NUMBER: US/08/500,611
4      FILING DATE: 11-JUL-1995
5      CLASSIFICATION: 435
6      ATTORNEY/AGENT INFORMATION:
7      NAME: Foley, Shawn P.
8      REFERENCE/DOCKET NUMBER: OCIRS 3.0-034
9      TELECOMMUNICATION INFORMATION:
10     TELEPHONE: 908-654-5000
11     TELEFAX: 908-654-7866
12     TELEX: 139-125
13     INFORMATION FOR SEQ ID NO: 1:
14     SEQUENCE CHARACTERISTICS:
15     LENGTH: 1379 base pairs
16     TYPE: nucleic acid
17     STRANDEDNESS: double
18     TOPOLOGY: linear
19     FEATURE:
20     NAME/KEY: CDS
21     LOCATION: 225..1163
22     FEATURE:
23     NAME/KEY: mutation
24     LOCATION: replace(233, "a")
25     FEATURE:
26     NAME/KEY: mutation
27     LOCATION: replace(349, "g")
28     FEATURE:
29     NAME/KEY: mutation
30     LOCATION: replace(435, "c")
31     US-08-500-611-1

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Query Match	66.9%	Score 632.4	DB 2	Length 1379
Best Local Similarity	80.0%	Pred. No. 3.9e-168		
Matches 757	Conservative 0	Mismatches 186	Indels 3	Gaps 1
QY	3	GAAGTGATGCTTGTAGTTGGTGAAGTTAATGACGTGCTCATGTGCGACCAATCTTC	62	
Db	221	GAAGATGAAGTCATGCTTGTGGTGAACAATATCAATATGCTCATTTTGTGACCAACTTC	280	
QY	63	AACCTTGGCCATAAATACGATCACCTTTGATGCTGGAATGCCACATTAAACAATATGC	122	
Db	281	AACTTGGGCTGTGAATCAATCAATCTCAATGTGGAAAGTACCAACATTAACCAATAGCC	340	
QY	123	CACCTTATGGAATCTCTTGSTATCAAGGAAAGATCCAAATCAATAATGCTATGCGAT	182	
Db	341	CACCTTTCGTATGATCTTGTATGAAAGCAAAAGATCCAAATGTTAAATCTATGGAAT	400	
QY	183	ACCAATGCTACCTGATATCTAATTTGACCCCTAGTACTTATGTGTTAAGTCCAAAGTGC	242	
Db	401	ACCAATGCTGCGCCAAATCAAAATACAAATCCAAATGATAGTGTGAGTCCAAAGTTTC	460	
QY	243	AAACCTTAAAAACCTTACACTAATGCTGAGACGAATATCTTAACTGATGAGGCTATTC	302	
Db	461	AAAAATAAAAAACCACTCACCTAAAGCTGAGACGAACAAATTTGATGTGAAGGGTTATTC	520	
QY	303	TGATCCCTTCGAATGACATAGTGTGCTTACATATATTTAATATATTTACAGACCGCA	362	
Db	521	TGATCCCTTTGAAACCAATTAATGTGTTACCAATCTTTATATATATCTCAGGTACTGCA	580	
QY	363	ACGCACTGATGTGAGAAATACCTTTTGTCTCAAGTTCTAGTTCGTGTGCAATGTCCAT	422	
Db	581	ACGCGAAGATGTAGAGCTACTCTTTTCCCAAAATGCCAAATTCGTGTGTAGTAAAAACAT	640	
QY	423	TAACTACAAATGCTTATATCCGACCATGGAAGAAAGCAAGTAAATCTCAAGAAATCA	482	
Db	641	AAATTTGGAATGTCGATATCCAAATTTGGAATCAAAAGCGGAGATAAATCAAGAGCA	700	
QY	483	AGTCCAAATTTGGAAATTCAAATATCTCAGCAGTGAACATTTGGAAGATTTCTGAGTGTGATTC	542	
Db	701	GGTCCAACTGGGAATTCAAATATCTCAGCAGTAAATTTTGGAAAGATTTCTGAGATGATGTC	760	
QY	543	ATTCCCTGTAAAAACGTAGGCTTTTTTTCTACTGCTAGTACCAATCCAAATGTGTTTCAAGGC	602	

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE: 11-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: 619_peptide
LOCATION: 225..290
US-09-005-273-1

Query Match 66.9%; Score 632.4; DB 3; Length 1379;
Best Local Similarity 80.0%; Pred. No. 3.9e-168;
Matches 757; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

QY 3 GAAGTGATGCTTGTGATGCTGATGCTTGAATAGCGTGGCTCATTCGACCAACTTC 62
DB 221 GAAGATGAAGTCGATCTGTGGTGAACAATATCATATGCGTCACTTGCACCACTTC 280
QY 63 AACTGTGCAATTAATACGATCCTTTGATGCTGGAATGCGACATTAACAAATATGC 122
DB 281 AACTGTGGCTGGAATACATCATCTACATGTTGGAAGTACCACTTAAGCAATATGC 340
QY 123 CACCTTTATGATCTCTTGTATGCAAGCAAGATCCAAACTAAATGCTATGCGAT 182
DB 341 CACTTTTGAATGATCTTGTATGGAAGCAAGATCCAAAGTTAAATGCTATGGAAT 400
QY 183 ACCAATGCTACGATCTAATTCGACCCCTTAAGTCTTATGTTAGCTCCAGGTGC 242
DB 401 ACCAATGCTGCCAATTAACAATCAATCCAAAGTGTGTTGAGCTCCAGGTGC 460
QY 243 AAACCTAAACCATTAACATATGCTGAGAGCAATTAATTAAGTATGGGCTATTC 302
DB 461 AAATTAACCAATCACTAATGCTGAGAGCAATTAATTAATGATGATGATGATTC 520
QY 303 TGAATCCCTTCAATGCAATGATGCTGATCAATATATTAATGATTAACAAGCAAG 362
DB 521 TGAATCCCTTGAACCAATTAATGCTGATCAATATCTTAATGATTAACAAGTATCA 580
QY 363 AGGCACTGATGAGGAATCTTTTGTCTCAAGTCTTATGTTCTGCTGTTGCAATGTCAT 422
DB 581 AGGCAAGATGAGGAATCTTTTGTCTCAAGTCTTATGTTCTGCTGTTGCAATGTCAT 460
QY 423 TAACCTAATGATGATTCGAGCAATGAGAAAGCAAGAGTAACTCAGAAATCA 482
DB 641 AAACCTTGAATGATTCGAGCAATGAGAAAGCAAGAGTAACTCAGAAATCA 700
QY 483 AGTCAATGGAATCAATCAATCACTGAGAGTGAATTTGAAATCTCTGAGTTGATTC 542
DB 701 GGTCCAACTGGGAATCAATCACTGAGAGTGAATTTGAAATCTCTGAGTTGATTC 760
QY 543 ATTCCCTGTAATAAGAGGCTTTTCTGATGTAAGCATCAATGTTTCAAGGC 602
DB 761 ATTCACTGGAATAAGAGGCTTTTCTGATGTAAGCATCAATGTTTCAAGGC 820
QY 603 AGGCGATTCAAGTATAGAGAAAGCAAGTCAAGATTAATTAATGAGCATTTCAACC 662
DB 821 AGCAAGATTCAGTATAGAGAAAGCAAGTCAAGATTAATTAATGAGCATTTCAACC 880

QY 663 TGATCCCAAGTAATTAATTTGGAGAGAGTGGGCAAAATCTGTAGGCAATTCACA 722
DB 881 TATCCCAAGTAATTAATTTGAGAGAGCATGGGTATGATTTCAACGCAATTCATGA 940
QY 723 TGCCAAGATGGGGCTTTACCCAAACCACTTGAAGTATGCAAGTATTCATCTTA 782
DB 941 TGCCAAGATGGGGCTTTACCCAAACCTTGAAGTATGCAAGTATTCATCTTA 1000
QY 783 GATGTTCTTAAGTGAATGAATCAATGATGAGGATGCTTAAGTATGATTAAG 842
DB 1001 GATGTTCTTAAGTGAATGAATCAATGATGAGGATGCTTAAGTATGATTAAG 1060
QY 843 AACTGTGACAACTT--ACCAAAATGCAATGTTCTGCAAGTATTAATTCATCTTA 899
DB 1061 GAGCTGTGACAACTTAAACCAAAATGCAATGTTCTGCAAGTATTAATTCATCTTA 1120
QY 900 TTAATTAATTAATGCTTAATCTTGTGATCTATTTGAAGATTTCA 945
DB 1121 TTAATTAATTAATGCTTAATCTTGTGATCTATTTGAAGATTTCTGA 1166

RESULT 7

PCT-US96-11546-1

Sequence 1, Application PC/TUS9611546
GENERAL INFORMATION:
APPLICANT: Turner, Nilsun E.
TITLE OF INVENTION: DNA Encoding Pokeweed Antiviral Protein
TITLE OF INVENTION: Mutants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE:

CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")

PCT-US96-11546-1

Query Match 66.9%; Score 632.4; DB 6; Length 1379;
Best Local Similarity 80.0%; Pred. No. 3.9e-168;
Matches 757; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

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Qy 3 GAAGGTGATGCTTGTAGTGTGTCGACCTTAATAGCGTGGCTCAATGCTGCACCAACTTC 62
Db 221 GAAGATGAAGTCGATGCTGTGTGTCGACCAATATGATGCTCAATGCTGCACCAACTTC 280
Qy 63 AACTTGTGCTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 122
Db 281 AACTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 340
Qy 123 CACCTTATGGAATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 182
Db 341 CACTTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 400
Qy 183 ACCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 242
Db 401 ACCAATGCTGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 460
Qy 243 AAACCTTAAACCACTTACCTAATGCTGATGATGATGATGATGATGATGATGATGATGATG 302
Db 461 AAATTAACCAACCACTTACCTAATGCTGATGATGATGATGATGATGATGATGATGATGATG 520
Qy 303 TGATCCCTTCAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 362
Db 521 TGATCCCTTGAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 580
Qy 363 ACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 422
Db 581 ACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 640
Qy 423 TAATCTAATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 482
Db 641 AAATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 700
Qy 483 AGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 542
Db 701 GGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 760
Qy 543 ATTCCCTGTAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 602
Db 761 ATTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 820
Qy 603 AGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 662
Db 821 AGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 880
Qy 663 TGATCCCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 722
Db 881 TAATCCCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 940
Qy 723 TGCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 782
Db 941 TGCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1000
Qy 783 GATAGTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 842
Db 1001 GATAGTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1060
Qy 843 AACCTGTCAGACCT---ACCAAAATGCAATGCTCAATGATGATGATGATGATGATGATGATG 899
Db 1061 GAGCTGTCAGACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1120
Qy 900 TTATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 945
Db 1121 TTATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1166
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RESULT 8
US-08-501-253A-1

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Sequence 1, Application US/08501253A
Patent No. 6146628
GENERAL INFORMATION:
APPLICANT: Uckun, Fatih
APPLICANT: Tumer, Nilgun
TITLE OF INVENTION: Biotechnological Agents Comprising
TITLE OF INVENTION: Recombinant PAP and PAP Mutants
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 6146628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: US
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,253A
FILING DATE: 11-JUL-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kettleberger, Denise M.
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 600.323US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
US-08-501-253A-1

Query Match 66.8%; Score 630.8; DB 3; Length 1379;
Best Local Similarity 79.9%; Pred. No. 1.1e-167;
Matches 756; Conservative 0; Mismatches 187; Indels 3; Gaps 1;
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Qy 3 GAAGGTGATGCTTGTAGTGTGTCGACCTTAATAGCGTGGCTCAATGCTGCACCAACTTC 62
Db 221 GAAGATGAAGTCGATGCTGTGTGTCGACCAATATGATGCTCAATGCTGCACCAACTTC 280
Qy 63 AACTTGTGCTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 122
Db 281 AACTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 340
Qy 123 CACCTTATGGAATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 182
Db 341 CACTTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 400
Qy 183 ACCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 242
Db 401 ACCAATGCTGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 460
Qy 243 AAACCTTAAACCACTTACCTAATGCTGATGATGATGATGATGATGATGATGATGATGATG 302
Db 461 AAATTAACCAACCACTTACCTAATGCTGATGATGATGATGATGATGATGATGATGATGATG 520
Qy 303 TGATCCCTTCAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 362
Db 521 TGATCCCTTGAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 580
Qy 363 ACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 422
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Db 581 ACCGCAAGATGAGAGTACTCTTTGCCCAATTCCTGCTTGTAGTAAAAATCAT 640
Qy 423 TAACTACATAGCTTATATCCAGCATGAGAAAAAGAGATAACTCAAGAAATCA 482
Db 641 AAAGTTGATAGTGCATATCCATCTTGATGATCAAAAACGGAGTAAATTCAGAAATCA 700
Qy 483 AGTCCAAATGGGAATTAATCTCAGAGTGCATTTGAAAAATCTCTGGAGTTGATTC 542
Db 701 GGTCCAACTGGGAATTAATCTCAGAGTGCATTTGAAAAATCTCTGGAGTGCATTC 760
Qy 543 ATTCCCTGTAATAAAGTGAAGCTTTTCTTACGTGGCCATCCAAATGGTTTCAGAGGC 602
Db 761 ATTCACTGAGAAAAACCAAGCCAAATTCCTTATGGTACCATACAAATGGTATCAGAGGC 820
Qy 603 AGCGCATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTATAGAGCATTTCAACC 662
Db 821 AGCAAGATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTATAGAGCATTTCAACC 880
Qy 663 TGATCCCAAGTAAATTAATTTGAGAGAAAGTGGGCAAAATCTCTGAGCAATTCACAA 722
Db 881 TAATCCCAAGTAAATTAATTTGAGAGAAAGTGGGCAAAATCTCTGAGCAATTCACAA 940
Qy 723 TGCCAAAGATGGGGCTTTACCAAAACCTTGAGCTGAGAGCCAAAGTACCAAGTG 782
Db 941 TGCCAAAGATGGGGCTTTACCAAAACCTTGAGCTGAGAGCCAAAGTACCAAGTG 1000
Qy 783 GATAGTCTTAGAGTGATGAAATCAATCGTATGTGCACTCCTTAAGTACGTTAATG 842
Db 1001 GATAGTCTTAGAGTGATGAAATCAATCGTATGTGCACTCCTTAAGTACGTTAATG 1060
Qy 843 AACCTGTCAAGCAACTT--ACCAAAATGCCATGTTCTGCAAGTTAATTTCTACTTA 899
Db 1061 GAGCTGTCAAGCAACTTATTAACCAAAATGCCATGTTCTGCAAGTTAATTTCTACTTA 1120
Qy 900 TTATTAATTAATGCTAATCTTGATCTTATTTGAAGATTCCTAA 945
Db 1121 TTATTAATTAATGCTAATCTTGATCTTATTTGAAGATTCCTAA 1166

RESULT 9

US-07-865-169-2
; Sequence 2. Application US/07865169
; Patent No. 6015940
; GENERAL INFORMATION:
; APPLICANT: Turner, Nigun E.
; APPLICANT: Lodge, Jennifer K.
; APPLICANT: Kanlewski, Wojciech K.
; TITLE OF INVENTION: Virus Resistant Potato Plants
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
; STREET: 700 Chesterfield Parkway No. 6015940th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/865,169
; FILING DATE: 19920407
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10547)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1379 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-07-865-169-2

Query Match 66.6%; Score 629.2; DB 3; Length 1379;
Best Local Similarity 79.8%; Pred. No. 3, 1e-167;
Matches 755; Conservative 0; Mismatches 188; Indels 3; Gaps 1;

Qy 3 GAAGTGAAGCTTGTAGTGTGTGACGTTAATAGCGTGTCTATGCTGCACCAATTC 62
Db 221 GAAGTGAAGCTTGTAGTGTGTGACGTTAATAGCGTGTCTATGCTGCACCAATTC 280
Qy 63 AACTTGTCCATTAATTCATGACCTTTGATGCTGGAAATGCCACCTTAACAAATATGC 122
Db 281 AACTTGTCCATTAATTCATGACCTTTGATGCTGGAAATGCCACCTTAACAAATATGC 340
Qy 123 CACCTTTATGAGATCTCTTGATCAAGGAAAGATCCAAATCTAAATGCTATGGCAT 182
Db 341 CACCTTTATGAGATCTCTTGATCAAGGAAAGATCCAAATCTAAATGCTATGGCAT 400
Qy 183 ACCAATGCTACCTGATATCTAATTCAGCCCTTAAGTCTTAATGCTTCAAGGTGC 242
Db 401 ACCAATGCTACCTGATATCTAATTCAGCCCTTAAGTCTTAATGCTTCAAGGTGC 460
Qy 243 AAACCTTAATAACATTAATCAATATGCTGAGACCAATTAATTAATGCTATGGCTATTC 302
Db 461 AAACCTTAATAACATTAATCAATATGCTGAGACCAATTAATTAATGCTATGGCTATTC 520
Qy 303 TGATCCCTTCAATGGAATAGTGTGCTTACCATATATTTAATGATATTAACAAGCCGA 362
Db 521 TGATCCCTTCAATGGAATAGTGTGCTTACCATATATTTAATGATATTAACAAGCCGA 580
Qy 363 AGCGACTGATGTGAGAAATCTTGTCTCAAGTTCTGATGCTGCTGCTGCAATGTCAT 422
Db 581 AGCGACTGATGTGAGAAATCTTGTCTCAAGTTCTGATGCTGCTGCTGCAATGTCAT 640
Qy 423 TAACTACATAGCTTATATCCAGCATGAGAAAAAGAGATAACTCAAGAAATCA 482
Db 641 AAAGTTGATAGTGCATATCCATCTTGATGATCAAAAACGGAGTAAATTCAGAAATCA 700
Qy 483 AGTCCAAATGGGAATTAATCTCAGAGTGCATTTGAAAAATCTCTGGAGTTGATTC 542
Db 701 GGTCCAACTGGGAATTAATCTCAGAGTGCATTTGAAAAATCTCTGGAGTTGATTC 760
Qy 543 ATTCCCTGTAATAAAGTGAAGCTTTTCTTACGTGGCCATCCAAATGGTTTCAGAGGC 602
Db 761 ATTCACTGAGAAAAACCAAGCCAAATTCCTTATGGTACCATACAAATGGTATCAGAGGC 820
Qy 603 AGCGCATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTATAGAGCATTTCAACC 662
Db 821 AGCAAGATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTATAGAGCATTTCAACC 880
Qy 663 TGATCCCAAGTAAATTAATTTGAGAGAAAGTGGGCAAAATCTCTGAGCAATTCACAA 722
Db 881 TAATCCCAAGTAAATTAATTTGAGAGAAAGTGGGCAAAATCTCTGAGCAATTCACAA 940
Qy 723 TGCCAAAGATGGGGCTTTACCAAAACCTTGAGCTGAGAGCCAAAGTACCAAGTG 782
Db 941 TGCCAAAGATGGGGCTTTACCAAAACCTTGAGCTGAGAGCCAAAGTACCAAGTG 1000
Qy 783 GATAGTCTTAGAGTGATGAAATCAATCGTATGTGCACTCCTTAAGTACGTTAATG 842
Db 1001 GATAGTCTTAGAGTGATGAAATCAATCGTATGTGCACTCCTTAAGTACGTTAATG 1060
Qy 843 AACCTGTCAAGCAACTT--ACCAAAATGCCATGTTCTGCAAGTTAATTTCTACTTA 899
Db 1061 GAGCTGTCAAGCAACTTATTAACCAAAATGCCATGTTCTGCAAGTTAATTTCTACTTA 1120
Qy 900 TTATTAATTAATGCTAATCTTGATCTTATTTGAAGATTCCTAA 945


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Query Match	57.5%	Score 543.8	DB 2	Length 918
Best Local Similarity	77.4%	Pred. No. 3.1e-143		
Matches 724, Conservative	0	Mismatches 197	Indels 12	Gaps 4

QY	8	YGAAGCTTGTAGTGTGTGTGACGCTTAATAGCGGTCTCATTTCTGCACCACTTCACATT	67
Db	2	TGAAGTGAATGCTTGTGTGTGACAAATTCAGTATGGCTCATTTCTGCACCAACATCTAATT	61
QY	68	GTGCATAAATPACGATACCTTTGATGCTGGAAATGCCACATTAACAATATGCACTT	12
Db	62	GGGGCGTGAATPACCATCATTTACCATGTTGGAAATGCAACCAATTGAAACATATGCACTT	123
QY	128	TTATGGAATCTCTTCTGTATCAAGCAAGATCCAAACTAAATAGCTATGGCATACCA	18
Db	122	TTGGATAT----CTTCGTACTGAAGGGGAAGATCC--AACTTATGTGTCTATGGAAATCCAA	178
QY	188	TGCTACTGTATCTAATTGCAACCCCTAAGTACTTATGTTGTTAAGTCCAGGTGCAACC	247
Db	176	TGCTGCCCAATATTGGATCAAAATCCAAATATGTTGTTAAGTCTCCAAAGTTCAATG	235
QY	248	TAAAAACATTAACACTAATGCTGAGACGAATTAACCTTAACGTATGGGCTATTTCTGATC	307
Db	236	AAGAGGCACTACACCTATGCTATAGACGAACCAATTTATGTGATGGGCTATTTCTGATC	295
QY	308	CTTTCAATGGCAATTAAGTGTGTTACCATATATTATATATATTAACAACACGACGCA	367
Db	296	CTTACAA---CAATTAAGGTGTGTTTCCATCTCTTTAAGGCTATTCAGGTACTGAACGG	355
QY	368	CTATGTGAGGAATPACTCTTTGTGTCAAGTTCTAAGTCTCGTGTGTGCAATGTCCATTAAT	427
Db	353	AAGATGTAGACATCACTCTTTGCCAAATAGCCGATTCGTGTGTGTTAAAAACATTAATCT	413
QY	428	ACAATAGCTTATATCCGACCATGGAAGAAAGAAAGCAAGATTAATCCAAAGATCAAGTCC	487
Db	413	ATGATGTGCAATATCCAACTTGGATTCAAAAGCAGAGATTAATTCAAGAGTGCAGATCC	472
QY	488	AATTGGGAATTCAAATATCTCAGACGTGCAATTGGAAAAATCTCTGAGTGAATTCATTTCC	547

Db 473 AACTGGGATTGGAATTACTCGACAGTGGCATTGGAGGATTTCTGAGTGAAGTCATTCA 5322

Qy 548 CTGTAAAACTGAGGCTTTTTTTTCTACTGTTAGCCATCCAAATGATTTCAAGGACGCG 6078

Db 533 CTGAGAGAACCGAAGCTGAATTTCTTAAGTGTAGCCATTACAAATGGTATCAGAGGACGCA 5922

Qy 608 GATTCAAGTACATAGAGAACCAAGTCACAGTAAATTTAATATAGAGCATTCCTGATC 6678

Db 593 GATTCAAGTACATAGAGGATCAAGTGAAGAACTAATTTTAAACAGACCATCAACCTTATC 6522

Qy 668 CCAAGTAATTAATTGTGGAGGAGAGTGGGGGCAAAATCTCTAGGCAATTCACAAAGCCA 7272

Db 653 CCAAAAGTACTTAATATTGACGAGAGCATGGGGTAAAGTTTCTTCACGAATTCATGAGCCA 7122

Qy 728 AGAATGGGGCTTTATCCCAAAACCACTTGAGCTAGTGGATGCCAAAGGTATCAAGTGGATAG 7878

Db 713 GGAATGGAGTTTACCCTAATCCTCTACAGCTAGTGCAATGCCAATGGTGCAGAAATGGATAG 7722

Qy 788 TTCTTAGAGTGAATGAATTCATCGTATGTGAGCACTCCTTAAGTACGTTAATGGAACCT 8478

Db 773 TGTTAGAGTGGATGAATTCAGAGCTGAATGTCTCACTCTTAATCTACGTTATGGAGCT 8322

Qy 848 GTGAGCAACTT--ACCAAAATGCCATGTCTCTCAAGTAAATTTCTACTTATTATA 9048

Db 833 GCCAGAGAACTAATACCAAAATGCGATGTTTCTCAACTTAATATGCTACTATTATA 8922

Qy 905 ATTATATGCTAATCTTGAT 927

Db 893 ATTACATGGCTAATCTTGAT 915

RESULT 12
US-08-319-622A-1
Semenza 1 Amplification 116/08319622A

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca insularis Nakai
TISSUE TYPE: leaf
IMMEDIATE SOURCE:
CLONE: PIP
US-08-319-622a-1

Query Match 57.5%; Score 543.8; DB 2; Length 918;
Best Local Similarity 77.4%; Pred. No. 3.1e-143;
Matches 714; Conservative 0; Mismatches 197; Indels 12; Gaps 4;

QY 8 TGAATCTTGTATGTTGGTGTGACGTTAATAGCGTGGCTCATTTGCTGACCAACTTCAACTT 67
DB 2 TGAAGTTGATGCTTGTGTGACAAATACAGTATGGCTCATTTGCTGACCAACTTCAACTT 61
QY 68 GTGCGAATTAATAGATGACCTTGTAGTGTGAAATGCGCAATTAACAATATGCGCACT 127
DB 62 GGGCGGTGAATACATCATCTACAGTGTGAAGTACACCATTAAGAACTATGCAACTT 121
QY 128 TTATGGAATCTCTTGTGATCAAGCGAAAGATCCAAACTAAATGCTATGCAATCA 187
DB 122 TTGGATA---CTTCGTACTGAAAGCGAATCC--AAGTTATGTGTAATGAAATCA 175
QY 188 TGTACCTGATTAATTTGACCCCTAAGTACTTATTTGTTAAGTTCGAAGTGAAC 247
DB 176 TGTGCGCCAAATATGATCAAAATCAAAATATGTTGTTGAGTTCGAAGTTCGAAGT 235
QY 248 TAAAAACATTAATCACTAATGCTGAGAGCAAAATTAATATATGAGTGTGATTTGATC 307
DB 236 AAGAGGCAATCACTAATGCTAAGAGCAAAATTAATATGAGTGTGATTTGATC 295
QY 308 CCTTCATGGCAATTAAGTGTGATCAATATTAATTAATTAATTAATTAATTAATTAAT 367
DB 296 CCGACA---CAATAGTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 352
QY 368 CTGATGTGAGAAATCTTTGCTCAAGTTCTAAGTCTGATTTGATTTGATTTGATTTGAT 427
DB 353 AAGATGTAGAGTACTCTTTGCTCAAGTTCTAAGTCTGATTTGATTTGATTTGATTTGAT 412
QY 428 ACAATAGCTTAATCCGACCATGAGAAAGAAAGCAAGAAATCAAGAAATCAAGTCC 487
DB 413 ATGATGTGAGATCAAAATGGAATCAAAATGGAATGGAATGGAATGGAATGGAATGGA 472
QY 488 AATTGGGAATCAATATCTGAGAGTGAATTTGGAATTTCTGAGAGTGAATTTCAATTC 547
DB 473 AACTGGGAATTCGAATCTGAGAGTGAATTTGGAATTTCTGAGAGTGAATTTCAATTC 532
QY 548 CTGTAATACTGAGGCTTTTCTAAGTGTGACCAATGATTTGAGAGGCAAGCG 607
DB 533 CTGAGAGAACCGAAGCTGAATTTCTAAGTGTGACCAATGATTTGAGAGGCAAGCG 592
QY 608 GATTCAAGTACATGAGAGCAAGTCAAGTCAATTTTAATGAGCAATTTCAATTCGATC 667
DB 593 GATTCAAGTACATGAGAGCAAGTCAAGTCAATTTTAATGAGCAATTTCAATTCGATC 652
QY 668 CCAAACTAATTAATTTGAGAGCAAGTGTGAGGCAAAATCTGAGGCAATTTCAATTCG 727
DB 653 CCAAACTAATTAATTTGAGAGCAAGTGTGAGGCAAAATCTGAGGCAATTTCAATTCG 712
QY 728 AGAATGGGCTTTAATCCCAACCTGAGCTAATGAGTCAAGGTAACCAAGTGAATG 787
DB 713 GGAATGAGTTTAAATCCCAATCTCTAAGCTAATGAGTCAAGTGAATGAGTGAATG 772
QY 788 TTCTTGAAGTGAATCAATGAGTGAATGAGTCAATTTGAGTGAATTTGAGTGAATTT 847
DB 773 TGTGAGAGTGAATCAATGAGTGAATGAGTGAATTTGAGTGAATTTGAGTGAATTT 832
QY 848 GTGAGCAACTT--ACCAAAATGCAATGTTCTCAAGTGAATTAATTTCTAATTAAT 904

DB 833 GCCAGAGACTTATATACCAAAATGCCATGTTTCTCACTTAATATGCTACTTATATA 892
QY 905 ATTAATGCTTAATCTTGTGAT 927
DB 893 ATTAATGCTTAATCTTGTGAT 915

RESULT 13

US-08-471-564-1
Sequence 1, Application US/08471564
Patent No. 5723326
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seoh
APPLICANT: Choi, Kyu-Wan
APPLICANT: Lee, Kwan Ho
APPLICANT: Kim, Man Keun
TITLE OF INVENTION: No. 5723326el Genome Coding Phytolacca Antiviral
TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 THIRD AVE.
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,564
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/210,396
FILING DATE:
APPLICATION NUMBER: US 08/138,636
FILING DATE: 15-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/18818US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca insularis
IMMEDIATE SOURCE:
CLONE: antiviral protein (PIP)
US-08-471-564-1

Query Match 57.5%; Score 543.8; DB 2; Length 918;
Best Local Similarity 77.4%; Pred. No. 3.1e-143;
Matches 714; Conservative 0; Mismatches 197; Indels 12; Gaps 4;

QY 8 TGAATCTTGTATGTTGGTGTGACGTTAATAGCGTGGCTCATTTGCTGACCAACTTCAACTT 67
DB 2 TGAAGTTGATGCTTGTGTGACAAATACAGTATGGCTCATTTGCTGACCAACTTCAACTT 61

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Qy 68 GTGCGATTAATGATCAGCTTGTGATGCTGGAATGCAACCATTAACAATATGCAACCT 127
Db 62 GGGCCGTGATATACATCATCTACCATGTTGGAAAGTACCAACATTAAGAACTATGCAACT 121
Qy 128 TTATGGAATCTCTCTGTAATCAAGCAAAAGATCCAAAATCTAAATGCTATGCAATCCA 187
Db 122 TTGGATA---CTTGTCTACTGAAAGGCGAAGATCC--AGTTATGTCTATGGAATGCA 175
Qy 188 TGTACTGTAATACTAATTAATGCAACCCCTAAGTAATTAATGTTAGTCCAAAGTCAAC 247
Db 176 TGTGCTCCAAATATGATGATCAAAATCAAAATACATATGTTGAGTCTCAAGGTTCAAA 235
Qy 248 TAAAAACATTAACATTAATGCTGAGAAGAAATTAATTAATGATGAGGCTATTCGATC 307
Db 236 AAGAAAGCATCACTAATGCTAAGACGAAACAAATTAATATGATGAGGCTATTCGATC 295
Qy 308 CTTCAATAGGCAATAGTGTCTTACCATTAATTAATTAATGATTAACAAGCAACCAACCA 367
Db 296 CTTACAA---CAATAGGTGTCTGTTCCATCTCTTAAAGGCTATCTCAGGTAACGAA 352
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Qy 428 ACAATAGCTTAATTCGACCATGGAAGAAAGCAAGTAATCTCAAGAAATCAAGTCC 487
Db 413 ATGATGTGATATCAACATTTGGAATCAAAAGCAAGATTAATTAAGAAAGTCAAGTCC 472
Qy 488 AATTGGGAATTCAAATATCTCAGAGTGAACATTTGGAATTAATCTGAGTGAATTC 547
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Db 533 CTGAGAGAAACGAAAGTGAATCTCTGTTGAGTGAACATTTGGAATTAATCTGAGTGAATTC 592
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Db 593 GATTCAGTATCATAGAAACCAAGTGAACATTTAATTTAACAAGATTCATCCCTGATC 652
Qy 668 CCAAGTATTAATTTGGAAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACATGCCA 727
Db 653 CCAAGTATTAATTTGGAAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACATGCCA 712
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Db 833 GCCAAGAACTTAATTAACCAAAATGCGATGTTCTCAACTTAATGATGCTACTTATTA 892
Qy 905 ATTATATGCTATCTTGGTAT 927
Db 893 ATTACATGCTATCTTGGTAT 915

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RESULT 14
US-08-356-161-6
Sequence 6, Application US/08356161
Patent No. 5916772

GENERAL INFORMATION:
APPLICANT: Leppl, Douglas A.
APPLICANT: Barthelemy, Isabel
APPLICANT: Baird, J. Andrew
APPLICANT: Sonowski, Barbara A.
TITLE OF INVENTION: RECOMBINANT PRODUCTION OF
TITLE OF INVENTION: SAPORIN-CONTAINING PROTEINS

```

? NUMBER OF SEQUENCES: 15
? CORRESPONDENCE ADDRESS:
? ADDRESSER: SEED AND BERRY LLP
? STREET: 701 Fifth Avenue, 6300 Columbia Center
? CITY: Seattle
? STATE: WA
? COUNTRY: USA
? ZIP: 98104
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/356,161
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/356,161
? FILING DATE: 13-APR-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: No. 5916772emburg, Carol
? REGISTRATION NUMBER: 39,317
? TELEPHONE: (206) 622-4900
? TELEFAX: (206) 682-6031
? INFORMATION FOR SEO ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 804 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: unknown
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..804
? NAME/KEY: misc feature
? LOCATION: 1..804
? OTHER INFORMATION: /note="Nucleotide sequence
? OTHER INFORMATION: corresponding to the clone M13 mp18-G7 in Example 1.B.2."
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 46..804
? OTHER INFORMATION: /product="Saporin"
? US-08-356-161-6

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Query Match 9.4%; Score 88.4; DB 2; Length 804;
Best Local Similarity 49.3%; Pred. No. 6, 6e-15;
Matches 376; Conservative 0; Mismatches 371; Indels 15; Gaps 5;

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Qy 47 TTGCTGACCACTTCACTTGTGCTAATTAATCAATCACTTGTGATGCTGGAATGCCA 106
Db 20 TTTCAGCTTGGCAACCACTGATGGGCTCACATCAATCACTTAATTAATTAATCCGA 79
Qy 107 CATTAACAAATATGCAACCTTATGGAATCTCTGTAATCAAGGAAAGATCCAAAC 166
Db 80 CCGGGGTCAATCACTCTTTTGTGATTAATCGAAACAACTTAAGATTCAAAC 139
Qy 167 TAAATGCTATGCAATCAATGC--TACCTGATTAATTAATGCAACCCCTAAGTACTAT 223
Db 140 TGAATTAAGGTGTGATCCGACATAGCGGTATGAGCCACCTCTTAAGAAATTCCTTA 199
Qy 224 TGTATAGCTCAAGTGTGAACCTTAATAACATTAACATTAATGCTGAGAGCAATTA 283
Db 200 GAATTAATTTCCAAAGTTC--CCGAGGAACGCTCTCACTTGGCTTAACCCGATTA 256
Qy 284 TATAGTGTGGGCTATCTGATCCCTTCAATGGCAATTAAGTGTGTTACATTAATTTA 343
Db 257 TGTATGTGTGCGGATCTTGTGAATGATTAACAGAAATGTTAATGGGCTATTA 316
Qy 344 ATGATATTAACAAGCAACGAAACGCACTGATGTGGAATTAATCTTTGCTCAAGTCTA 403

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Db 317 GATCAGAAATTACTTCCCGCAGATTACCGCCCTTTTCCAGAGGCCACAACCTGCAATC 376
Qy 404 CTCGTGTGCAATGTCATTAAGTACATTAATATCCAGCCATGAGAAAGAAAGAG 463
Db 377 AGAAGCTTTTGAATACACAGAGATTTTCACTGATGAGAAAGATCCAGATMACAC 436
Qy 464 AAGTA---AACTCAAGAAATCAAGTCCAAATTTGGGAATTCAAATACTGACAGTGA 520
Db 437 AGGAGATTAATCAAGAAAGAAAGAACTCGGCTTGGGATGACCTTACTTTGACGTGAG 496
Qy 521 GAAAAATCTCTGAGCTGATTCATTCCTGTAAAACTGAGGCTTTTCTTACTGTAG 580
Db 497 AAGCAGTGAACAGAA---AGCAGCTGTGTAAAAAGAACTGATGATTCCTTTATCG 553
Qy 581 CCATCCAAATGTTTCAAGAGGACGGGATTCAGTACATAGAGAACCAATCAAGACTA 640
Db 554 CTATTCAGATGACGGCTGAGGACGACGATTTAGTACATCAAAAACCTTGATATCAGA 613
Qy 641 ATTTAATAGACATTTCTACCTGATCCCAAGTAATTAATTTGAGAGAGAGAGGAGCA 700
Db 614 ACTTCCCAACAAGTTCACTCGGAAAAACAAGTCACTTGAAGTTTAACGTGAAAA 673
Qy 701 AAATCTGAGGCAATTCAC---AATGCCAAGAAATGGGCTTTTACCCAAACCACTGAGC 757
Db 674 AAATTTCTACGGCAATATACGGGGATGCCAAAAACGGGCTTTAATTAAGATTATGATT 733
Qy 758 TAGTGATGCCAAGGTACCAAGTGAATGTTCTTAAGTGG 799
Db 734 TCGGCTTGGAAAAGTGAAGGATGAAGACTTGCAAAATGG 775
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RESULT 15

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US-08-356-161-7
; Sequence 7, Application US/08356161
; Patent No. 5916772
; GENERAL INFORMATION:
; APPLICANT: Lappi, Douglas A.
; APPLICANT: Barthelemy, Isabel
; APPLICANT: Baird, J. Andrew
; APPLICANT: Soenowaki, Barbara A.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: SEED and BERRY LLP
; STREET: 701 Fifth Avenue, 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,161
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/356,161
; FILING DATE: 13-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5916772 Leuburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 760100, 404US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 804 base pairs
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..804
NAME/KEY: misc feature
LOCATION: 1..804
OTHER INFORMATION: /note= "Nucleotide sequence
OTHER INFORMATION: corresponding to the clone M13 mp18-69 in Example 1.B.2."
FEATURE:
NAME/KEY: mac peptide
LOCATION: 46..804
OTHER INFORMATION: /product= "Saporin"
US-08-356-161-7
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Query Match 9.4%; Score 88.4; DB 2; Length 804;
Best Local Similarity 49.3%; Pred. No. 6.6e-15;
Matches 376; Conservative 0; Mismatches 371; Indels 15; Gaps 5;

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Qy 47 TTGCTGACCAACTTCACTTGTGCCATTAATACATCACCTTGTGATGCTGAATGCA 106
Db 20 TTTCAGCTTGAACAACATGATGCGGTCAATCAATCACTTAATGATCTAATATCCGA 79
Qy 107 CCATTAACAATATGCACTTTATGGAATCTCTGTAATCAAGCGAAGATCCAAAC 166
Db 80 CCGGGGTCAATCTCATCTTTGTGATTAATCCGAAACACGTAAGATCCAAAC 139
Qy 167 TAAATGCTATGCGATACCAATGC---TACCTGATCAATTAATGCAACCCCTAATGAT 223
Db 140 TGAATATCGGTGTATCCGACATAGCGGTATAGGCCACCTTTAAAGAAATTCCTTA 199
Qy 224 TGGTTAGCTCAAGGTGCAAACTTAATAACATTAACATTAATGCTGAGAGCAATTA 283
Db 200 GAATTAATTTCCAAAGTTC---CCAGAGACGGTCTCACTTGGCTTAAGCGGATTA 256
Qy 284 TATACGATGCGGTATTTCTGATCCCTTCAATGCAATTAAGTGTCTTACATATATTA 343
Db 257 TGTATGTGTCGGGTATCTTGTGCAATGATTAACGAAATGTAATCGGGCATATTA 316
Qy 344 ATGATATTACAAGACCGAAGCACTGATGAGAAATCACTTTGTCAAGTTCTAGTT 403
Db 317 GATCAGAAATTAATCTTCGCGCAAGTTAACGCCCTTTTCCAGAGGCCACAACCTGA 376
Qy 404 CTCGTGTGCAATGTCATTAATTAATTAATTAATCCAGCAGTGAAGAAAGAGCAG 463
Db 377 AGAAGCTTTAAGATACACAGAGATTAATCAATGATGATGAAGAAAGATGCCAGTAA 436
Qy 464 AAGTAATCTCA---AGAAATCAAGTCCAAATTTGGAATTCAAATACTGACAGTGA 520
Db 437 AAGAGATCAAAAGTGAAGAAAGAACTCGGCTTGGGATGATCACTTCAACCTCAATG 496
Qy 521 GAAAAATCTCTGAGTGTGATTCATTCCTGTAAAACTGAGGCTTTTCTTCTACTGTAG 580
Db 497 AAGCAGTGAACAGAA---AGCAGCTGTGTAAAAAGAACTGATGATTCCTTTATCG 553
Qy 581 CCATCCAAATGTTTCAAGAGGACGGGATTCAGTACATAGAGAACCAATCAAGACTA 640
Db 554 CTATTCAGATGACGGCTGAGGACGCGGATTTAGTACATCAAAAACCTTGATATCAGA 613
Qy 641 ATTTAATAGACATTTCTACCTGATCCCAAGTAATTAATTTGAGAGAGAGTGGGCA 700
Db 614 ACTTCCCAACAAGTTCACTCGGAAAAACAAGTGAATCAAGTTGAGGTTAATCGAAAA 673
Qy 701 AAATCTGAGGCAATTCAC---AATGCCAAGAAATGGGCTTTTACCAACAACCACTGAGC 757
Db 674 AAATTTCTACGGCAATATACGGGGATGCCAAAAACGGCTTTAATTAAGATTATGATT 733
Qy 758 TAGTGATGCCAAGGTACCAAGTGAATGTTCTTAAGTGG 799
Db 734 TCGGCTTGGAAAAGTGAAGGATGAAGACTTGCAAAATGG 775
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Mon Apr 10 07:26:45 2006

us-09-978-274a-1.rn1

Page 14

Search completed: April 8, 2006, 09:49:00
Job time : 331.047 secs

QY 301 TCTGATCCCTTCAATGAGCATATAGTTCGTACCATATATTTATGATATATACAGACACC 360
DB 301 TCTGATCCCTTCAATGAGCATATAGTTCGTACCATATATTTATGATATATACAGACACC 360
QY 361 GAACGCACTGATGTGGAGAACTCTTTTGTCTCAAGTTCTAGTTCTGCTGTGGATGTCC 420
DB 361 GAACGCACTGATGTGGAGAACTCTTTTGTCTCAAGTTCTAGTTCTGCTGTGGATGTCC 420
QY 421 ATTAATCAATAGTCTTATATCCGACCATGAGAAAGAGAGAGAACTGAAGTAACTGAAGAA 480
DB 421 ATTAATCAATAGTCTTATATCCGACCATGAGAAAGAGAGAGAACTGAAGTAACTGAAGAA 480
QY 481 CAAGTCAATTTGGAAATTCATAATCTCAGCAGTGAATTTGGAAAAATCTCTGGAGTTGAT 540
DB 481 CAAGTCAATTTGGAAATTCATAATCTCAGCAGTGAATTTGGAAAAATCTCTGGAGTTGAT 540
QY 541 TCATTTCCCTGTAAAACTGAGGCTTTTTTTCTACTGTGTAGCCATCCAAATGTTTCAAG 600
DB 541 TCATTTCCCTGTAAAACTGAGGCTTTTTTTCTACTGTGTAGCCATCCAAATGTTTCAAG 600
QY 601 GGAAGCGAGTTCAATGATAGAGAACCAAGTCAAGCTTAATTTATAGAGATCTAC 660
DB 601 GGAAGCGAGTTCAATGATAGAGAACCAAGTCAAGCTTAATTTATAGAGATCTAC 660
QY 661 CCTGATCCCAAGTAATTAATTTGAGAGAGAGTGGGCAAAATCTCTGAGCAATTCAC 720
DB 661 CCTGATCCCAAGTAATTAATTTGAGAGAGAGTGGGCAAAATCTCTGAGCAATTCAC 720
QY 721 AATGCCAAGATGGGGCTTTTACCCAACCACTTGAGCTAGTGAATGCCAAAGTACCAAG 780
DB 721 AATGCCAAGATGGGGCTTTTACCCAACCACTTGAGCTAGTGAATGCCAAAGTACCAAG 780
QY 781 TGGATAGTTCTTGAAGTGAATCAATCGTATGTGSCACTCCCTTAAGTACGTTAAT 840
DB 781 TGGATAGTTCTTGAAGTGAATCAATCGTATGTGSCACTCCCTTAAGTACGTTAAT 840
QY 841 GGAACCTGTCAAGCACTTAACCAAAATGCCATGTTCTCTCAAGTTAATTTTACTTAT 900
DB 841 GGAACCTGTCAAGCACTTAACCAAAATGCCATGTTCTCTCAAGTTAATTTTACTTAT 900
QY 901 TATTAATTAATGCTTAATCTGTGATCTATTTGAAGATCTTAA 945
DB 901 TATTAATTAATGCTTAATCTGTGATCTATTTGAAGATCTTAA 945

RESULT 2

US-09-978-274A-3
Sequence 3, Application US/0978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patent version 3.1
SEQ ID NO 3
LENGTH: 792
TYPE: DNA
ORGANISM: Phytolacca americana
US-09-978-274A-3

Query Match 83.2%; Score 786.4; DB 3; Length 792;
Best Local Similarity 99.9%; Pred. No. 4,7e-211;
Matches 787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 73 ATAAATACATGACCTTTGATGCTGGAATGCGACCATTAACAAATATGCACTTTATG 132
DB 4 ATAAATACATGACCTTTGATGCTGGAATGCGACCATTAACAAATATGCACTTTATG 63
QY 133 GAATCTCTTCTGATATACAGGAAGATCCAAACTTAAATGCTATGTGCATACCAATGCTA 192
DB 64 GAATCTCTTCTGATATACAGGAAGATCCAAACTTAAATGCTATGTGCATACCAATGCTA 123
QY 193 CCTGATACATTAATTCGACCCCTTAAGTACTTATTTGTTAGCTCCAAAGTCAAACTTAAA 252
DB 124 CCTGATACATTAATTCGACCCCTTAAGTACTTATTTGTTAGCTCCAAAGTCAAACTTAAA 183
QY 253 ACCATTACATTAATGCTGAGAGCAATTAATTAATGATAGGCTATTTCTGATCCCTTC 312
DB 184 ACCATTACATTAATGCTGAGAGCAATTAATTAATGATAGGCTATTTCTGATCCCTTC 243
QY 313 AATGGCAATTAATGCTGATACCAATATTTAATGATATTAACAAGCAGCAAGCACTGAT 372
DB 244 AATGGCAATTAATGCTGATACCAATATTTAATGATATTAACAAGCAGCAAGCACTGAT 303
QY 373 GTGGAAATATCTTTGCTCAAGTTCTAGTTCTCGTGTGCAATGTCATTAATTAATCAAT 432
DB 304 GTGGAAATATCTTTGCTCAAGTTCTAGTTCTCGTGTGCAATGTCATTAATTAATCAAT 363
QY 433 AGCTATATCCGACCATGAGAAAGAGAGCAAGTAATCTCAAGAAATCAAGTCAATG 492
DB 364 AGCTATATCCGACCATGAGAAAGAGAGCAAGTAATCTCAAGAAATCAAGTCAATG 423
QY 493 GGAATTCAAATATCTCAGCATGATCATTTGGAATAATCTCTGAGTGTATTCATTTCCCTGTA 552
DB 424 GGAATTCAAATATCTCAGCATGATCATTTGGAATAATCTCTGAGTGTATTCATTTCCCTGTA 483
QY 553 AAAATGAGGCTTTTTTTTCTACTGTGAGCATCCAAATGTTTCAAGAGCAGGCGCATTC 612
DB 484 AAAATGAGGCTTTTTTTTCTACTGTGAGCATCCAAATGTTTCAAGAGCAGGCGCATTC 543
QY 613 AAGTACATAGAGAACCAAGTCAAGTAATTTAATAGCATTTCTACCTGATCCCAAA 672
DB 544 AAGTACATAGAGAACCAAGTCAAGTAATTTAATAGCATTTCTACCTGATCCCAAA 603
QY 673 GTAATTAATTTGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCCAAGAT 732
DB 604 GTAATTAATTTGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCCAAGAT 663
QY 733 GGGGCTTTACCCAAACCACTTGAGTATGATGCAAAAGTACCAAGTGAATGTTCTT 792
DB 664 GGGGCTTTACCCAAACCACTTGAGTATGATGCAAAAGTACCAAGTGAATGTTCTT 723
QY 793 AGAGTGAATGAATCAATGATGATGAGCACTCTTAATGATGATGAACCTGTGAG 852
DB 724 AGAGTGAATGAATCAATGATGATGAGCACTCTTAATGATGATGAACCTGTGAG 783
QY 853 ACAACTTA 860
DB 784 ACAACTTA 791

RESULT 3

US-09-978-274A-19
Sequence 19, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32

Db 1001 GAATGCTTGAAGTGTGATGAATCAAGCTGTGATGCACTCTTAACATCACTGTGTG 1060
Qy 843 AACCTGTGAGACAACTT---ACCAAAATGCGATGTTCTCAAGTTATATTTCTCTTA 899
Db 1061 GAGCTGTGACAACTTATATACCAAAATGCGATGTTCTCTCAAGTTATATTTCTCTTA 1120
Qy 900 TTATAATTATATGTCTAATCTGTGTGATCTTATTTGAAGATCTTAA 945
Db 1121 TTATAATTATATGTCTAATCTGTGTGATCTTATTTGAAGATCTTGA 1166

RESULT 5
US-11-106-187-1
; Sequence 1, Application US/11106187
; Publication No. US20050183162A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NILGUN E.
; APPLICANT: WANG, PINGER
; TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
; FILE REFERENCE: OCIRS 3.9-060 CONT
; CURRENT APPLICATION NUMBER: US/11/106,187
; CURRENT FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US/09/721,047
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: PCT/US99/11301
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/086,374
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: *Phytolacca americana*
; NAME/KEY: CDS
; LOCATION: (225)..(1163)
US-11-106-187-1

Query Match 66.9%; Score 632.4; DB 10; Length 1379;
Best Local Similarity 80.0%; Pred. No. 1.9e-167;
Matches 757; Conservative 0; Mismatches 186; Indels 3; Gaps 1;
Qy 3 GAAAGTATGCTTGTAGTGTGTGACGTTAATAGCGTGCCTATGCTGACCAACTTC 62
Db 221 GAATGATGAGTGTGATGCTGTGTGACAAATATGCTCATTTCTGACCAACTTC 280
Qy 63 AACTTGTGCATTAATATGATCACTTTGATGCTGGAATGCAACATTAACAATATGC 122
Db 281 AACTTGTGTGATTAATATGATCACTTTGATGCTGGAATGCAACATTAACAATATGC 340
Qy 123 CACCTTTATGGAATCTCTTGTATCAAGGAAAGATCCAAACTAAATGCTATGCGAT 182
Db 341 CACTTTTCTGAATGATCTTGTATGAGGAAAGATCCAAACTAAATGCTATGCGAT 400
Qy 183 ACCAATGCTACTGATATTAATTCGACCCCTAAGTACTTATGCTTAAAGTCCAAAGTGC 242
Db 401 ACCAATGCTGCCAATTAATTAATCAATCAATCAAGTACGTTGAGTCCAAAGTGC 460
Qy 243 AAAACCTAAACCAATTAATGCTGAGAGCAAAATTAATTAAGTATGAGGCTATTC 302
Db 461 AAATTAATTAATTAATTAATGCTGAGAGCAAAATTAATTAAGTATGAGGCTATTC 520
Qy 303 TGATCCCTTCAATGGAATATGATGCTTATCAATATTAATGATATTAACAAGCCGA 362
Db 521 TGATCCCTTGAACCAATTAATGCTTATCAATATTAATGATATTAACAAGTATCA 580
Qy 363 AGCACTGATGAGGAATATCTTGTGCTCAAGTTCTAGTCTGCTGCTCAATGCTATTC 422
Db 581 AGCCCAAGATGATGAGATCTCTTGTGCTCAAGTTCTAGTCTGCTGCTCAATGCTATTC 640
Qy 423 TAACTTAATATGCTTATATTCGACATGAGAAAGAAAGCAAGATTAATCTCAAGAAATCA 482

Db 641 AAACCTTTATGATGATATTCACCAATTTGAATTCAAAAGGGAGTAAATCAAGAAATCA 700
Qy 483 AGTCCAAATGGGAATTAATTAATCTGACAGTGAATTTGAAAAATCTGCAAGTATTC 542
Db 701 GGTCCAACTGGGAATTAATTAATCTGACAGTGAATTTGAAAAATCTGCAAGTATTC 760
Qy 543 ATTCCCTTAATTAATTAATGAGGCTTTTCTTACTGATGAGCAATCAATGATTTCAAGGC 602
Db 761 ATTCACTGAGAAAACCGAAGCCGAATTTCTTATTTGATGAGCAATCAATGATTTCAAGGC 820
Qy 603 AGCCGATTCAGTATGATGAGAACCAAGTCAAGTAAATTTAATGAGCAATTCACCC 662
Db 821 AGCAAGATTCAGTATGATGAGAACCAAGTCAAGTAAATTTAATGAGCAATTCACCC 880
Qy 663 TGATCCCAAGTAAATTAATTTGAGGAGAGGAGGCAAAATCTCGAAGCAATTCACA 722
Db 881 TAATCCCAAGTAAATTAATTTGAGGAGAGGAGGCAAAATCTCGAAGCAATTCACA 940
Qy 723 TGCCAAAGATGGGCTTTTACCACCACTGAGTATGATGCAAGGATCAAGTATTC 782
Db 941 TGCCAAAGATGGGCTTTTACCACCACTGAGTATGATGCAAGGATCAAGTATTC 1000
Qy 783 GATAGTCTTATGATGATGAGAAATCAATGATGATGCACTCTTAAGTATGATG 842
Db 1001 GATAGTGTGAGATGATGAGAAATCAAGCTGATGATGCACTCTTAAGTATGATG 1060
Qy 843 AACCTGTGAGACAACTT---ACCAAAATGCGATGTTCTCAAGTTATATTTCTCTTA 899
Db 1061 GAGCTGTGACAACTTATATACCAAAATGCGATGTTCTCTCAAGTTATATTTCTCTTA 1120
Qy 900 TTATAATTATATGTCTAATCTGTGTGATCTTATTTGAAGATCTTAA 945
Db 1121 TTATAATTATATGTCTAATCTGTGTGATCTTATTTGAAGATCTTGA 1166

RESULT 6
US-09-978-274A-31
; Sequence 31, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: *Phytolacca americana*
US-09-978-274A-31

Query Match 66.6%; Score 629.2; DB 3; Length 1368;
Best Local Similarity 79.8%; Pred. No. 1.5e-166;
Matches 755; Conservative 0; Mismatches 188; Indels 3; Gaps 1;
Qy 3 GAAAGTATGCTTGTAGTGTGTGACGTTAATAGCGTGCCTATGCTGACCAACTTC 62
Db 221 GAATGATGAGTCAATGCTTGTGTGACAAATATGATGCTCATTTCTGACCAACTTC 280
Qy 63 AACTTGTGCATTAATATGATCACTTTGATGCTGGAATGCAACATTAACAATATGC 122
Db 281 AACTTGTGTGATTAATATGATCACTTTGATGCTGGAATGCAACATTAACAATATGC 340
Qy 123 CACCTTTATGGAATCTCTTGTATCAAGGAAAGATCCAAACTAAATGCTATGCGAT 182

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Db      341 CACTTTTGGAGTATGCTGTATGAGAGGAAAGATCAAGTTAAATGCTATGAAAT 400
Qy      183 ACCAATGCTACGTATCTATTTGACCCCTTAATCTATTTGTTAAAGTCCAGGTGC 242
Db      401 ACCAATGCTGCGCAATCAATATCAATATCCAAAGCAGTGTGTGATGCTCAAGGTTC 460
Qy      243 AAAAATAAAAAACATTAACATTAATGCTGAGAGCAAAATTAATTAACGTTAGGCTATTC 302
Db      461 AAAATAAAAAACATTAACATTAATGCTGAGAGCAAAATTAATTAATGTTATGTTATTC 520
Qy      303 TGATCCCTTCAATGCGCAATATGCTGTACATATATTTATATATATCAACAGCAGCA 362
Db      521 TGATCCCTTCAATGCGCAATATGCTGTACATATATTTATATATATCAACAGCAGCA 580
Qy      363 ACCGACTGATGAGAGATCTCTTGTCTCAAGTTCTGATGCTGTGCAATGTCAT 422
Db      581 ACCGCAAGATGTAGATCTCTTGTCTGCAATGCTGCAATGCTGTGATGTTAAATCAT 640
Qy      423 TAACTCAATAGCTTATATCCGACCATGAGAAAGAAAGCAAGATTAATCAAGAAATCA 482
Db      641 AAATCTTGATATGATATCAATCAATGATGAAATCAAAAGCGGAGATTAATCAAGATCA 700
Qy      483 AGTCCAAATGGGAATTAATTAATCTGAGAGTGAATGGAATTAATCTGAGAGTTGATC 542
Db      701 GGTCCAACTGGGAATTAATTAATCTGAGAGTGAATGGAATTAATCTGAGAGTTGATC 760
Qy      543 ATTCCCTGTAATAATGAGGCTTTTCTTCTGATGCTGCAATGCTGCAAGGC 602
Db      761 ATTCACTGAGAAACCGAAGCCGAAATCTTATGATGCTGCAATGCTGCAAGGC 820
Qy      603 AGGCGAATTCAGATACATAGAGAAACCAAGTCAAGATTAATTAATGAGATTCATCC 662
Db      821 AGCAAGATTCAGATACATAGAGAAACCAAGTCAAGATTAATTAATGAGATTCATCC 880
Qy      663 TGATCCCAAGTATTAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 722
Db      881 TAATCCCAAGTATTAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 940
Qy      723 TGCAGAAATGGGGCTTACCAACCACTTGAGCTGATGAGTCCAAAGTACCAAGT 782
Db      941 TGCAGAAATGGGGCTTACCAACCACTTGAGCTGATGAGTCCAAAGTACCAAGT 1000
Qy      783 GATAGTCTTGAAGTGAATTAATCAATGCTGATGAGTCCCTTAATGATGATTAATG 842
Db      1001 GATAGTCTTGAAGTGAATTAATCAATGCTGATGAGTCCCTTAATGATGATTAATG 1060
Qy      843 AACCTGTGAGACAATTT--ACCAAAATGCGATGCTCTCAAGTTAAATTTCTACTTA 899
Db      1061 GACCTGTGAGACAATTTAAACCAAAATGCGATGCTCTCAACTTAAATGCTACTTA 1120
Qy      900 TTATTAATTAATGCTTAATCTGATGATGATGATGATGATGATGATGATGATGAT 945
Db      1121 TTATTAATTAATGCTTAATCTGATGATGATGATGATGATGATGATGATGATGAT 1166

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RESULT 7

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US-10-467-009-1
; Sequence 1, Application US/10467009
; Publication No. US20040241673A1
; GENERAL INFORMATION:
; APPLICANT: RUTGERS, THE STATE UNIVERSITY
; TITLE OF INVENTION: NON-CYTOTOXIC PAP MUTANTS
; FILE REFERENCE: OCIRS 3 4-076
; CURRENT APPLICATION NUMBER: US/10/467, 009
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: 60/266,396
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: Phytolacca americana

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (225) .. (1160)
US-10-467-009-1
Query Match      65.4%; Score 618; DB 8; Length 1376;
Best Local Similarity 79.8%; Pred. No. 2.2e-163;
Matches 755; Conservative 0; Mismatches 185; Indels 6; Gaps 2;
Qy      3 GAAAGTATGCTGTTGATGTTGCTGATGATGATGATGATGATGATGATGATGATG 62
Db      221 GAAAGTATGCTGATGTTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 280
Qy      63 AACCTGTGAGACAATTTAAACCAATGCTCTCAAGTTAAATTTCTACTTA 122
Db      281 AACCTGTGAGACAATTTAAACCAATGCTCTCAAGTTAAATTTCTACTTA 340
Qy      123 CACCTTATGGAATCTCTGATATCAAGGAAAGATCCAAATTAATGCTATGAGCAT 182
Db      341 CACTTTTCTGAATGATCTTGTATGAGGAAAGATCCAAATTAATGCTATGAGCAT 400
Qy      183 ACCAATGCTACGTATATTAATTCACCCCTTAAGTCTTATGTTAAGTCCAGGTGC 242
Db      401 ACCAATGCTGCGCAATCAATTAATCAATCCAAAGTACGTGTGTTGAGCTCCAGGTTC 460
Qy      243 AAACTTAATAACCAATTAATCAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 302
Db      461 AAATTAATAATAACCAATTAATCAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 520
Qy      303 TGATCCCTTCAATGGAATTAAGTGTGCTTACATATATTAATTAATTAATTAATTAATCA 362
Db      521 TGATCCCTTCAATGGAATTAAGTGTGCTTACATATATTAATTAATTAATTAATTAATCA 580
Qy      363 AGCACTGATGAGAGATTAATCTTGTGCTCAAGTTCTAGTTCTGTTGCAATGTCAT 422
Db      581 ACCGCAAGATGATGAGAGATTAATCTTGTGCTCAAGTTCTAGTTCTGTTGCAATGTCAT 637
Qy      423 TAATCCCAAGTATTAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 482
Db      638 AAATCTTGAATGATGATATCAATGATGATGATGATGATGATGATGATGATGATGAT 697
Qy      483 AGTCCAAATGGGAATTAATTAATCTCAAGTGAATTTGAGAGAGAGAGAGAGAGAGAGAG 542
Db      698 GGTCCAACTGGGAATTAATTAATCTCAAGTGAATTTGAGAGAGAGAGAGAGAGAGAGAG 757
Qy      543 ATTCCCTGTAATAATGAGGCTTTTCTTCTACTGATGAGTCCAAATGCTTCAAGGC 602
Db      758 ATTCACTGAGAAACCGAAGCCGAATTCCTATGATGAGTCCAAATGCTTCAAGGC 817
Qy      603 AGGCGAATTCAGATACATAGAGAAACCAAGTCAAGATTAATTAATGAGATTCATCC 662
Db      818 AGCAAGATTCAGATACATAGAGAAACCAAGTCAAGATTAATTAATGAGATTCATCC 877
Qy      663 TGATCCCAAGTATTAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 722
Db      878 TAATCCCAAGTATTAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 937
Qy      723 TGCAGAAATGGGGCTTACCAACCACTTGAGCTGATGAGTCCAAAGTACCAAGT 782
Db      938 TGCAGAAATGGGGCTTACCAACCACTTGAGCTGATGAGTCCAAAGTACCAAGT 997
Qy      783 GATAGTCTTGAAGTGAATTAATCAATGCTGATGAGTCCCTTAATGATGATTAATG 842
Db      998 GATAGTCTTGAAGTGAATTAATCAATGCTGATGAGTCCCTTAATGATGATTAATG 1057
Qy      843 AACCTGTGAGACAATTT--ACCAAAATGCGATGCTCTCAAGTTAAATTTCTACTTA 899
Db      1058 GACCTGTGAGACAATTTAAACCAAAATGCGATGCTCTCAACTTAAATGCTACTTA 1117
Qy      900 TTATTAATTAATGCTTAATCTGATGATGATGATGATGATGATGATGATGATGAT 945
Db      1118 TTATTAATTAATGCTTAATCTGATGATGATGATGATGATGATGATGATGATGAT 1163

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D	67	GGTTCTTCAAAACATA-----GTTTGAAGTTGAAGATGCAACACGAAGAACTTAC	117
Q	121	GGCACCCTTATGGAATCTCTTGATATCAAGCAAAAGATCCAAACTAAATGCTATGGC	180
D	118	TCTAATTTTCTACTAGTTTGGAGGAAGCTGTGTAAGACAAAGAAATTGACATGCAATGA	177
Q	181	ATACCAATGCTACTGATATCTAATTTGACCCCTTAAGTACTATTTGGTTAAAGTCCAAAGT	240
D	178	ATGATATATGCGCAACACCTCTACTGAACCAACCAATATGTGTGGTTGACTCTCAATTC	237
Q	241	GCAAACCTTAAAAACATTAACACTATATGCTGAGCGAATTAATCTTATATCGTATGGCTAT	300
D	238	GGATCTGAAACATTC---ACATTAGCAATCAGAGGGGAAACTTATATTGGAGGCTAT	294
Q	301	TCTGATCCCTTAAATGGCAATAGTGTCTTACATATATTTAATATATATTAACAGACC	360
D	295	TCTGACATTTACAAATGG---AAAATGTGTATTCGATCTTCAAGAT-----	339
Q	361	GAACGCACTGATGTGAGATATCTCTTGTCTCAAGTTCTAGTCTGTGTGCAATGCC	420
D	340	TCAGAAATCGAATGCCAAGACAGACCGTTTCCCGGGGACAAAAGCAAGCTGGCACTCAG	399
Q	421	ATTAACTACAAATAGCTTATATCCGACATGGAAGAAAGAAAGCAGAGTAACTCAAGAAAT	480
D	400	AATATATATCCCTATGAAGAAAGATTACAAAGGATGAAATCAAAAGGTGGGCTAGAACT	459
Q	481	CAAGTCCAATTTGGGAATCAAAATCTCAGCAGTGAATTTGGAAGAAATCTCTGAGTTGAT	540
D	460	AAATTATGGGTTAGGAAGATTAACCTCAGAGATCGAATGGTAAATCTACGCGCAAGAT	519
Q	541	TCA-----TTCCCTGTAAAACTGAAGGCTTTTCTTACTGTGAGCCATCCA	588
D	520	GCAACGCAATCAGAGCAGATCAAAAAATGAGGCTGAATTTCTTATATGCGCTTCAA	579
Q	589	ATGGTTTCAAGAGCGCGGATTCAGTACATAGACAAACCAAGTCAAGCTAATTTTAAT	648
D	580	ATGGTTACTGAGGCAATCAAGTTCAAAATCAATGGAACAAGGTGAAGCTTAATTTGAT	639
Q	649	-----AGAGCAATCTACCCCTGATCCCAAGTAAATTAATTTGGAGAGAAAGTGGGCAAA	702
D	640	GATGCAATGGGTATCAGCCAGATCCTTAAGCATTTCCCTAGAGAAAAATTGGACAGT	699
Q	703	ATCTCTGAGGCAATTCAAATGCCAAGATGGGGCTTTAACCCAAACACTTGAGCTAGTG	762
D	700	GTTTCTTAAGTCAATTCCAAAAGTTGGCACCTCCGGTGAATGATCTGTTACTTTAACCTTGA	759
Q	763	GATGCCAAGGTAAACCAAGGATAGTGTCTTAGAGTGATGAATCAATGTATATGAGCA	822
D	760	GACCTTAAAGATGAGATATATAACTTTGACCTAGCGCCACATGAACGACTTAAAGAAC	819
Q	823	CTCCTTAAGTACGTTAATGGAACCTGTGACAGCAACTTACCAAAATGCCAATGTTCTTCAA	882
D	820	GACATTTATGCGACTCTTAAACCAAGCTTACTTGCAAGGTTAAAAAGTTCCATGTTCCCTGAA	879
Q	883	GTTAATATTTCTACTATTTAATATATATATGCTAATCTTGGTGA	926
D	880	ATTATGTCTATTTATTAAGACTGATATTAAGTAACTTGGTGA	923

RESULT 11
 US-11-106-187-3
 ; Sequence 3, Application US/11106187
 ; Publication No. US20050183162A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TURNER, NILGUN B.
 ; APPLICANT: WAND, PINGRAN
 ; TITLE OF INVENTION: TRANSGENIC PLANTS PRO-
 ; FILE REFERENCE: OCSRS 3.9-060 CONT
 ; CURRENT APPLICATION NUMBER: US/11/106,187
 ; CURRENT FILING DATE: 2005-04-11
 ; PRIOR APPLICATION NUMBER: US/09/721,047
 ; PRIOR FILING DATE: 2000-11-22
 ; PRIOR APPLICATION NUMBER: PCT/US99/11301

```

? PRIOR FILING DATE: 1999-05-21
? PRIOR APPLICATION NUMBER: 60/086,374
? PRIOR FILING DATE: 1998-05-22
? NUMBER OF SEQ ID NOS: 21
? SOFTWARE: PatentIn Ver. 3.3
? SEQ ID NO 3
? LENGTH: 934
? TYPE: DNA
? ORGANISM: Phytolacca americana
? FEATURE:
? NAME/KEY: sig_peptide
? LOCATION: (1)..(75)
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: (76)..(930)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(930)
US-11-106-187-3

```

Query Match	11.7%	Score 110.8	DB 10	Length 934
Best Local Similarity	50.0%	Pred. No. 3e-20		
Matches 472; Conservative	0	Mismatches 427	Indels 45	Gaps 67

Qy	1	ATGAAGGAGTACCTGGTAGTTGTTGGTGAACGGTAAATAGGGGCTCATTTGCTGCACAACT	60
Db	7	ATGAAGGAGTGAAGAGTAGTTGGTTGGTGCATATGCATATGGCTGAATGCTTAACACCA	66
Qy	61	TCAACTGTGGCCATTAATACGATACCTTTGATGCTGGAATGCCACCATTTACAAATAT	120
Db	67	GCTTCTTCAAAAGATA-----GTGTTTGAAGCTTAGAATGCAACCAAGAAACCTAC	117
Qy	121	GCCACCTTTATGGAATCTTTCGTATCAAGCGAAGATCCAAACTTAAATGCTATGGC	180
Db	118	TCTAATTTTCTGACTAGTTTGGCGAAGACTGTGTAAGACAAAGAAATTTGACATGCGATGSA	177
Qy	181	ATTACCAATGCACTGATTAATTAATTCGACCCCTTAAGTACTTAATTTGTTAAGTCCAAAGT	240
Db	178	ATGATTAATGGCCACACCTTCACTGAACCAACCCAGATGATGTTGTTGACTCAAAATTC	237
Qy	241	GCAAACTTAAAAACCATTAACATAATGCTGAGACGAATTAATTAATACGTATGGGCTAT	300
Db	238	GGATCTGGAACTTC---ACATTAGCAATCAGAAAGGGAACTTAATTTTGAGAGGCTAT	294
Qy	301	TCTGATCCCTTCAATGGCAATAAGTGTGTTACCAATTAATTTAATTAATTAACAAGACC	360
Db	295	TCTGACATTTACAATGG---AAATGTGTTATTCGATCTTCAAGAT-----	339
Qy	361	GAAGCGACTGATGTGGAGATTACTCTTTGCTCAAGTTCTAGTTTCTGGTGTGCATATGC	420
Db	340	TCGAAATCCGATGCCCAAGAGACCGTTTGGCCCGGGGACAAAGCAAGCCCTGGACCTCAG	399
Qy	421	ATTAACTACAAATGCTTAATTCGACCATGGAAGAAAGACAGAGTAATCTCAAGAAAT	480
Db	400	AATATAATCCCCATATGAAAAAGATTACAAAGGAGTGAATCAAAAGGTGGGGCTGAGACT	459
Qy	481	CAAGTCCAAATTTGGGAATTCAAATTACTCAGCAGTGCACATTTGGAAAAATCTCTGAGTTGAT	540
Db	460	AAATTAAGGTTAGGAAAGATTAACACTCTCAAGAGTCGATGGGTAAATCTTACGCAAGAGAT	519
Qy	541	TCA-----TTCCTGTAAAAACTGAGGCTTTTCTTCTACTGTAAGCCATCCAA	588
Db	520	GCAACGGATGAGAGCAGTATTCAAAAAAATGAGGCTGAATTTCTTCTTAAGCGCTTCAA	579
Qy	589	ATGGTTTCAAGGAGGCGCAATTCAGTATCATATGAGAACCAAGTCAAGACTAATTTTAT	648
Db	580	ATGGTTACTAGGAGATCAAGGTTCAAAATTAATTAATTAATTAATTAATTAATTAAT	639
Qy	649	-----AGACATTTCTACCTGATCCCAAGTAAATTAATTTGAGGAGAGTGGGGCAAA	702
Db	640	GATGCCAATGGGTATCAGCGAGATCTTAAAGCTATTTCCCTAAGAGAAAATTTGGGACAGT	699
Qy	703	ATCTCTGAGCAATTCAAATGCCAAGATGGGGCTTTACCAAAACCATTTGACTGATGTG	762

Db 700 GTTCTAAGGTCATTGCAAAAGTTGGCACTCCGGTATAGTACTGTTACTTAACTGGA 759
Qy 763 GATGCCAAAGGTACAAGTGAATAGTCTTAAAGTGAATGAATCAATCGTGAATGGCA 822
Db 760 GACCTTAAAGATAGAAATTAATTAACCTTGAATGCGCACCAATGAACGACTTAAAC 819
Qy 823 CTCCTTAAGTACGTTAATGAGACCTGTCAAGCACTTACCAAAATGCGATGTTCTCA 882
Db 820 GACATTATGGCACTCCTAACCAAGTTACTTGAAGSTTAAAGTTCCATGTTCCCTGA 879
Qy 883 GTTATATTTCTACTTATTAATTAATATGTCCTAATTTGGTGA 926
Db 880 ATTATGTCCTATTAATTAATGAGTATGATTAATGAACTTGGTGA 923

RESULT 12

US-11-106-187-20
; Sequence 20, Application US/11106187
; Publication No. US20050183162A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NILGUN E.
; APPLICANT: WANG, PINGER
; TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
; FILE REFERENCE: OCINS 3.9-060 CONT
; CURRENT FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US/09/721,047
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: PCT/US99/11301
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/086,374
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 20
; LENGTH: 855
; TYPE: DNA
; ORGANISM: Phytolacca americana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(855)
US-11-106-187-20

Query Match 11.1%; Score 104.6; DB 10; Length 855;
Best Local Similarity 49.8%; Pred. No. 1.6e-18;
Matches 427; Conservative 0; Mismatches 394; Indels 36; Gaps 5;

Qy 88 TTTGATGCTGGAATGCCACCATTAACAATATGCCACTTATGGAATCTCTGTAAT 147
Db 10 TTTGAGTTGAGATGCCACACCAAGAACTACTTAATTTCTGACTAGTTGGCGAA 69
Qy 148 CAAGCAAGATCCAAATCTAAATGCTATGCAATCAATGCTACTGATTAATGCG 207
Db 70 GCTGTAAAGACAAGAAATGACATGCCATGATATATATGCGCAACCTCACTGAA 129
Qy 208 ACCCTTAAGTACTTATTTGTTAGTCAAGTGCAGAACTTAAACCATTAACATAAG 267
Db 130 CAACCAAGTATGTGTGTTGCTCAATTTGGAATTCGAAATTC--ACATTTGCA 186
Qy 268 CTGAGACGAATTAATCTTAATCGTATGGCTATTTGATCCCTCAATGGCAATTAAGT 327
Db 187 ATCAGAGGGGAACTTAATTTGAGGGCTATTTGACATTTTAAATG--AAATGT 243
Qy 328 CATTACCATTAATTTTATATATTAACAAGACGAACGACATGATGTGAATTAATCTT 387
Db 244 CGTATCGATCTTCAAGATTCAGATCC-----GATGCCAAGAGACCGTT 291
Qy 388 TCTCAAGTTCTAGTCTCGTGTGCAATGTCCATTAATCAATAGCTTAATTCGACC 447
Db 292 TGGCCCGGGGAGCAAGCAAGCTGGCACTCAGAAATTAATTCCTCATGAAAGAGTTAC 351
Qy 448 ATGAAAGAAAGCAGAGTAACTCAAGAAATCAAGTCAATGGGAATTCAAATATCTC 507

Db 352 AAAGGATGGAATCAAAAGGTGGGGCTAGAACTAAATTAAGGTTAGAAAGATTAACATC 411
Qy 508 AGAGTGAATTTGAAAAAATCTCTGAGTTGATTAATCTCCCTG-----AAAA 555
Db 412 AAGATGCAATGTGTTAAATCTAAGCGCAAGATGCAACGATCAAGAGATCAAAA 471
Qy 556 ACTGAGCTTTTCTTCTAGTGGATCAAAATGTTTCAAGAGGAGGCGATTCAG 615
Db 472 AATGAGGCTGAATTTCTTCTTATAGCCGTTCAAAATGTTTACTGAGGATCAAGTTCAA 531
Qy 616 TACATAGAACCAAGTCAAGACTAAATTTTAAATAGCA-----TTTACCTGATCCC 669
Db 532 TACATAGAACCAAGTCAAGGCTAAATTTGATGATGCAATGGTATACAGCAATCTC 591
Qy 670 AAGTAAATTAATTTGAGAGGAGAGTGGGCAAAATCTCTGAGGCAATTCAGATGCCAG 729
Db 592 AAGCTAATTTCCCTAAGAAAATTTGGACAGTGTCTTAAGTCAATCAAAAGTTGGC 651
Qy 730 AATGGGCTTTTACCACCAACTTGAAGTATGATGCGCAAGTACCAAGTGAATAGTT 789
Db 652 ACCTCGGTGATAGTACTGTACTTAACTTGAAGACTTAAAGATGAAATTAATTAACCT 711
Qy 790 CTGAGTGAATGAATCAATCGTATGTCGACTTCAAGTACGTTAATGGAACCTGT 849
Db 712 TGGACTAAGGCGCACATGACGACCTTAAGAACGACATTAATGCACTCTTAACCGACGT 771
Qy 850 CAGACAACTTACCAAAATGCAATGTTCTCTCAAGTATTAATTTCTATTAATTAAT 909
Db 772 ACTTGAAGTTAAAGTTCATGTTCCCTGAAATTAATGTCCTTAATTAATGAGTACT 831
Qy 910 AAGTCAATCTTGGTGA 926
Db 832 ATTATGAACCTTGGTGA 848

RESULT 13

US-10-919-750-4
; Sequence 4, Application US/10919750
; Publication No. US20050120414A1
; GENERAL INFORMATION:
; APPLICANT: Diamond, Paul
; TITLE OF INVENTION: REGULATION OF POLYNUCLEIC ACID ACTIVITY AND EXPRESSION
; FILE REFERENCE: PT100-4US
; CURRENT APPLICATION NUMBER: US/10/919,750
; PRIOR FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: US 10/644,288
; PRIOR FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US 10/354,903
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US 60/352,705
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Microsoft Wordpad
; SEQ ID NO 4
; LENGTH: 935
; TYPE: DNA
; ORGANISM: Saponaria officinalis
US-10-919-750-4

Query Match 10.2%; Score 96; DB 9; Length 935;
Best Local Similarity 49.3%; Pred. No. 4.5e-16;
Matches 398; Conservative 0; Mismatches 395; Indels 15; Gaps 5;

Qy 1 ATGAAGTGAATCTTGTATGTTGTGAGCTTAATTAAGCTGCTCAATGCGCAACT 60
Db 85 ATGAAGATTAATGTTGTATGACCAATTAAGATGATCTGCTTCAATTTCACTTGGACA 144
Qy 61 TCAACTGTCATTAATTAATGATCACTTGAATGCTGGAATGCCATTAACAAATAT 120
Db 145 ACAATGATGCGGTCACTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 204
Qy 121 GCCACTTATGAATCTCTGTATTAACAGGAAAGATCAAACTAAATGCTATGGC 180

205 TCATCTTTTGTGATAAAATCCGAACAGTAAAGATCCAACTGAAATAGCGTGT 264
Db
181 ATACCAAT---GCTACTGTAATCAATTCGACCCCTTAAGTACTTATGTTAGCTCAA 237
Qy
265 ACCGACATAGCCGGATGATGAGCCCTTCTTAAGAAAATTTCTTAGAATTTATTTCCAA 324
Db
238 GGTGCAAACTTAAACCATTAACATATGCTGAGAGCAAAATTAATTAATAGTATGAGGC 297
Qy
325 AGTTC---CCGAGGAAGGTCTCACTTGCGCTTAAAGCCGATTAATCTGTATGTGTGCG 381
Db
298 TATTCGATCCCTTCAATGCGATTAAGTGTCTTACCAATATTTAATTAATTAATTAAC 357
Qy
382 TATCTTGAATGATTAACAGAAATGTAATCGGCATATTAATTAATTAATTAATTAATTA 441
Db
358 ACCGACGCACTAATGAGAAATCTTTGCTCAAGTCTTAATTTCTCGTGTGCAATG 417
Qy
442 TCCGCGAGTCAACCGCCCTTTTCCAGAGGCCCAATCGCAATTCAGAAAGCTTTAGAA 501
Db
418 TCCATTAATCAATAGCTTAATTAATCCGACATGAGAAAGAAAGCAAGTAACTCA--- 474
Qy
502 TACACGAAATATTAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 561
Db
475 AGAATCAATGCTCAATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 534
Qy
562 AGAAAGAACTCGGGTGGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 621
Db
535 GTTGAATTCATTCCTGTAATAAACTGAGCTTTTCTTCTGTAATTAATTAATTAATTAAT 594
Qy
622 AAGG---CAGGTGTGTTAAAGCAAGCTAGATTTCTTCTTCTGTAATTAATTAATTAAT 678
Db
595 TCAGAGGCAAGGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 654
Qy
679 GCTGAGGCAAGGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 738
Db
655 TTCTACCTGATCCCAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 714
Qy
739 TTCAACTCGGAAACAAAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 798
Db
715 ATTAC---AATGCAAGAAATGAGGCTTTACCCAACTGATGATTAATTAATTAATTAAT 771
Qy
799 ATATACGAGGAGTCCCAAAACGCGTGTTAATTAATTAATTAATTAATTAATTAATTAAT 858
Db
772 GGTACCAAGTGAATGATTTCTTAAGATGG 799
Qy
859 GTTAGGCAAGTGAAGACTTGCAATGG 886
Db
RESULT 14
US-09-861-257-37
; Sequence 37, Application US/09861257
; Publication No. US20030040496A1
; GENERAL INFORMATION:
; APPLICANT: Chandler, Lois Ann
; APPLICANT: Soenowski, Barbara A.
; APPLICANT: Baird, J. Andrew
; APPLICANT: Pierce, Glenn
; TITLE OF INVENTION: TREATMENT OF TUMORS USING
; LIGAND-DIRECTED NUCLEIC ACID DELIVERY VEHICLES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/861,257
FILING DATE: 17-MAY-2001
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Christensen Ph.D., William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 760100.423C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULAR TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..804
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..804
OTHER INFORMATION: /note= "Nucleotide sequence
corresponding to the clone M13 mp18-67"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 46..804
OTHER INFORMATION: /product= "Saporin"
US-09-861-257-37

Query Match 94%; Score 88.4; DB 3; Length 804;
Best Local Similarity 49.3%; Pred. No. 5.8e-14;
Matches 376; Conservative 0; Mismatches 371; Indels 15; Gaps 5;

Qy 47 TTGCTGACCACTTCACTTGTCCATTAATACATCACTTGTGATGCTGAATGCCA 106
Db 20 TTTCAGCTTGAACAACATGATGCGGTCAATCAATCAATTAATTAATTAATTAAT 79
Qy 107 CCATTAACAATATGCACTTTATGAAATCTTTGTAATCAAGGAAAGATCCAAAC 166
Db 80 CCGCGGGTCAATCTCATCTTTTGTGATTAATAATCCGAAACAACTGAAGATCCAAAC 139
Qy 167 TAAATGCTATGSCATTAACAATGC---TACCTGATTAATTAATTAATTAATTAAT 223
Db 140 TGAATTAACGCTGATACCAATATGCGGTATAGGCCCACTTTTAAAGAAAATTCCTTA 199
Qy 224 TGGTAACTCCAAAGTGCAAACCTTAAACCATTAACATTAATGCTGAGCAAAATTAAT 283
Db 200 GAATTAATTTCCAAATTC---CCGAGGAACGCTCTCACTTGCCCTTAAACGCGATTAAT 256
Qy 284 TATAGCTATGAGCTATTTGATCCCTTCAATGCAATTAATGATGCTTAATTAATTA 343
Db 257 TGTATGTGTGCGGTATCTTGTCAATGATTAACGAATGTTAATCGGCGATATTAATTA 316
Qy 344 ATGATATTAACAAGCAAGCAAGCACTGATGATGAGAAATCTTTGCTCAAGTTTAAAT 403
Db 317 GATCAAAATTAATTTCCGCGAGTAAACGCGCTTTTCCAGAGGCCAACAATGCAATTC 376
Qy 404 CTCGTGTCGAATGCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 463
Db 377 AGAAGCTTTGAATTAACAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 436
Qy 464 AAGTA---AATCAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 520
Db 437 AGGAGATTAATTAACAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 496
Qy 521 GAAATATCTGTGAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 580
Db 497 AAGCAGTGAACAAGA---AGGCACTGTGTTAAACAAAGCTAGATTCCTTCTTAATTCG 553
Qy 581 CCATCCAAATGTTTCAAGAGCAGCGCAATTCAGATTAATTAATTAATTAATTAATTAATTA 640

Db 554 CTTTCAGATGACGCTGAGGCGACAGATTAGTACATACAAAAGCTGTATACAGA 613
QY 641 ATTTAATGAGCATCTTACCTGTATCCCAAGTAATTAATTTGAGAGAGAGTGGGCA 700
Db 614 ACTTCCCAACAGATTCAGTGGGAAACAAAGTATTCAGTTGAGTTAACTGGAAAA 673
QY 701 AATCTCTGAGGCAATTCAC--AATGCCAAGATGGGGCTTTACCAACCACTTGAGC 757
Db 674 AATTTCTACGGCAATATACGGGAGATGCCAAAAACGGCGTGTAAATTAAGATTATGATT 733
QY 758 TAGTGATGCCAAGGATACAGTGAATAGTTCTTAGAGTGG 799
Db 734 TCGGGTTTGAAAAAGTGAAGGAGGTGAAGACTTGCAAAATGG 775

RESULT 15
US-09-861-257-38
Sequence 38, Application US/09861257
Publication No. US20030040496A1
GENERAL INFORMATION:
APPLICANT: Chandler, Lois Ann
APPLICANT: Sosnowski, Barbara A.
APPLICANT: Baird, J. Andrew
APPLICANT: Pierce, Glenn
TITLE OF INVENTION: TREATMENT OF TUMORS USING
NUMBER OF SEQUENCES: 103
TITLE OF INVENTION: LIGAND-DIRECTED NUCLEIC ACID DELIVERY VEHICLES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/861,257
FILING DATE: 17-MAY-2001

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Christensen Ph.D., William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 760100,423C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..804
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..804
OTHER INFORMATION: /notes= "Nucleotide sequence
OTHER INFORMATION: corresponding to the clone M13 mp18-C9"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 46..804
OTHER INFORMATION: /product= "Saporin"
US-09-861-257-38

Query Match 9.4%; Score 88.4; DB 3; Length 804;
Best Local Similarity 49.3%; Freq. No. 5.8e-14;

Matches 376; Conservative 0; Mismatches 371; Indels 15; Gaps 5;
QY 47 TTGCTGACCAACTTCACTTGTGCAATTAATGATGATCCCTTGTAGTGTGAAATGCCA 106
Db 20 TTTCAGCTTGACACAACTGATGCGGTGATCATCAATTCATTAATGATGATGATCCGA 79
QY 107 CCATTAACAAATATGCGACCTTTATGAAATCTCTTGATATCAAGGAAAGATCCAAAC 166
Db 80 CCGCGGGTCAATATCATCTTTTGTGATTAATAATCCGAAACAAAGTAAGATCCAAAC 139
QY 167 TAAAAATGCTATGCTATCAATGCG--TACCTGATATCTAATTTGACCCCTTAATTTAT 223
Db 140 TGAATATACGGTGTATACGATAGCCGTATAGGCCACCTTTTAAAGAAATTCCTTA 199
QY 224 TGGTAAAGCTCCAAAGGTGCAACCTTAAACCACTTACATTAATGCTGAGCGAAATTACT 283
Db 200 GAATTAATTTCCAAAGTTC---CCAGGAACGGTCTACCTTGCCCTAAACCGGATTACT 256
QY 284 TATACGTATGAGCTATTTCTGATCCCTCAATGGCAATTAAGTGTGTTACATATATTTA 343
Db 257 TGTATGTGGTGGGTATCTTGCAATGATTAACGAAATGTTAATGGGATATTAATCTCA 316
QY 344 ATGATATTTACAGCACCGCAACGCACTGATGTGAAGATCTCTTGCTCAAGTTCTAGTT 403
Db 317 GATCAGAAATTACTTCCGCCAGTTAACCGCCCTTTTCCAGAGGCCAACACTGCAAAATC 376
QY 404 CTGCTGTGCAATGTCATTAACTAATAGCTTATATCCGACCATGAAAGAAAGCAAG 463
Db 377 AGAAAGCTTTGAATACAGAAAGATTAATCACTGATTAATAAAGATCCCAATTAAC 436
QY 464 AAGTAAACTCA--AGAAATCAAGTCCAAATGGGAATTCAAATACTCAGACGTACATTTG 520
Db 437 AAGAGATCAAGATGAAAGAAAGAACTGGGTGGGATGATTAATCTTCAAGTCATAG 496
QY 521 GAAAAATCTGGAATGATTTCACTCCCTGTAAAACTGAGCTTTTCTTACTGTGTAG 580
Db 497 AAGCAAGTGAACAAGA--AGGACGCTGTGTAAAGACAACTGATTCCTTCTTATG 553
QY 581 CCATCCAAATGTTTCAGAGGACGCGCATTAAGATACATAGAAACCAAGTCAAGACTTA 640
Db 554 CTTTCAGATGACGCTGAGGCGAGCGCATTTAGTACTACAAACCTTGTATATCAAGA 613
QY 641 ATTTAATGAGCATTTACCTGTATCCCAAGTAAATTAATTTGAGGAAAGTGGGCA 700
Db 614 ACTTCCCAACAGATTCAGCTCGGAAACAAAGTATTCAGTTGAGTTAACTGAAAAA 673
QY 701 AATCTCTGAGGCAATTCAC--AATGCCAAGATGGGGCTTTACCAACCACTTGAGC 757
Db 674 AATTTCTACGGCAATATACGGGAGATGCCAAAAACGGCGTGTAAATTAAGATTATGATT 733
QY 758 TAGTGATGCCAAGGATACAGTGAATAGTTCTTAGAGTGG 799
Db 734 TCGGGTTTGAAAAAGTGAAGGAGGTGAAGACTTGCAAAATGG 775

Search completed: April 9, 2006, 01:44:59
Job time : 1094.88 secs

Oy	168	TGCTACCTGATCTTAATTCGACCCCTTAAGTACTTTATGGTTAAGTCCCAAGGTGCAACC	247
Db	368	TGCTGCCCAATCAATCAATCAATCAATCAAGTACGTGTGTTAAGCTCCAAAGTTCAATA	447
Oy	248	TAAAAACCAATTACCTAATGTCTGAGACGAAATTAATCTAATACGTGATGGCTATTCTGATC	307
Db	448	AAAAAACATCACTCAATATGCTGACAGCAAAATTGTATGTATGGATTATTTCTGATC	507
Oy	308	CCTTCAATGGCAATAGTGTGGTTACATATATTTAATGAATATTCACGACCCGAACGCA	367
Db	508	CCTTTGAAACCAATTAATGTGCTTACCATATCTTTAATGAATATCTCAGGTACTGAACGCC	567
Oy	368	CTGATGTGAGAAATATCTCTTGGCTCAAGTTCTTGAATCTCTGTGTTCAATGTCATTAATC	427
Db	568	AAGATGTAGAGACTACTCTTGGCCAAATGCGCAATTTCTGTGTTAATAAAACATTAATC	627
Oy	428	ACAAATGCTTATATCCGACATGAGAAAAGAAAGCAAGATTAATCTCAAGAAATCAATGCC	487
Db	628	TTGATATGTGCAATATCAATTTGGAATCAAAAGCGGGAGTAAATCAAGAAATCTAGGTCC	687
Oy	488	AATGGGAATTCAAATTAATCTCAGCAGTGAATTTGAAATAATCTCTGAGTGTGATTCATCC	547
Db	688	AACTGGGAATTCAAATTAATCTCAGCAGTGAATTTGAAATAATTTCTGAGTGTGATTCATCA	747
Oy	548	CTGTAAAACTGAGGCTTTTTTTCTACTGTGATGACCATCCAAATGGTTTCAAGAGCAGCC	607
Db	748	CTGAGAAAAACGAAACCGCAATCTTATGTGTGACCATCAAAATGGTATCAGAGGACGAA	807
Oy	608	GATTCAATGATCATAGAAACCAAGTCAAGACTAATTTTAATGACATTTTACCCCTGATC	667
Db	808	GATTCAATGATCATAGAAATCAAGTGAATCAATTTTAATGACATTTCAACCTCATATC	867
Oy	668	CCAAAGTAATTAATTTGAGAGAGAGAGTGGGGCAAAATCTCTGAGGCAATTCACATGCCA	727
Db	868	CCAAAGTACTTAATTTGCAAGAGACATGGGGGTAATTTCAACAGCAATTCATGATGCCA	927
Oy	728	AGAAATGGGCTTTTACCACCAACACTTGATGCTGTGATGTCAGCAAGGTACCAAGTGAATAG	787
Db	928	AGAAATGGGCTTTTACCACCAACCTCTCGAGCTGATGTAATGCCAGTGTGCCAAAGTGAATAG	987
Oy	788	TTCTTAGAGTGAATCAATCGTGAATGTGGCACTCCTTAAGTACGTTAATGGAACCT	847
Db	988	TGTTGAGAGTGGATGAATCAAGCTGATGTGACACTTTAAATCTACGTTGGTGGAGCT	1047
Oy	848	GTCAGACACTT--ACCAAAATGCCATGTTCTCTCAAGTTAATTAATTTCTACTATTATA	904
Db	1048	GTCAGACAACTTAATCAACAAATGCGCATGTTTCCCACTTAATATATGCTACTATTATA	1107
Oy	905	ATTATATGCTAATCTTGTGATCTAATTTGAAGATTTCTAA	945
Db	1108	ATTACATGCTTAATCTTGTGATCTAATTTGAAGATTTCTGA	1148
RESULT 2			
US-11-010-795-21			
: Sequence 21, Application US/11010795			
: Publication No. US20060005271A1			
: GENERAL INFORMATION:			
: APPLICANT: TUMER, NILDUN E.			
: APPLICANT: DI, RONG			
: TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE			
: FILE REFERENCE: OCIRS 3 0-085			
: CURRENT APPLICATION NUMBER: US/11/010,795			
: CURRENT FILING DATE: 2004-12-13			
: PRIOR APPLICATION NUMBER: 60/529,348			
: NUMBER OF SEQ ID NOS: 44			
: SOFTWARE: PatentIn Ver. 3.3			
: SEQ ID NO 21			
: LENGTH: 934			
: TYPE: DNA			
: ORGANISM: Phytolacca americana			

[illegible]

RESULT 3
US-10-893-584-273
; Sequence 273, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 273
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ricin-like toxin (TST10054)
US-10-893-584-273

Query Match 6.7%; Score 63; DB 8; Length 1623;
Best Local Similarity 54.0%; Pred. No. 7.7e-06;
Matches 154; Conservative 0; Mismatches 125; Indels 6; Gaps 1;
QY 555 AACTGAGCCTTTTCTACTGTAGCCATCAAAATGGTTTCAGAGCGCGCATTCAA 614
DB 486 AACTGAGCCTTTTCTACTGTAGCCATCAAAATGGTTTCAGAGCGCGCATTCAA 545
QY 615 GTACATGAGAACCAACTCAAGACTAATTTT-----AATAGACATTTCACTGATCC 668
DB 546 ATATATTGAGGAGAAATGCGGACGAGAAATTAAGTACACCGAGATCTGCACCAATCC 605
QY 669 CAAAGTAATTAATTTGGAGGAGAGTGGGCAAAATCTCGAGCAATTCAGATGCCAA 728
DB 606 TAGGTATTAATCACTTGAAGTAAGTGGGGAGACTTCCACTCAATTCAGAGCTTAA 665
QY 729 GAATGGGCTTTTACCCAAACCACTTGAGCTAGTGATGCCAAAGGTACCAAGTGATAGT 788
DB 666 CCAAGGAGCCTTTGCTAGTCCAAATTCAGATGCAAGAGATGTTCCAAATTCAGATGT 725
QY 789 TCTTAGTGTGATCAATCAATGCTGATGTGGGCACTCTTAAGTA 833
DB 726 GTACGATGTGATATTAATTCCTATCATAGCTCTCATGTGTGA 770

RESULT 4
US-10-893-584-83
; Sequence 83, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752

PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PAP-268 insert
US-10-893-584-83

Query Match 6.6%; Score 62.4; DB 8; Length 1855;
Best Local Similarity 50.0%; Pred. No. 1.2e-05;
Matches 187; Conservative 0; Mismatches 181; Indels 6; Gaps 1;
QY 555 AACTGAGCCTTTTCTACTGTAGCCATCAAAATGGTTTCAGAGCGCGCATTCAA 614
DB 597 AACTGAGCCTTTTCTACTGTAGCCATCAAAATGGTTTCAGAGCGCGCATTCAA 656
QY 615 GTACATGAGAACCAACTCAAGACTAATTTT-----AATAGACATTTCACTGATCC 668
DB 657 ATATATTGAGGAGAAATGCGGACGAGAAATTAAGTACACCGAGATCTGCACCAATCC 716
QY 669 CAAAGTAATTAATTTGGAGGAGAGTGGGCAAAATCTCGAGCAATTCAGATGCCAA 728
DB 717 TAGGTATTAATCACTTGAAGTAAGTGGGGAGACTTCCACTCAATTCAGAGCTTAA 776
QY 729 GAATGGGCTTTTACCCAAACCACTTGAGCTAGTGATGCCAAAGGTACCAAGTGATAGT 788
DB 777 CCAAGGAGCCTTTGCTAGTCCAAATTCAGATGCAAGAGATGTTCCAAATTCAGATGT 836
QY 789 TCTTAGTGTGATCAATCAATGCTGATGTGGGCACTCTTAAGTAAGTAAGTAAGT 848
DB 837 GTACGATGTGATATTAATTCCTATCATAGCTCTCATGTGTATGATGCCACCTCC 896
QY 849 TCAGAACCTTACCAAAATGCCAGTTCCTCAAGTATTAATTTCACTAATATATTA 908
DB 897 ACCATGCTCAAGTTTAAGGGGTGAGATGCTAGAGCCCAATACGCTTAATGCTGATGT 956
QY 909 TATGCTAATCTTG 922
DB 957 TTGTATGATCTCG 970

RESULT 5
US-10-893-584-266
; Sequence 266, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 266
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: B. coli
US-10-893-584-266

Query Match 6.6%; Score 62.2; DB 8; Length 1837;
Best Local Similarity 52.0%; Pred. No. 1.3e-05;
Matches 167; Conservative 0; Mismatches 148; Indels 6; Gaps 1;

QY 555 AACTGAGGCTTTTCTCTAGTGGATCCCAATGCTTTCAGAGGCGCGGATTCAA 614
DB 597 AACTGAGGCTTCTCTTATTAATTTGCAATGATTTCCAGAGCGCAAGATTCCA 656
QY 615 GTACATAGAGAACCAAGTCAAGCTAATTTT-----AATAGAGCATTTTACCTGATCC 668
DB 657 ATATATAGGAGGAAGATGCGACGAGATTAAGTACACCGAGATCTGACCAATCC 716
QY 669 CAAAGTAATTAATTGAGAGAGAGTGGGCAAAATCTTGAGGCAATTCACAATGCCAA 728
DB 717 TAGCGTAATTAACCTTGAGAAATGTTGGGGGAGACTTTCACATGCAATTCAGAGCTTAA 776
QY 729 GAATGGGGCTTACCCAAACCACTTGAGCTAGTGATGCCAAAGGTACCAAGTGATAGT 788
DB 777 CCAAGAGGCTTTGCTAGTCCAAATTCGAAAGCGTAATGTTCCAAATTCAGTGT 836
QY 789 TCTTAGAGTGATGAATCAATCGTATGTCGACTCTTAAGTAACTTAATGGAACCTG 848
DB 837 GTACGATGTGAGTATTAATCCCTATCATAGCTCTCATGTGTATATAGATCGGAGCGG 896
QY 849 TCAGACAACTTACCAAAATGC 869
DB 897 GACTCCACCGCAAGAAATGC 917

RESULT 6

US-11-010-795-23
; Sequence 23, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TURNER, NIGUN E.
; APPLICANT: DI, KONG
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 23
; LENGTH: 807
; TYPE: DNA
; ORGANISM: *Ricinus communis*
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(804)
US-11-010-795-23

Query Match 6.5%; Score 61.4; DB 14; Length 807;
Best Local Similarity 53.7%; Pred. No. 1.5e-05;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 555 AACTGAGGCTTTTCTCTAGTGGATCCCAATGCTTTCAGAGGCGCGGATTCAA 614
DB 489 AACTGAGGCTTCTCTTATTAATTTGCAATGATTTCCAGAGCGCAAGATTCCA 548
QY 615 GTACATAGAGAACCAAGTCAAGCTAATTTT-----AATAGAGCATTTTACCTGATCC 668
DB 549 ATATATAGGAGGAAGATGCGACGAGATTAAGTACACCGAGATCTGACCAATCC 608
QY 669 CAAAGTAATTAATTGAGAGAGAGTGGGCAAAATCTTGAGGCAATTCACAATGCCAA 728
DB 609 TAGCGTAATTAACCTTGAGAAATGTTGGGGGAGACTTTCACATGCAATTCAGAGCTTAA 668
QY 729 GAATGGGGCTTACCCAAACCACTTGAGCTAGTGATGCCAAAGGTACCAAGTGATAGT 788

DB 669 CCAAGAGGCTTTGCTAGTCCCAATTCAGTCAAGAGCGTAATGTTCCAAATTCAGTGT 728
QY 789 TCTTAGAGTGATGAATCAATCGTATGTCGACTCTTAAGTA 833
DB 729 GTACGATGTGAGTATTAATCCCTATCATAGCTCTCATAGTGTGA 773

RESULT 7

US-10-893-584-196
; Sequence 196, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Adam
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 196
; LENGTH: 1807
; TYPE: DNA
; ORGANISM: *E. coli*
US-10-893-584-196

Query Match 6.5%; Score 61.4; DB 8; Length 1807;
Best Local Similarity 53.7%; Pred. No. 2.1e-05;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 555 AACTGAGGCTTTTCTCTAGTGGATCCCAATGCTTTCAGAGGCGCGGATTCAA 614
DB 597 AACTGAGGCTTCTCTTATTAATTTGCAATGATTTCCAGAGCGCAAGATTCCA 656
QY 615 GTACATAGAGAACCAAGTCAAGCTAATTTT-----AATAGAGCATTTTACCTGATCC 668
DB 657 ATATATAGGAGGAAGATGCGACGAGATTAAGTACACCGAGATCTGACCAATCC 716
QY 669 CAAAGTAATTAATTGAGAGAGAGTGGGCAAAATCTTGAGGCAATTCACAATGCCAA 728
DB 717 TAGCGTAATTAACCTTGAGAAATGTTGGGGGAGACTTTCACATGCAATTCAGAGCTTAA 776
QY 729 GAATGGGGCTTACCCAAACCACTTGAGCTAGTGATGCCAAAGGTACCAAGTGATAGT 788
DB 777 CCAAGAGGCTTTGCTAGTCCAAATTCGAAAGCGTAATGTTCCAAATTCAGTGT 836
QY 789 TCTTAGAGTGATGAATCAATCGTATGTCGACTCTTAAGTA 833
DB 837 GTACGATGTGAGTATTAATCCCTATCATAGCTCTCATAGTGTGA 881

RESULT 8

US-10-893-584-168
; Sequence 168, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Adam
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584


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; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 182
; LENGTH: 1822
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-182

Query Match      6.5%; Score 61.4; DB 8; Length 1822;
Beet Local Similarity 53.7%; Pred. No. 2,1e-05;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

OY 555 AACTGAGGCTTTTCTTCTACTGTCGATGCCATCCAAATGGTTTCAGAGGCGAGCATTCAA 614
Dd 597 AACTCTGGCTCGTTCCTTATTAATTGSCATCCAAATGATTTTCAGAGGAGCAAGATTCCA 656
OY 615 GTACATAGAGAACCAAGTCAAGACTAATTTT-----AATAGACATTCTACCTGATCC 668
Dd 657 ATATATTGAGGAGGAGAAATGCGCAGAAATTTAGTACAAACCGGAGATCTGACACGATCC 716
OY 669 CAAGTAATTATTTGGAGAGAGAGGCGGCAAAATCTGAGGCAATTCAGAAATGCCAA 728
Dd 717 TAGGTAATTAACCTTAGAATAGTTGGGGAGCTTTCACATGCAATTCAGAGTCTAA 776
OY 729 GAATGGGCTTTTACCACCAACCACTGAGCTAATGATGATCCAAAGTCAAGATGATAGT 788
Dd 777 CCAAGAGCCTTTGCTAGTCCAAATTCACATGCAAGACGTAATGGTTCCAAATTCAGTGT 836
OY 789 TCTTAGAGTGATCAATCAATGCTGATGTCGACATCTCCTTAAGTA 833
Dd 837 GTACAGATGATGATTAATTAATCCCTATCATAGCTTCATGATGTA 881

RESULT 13
US-10-893-584-231
; Sequence 231, Application US/10893584
; Publication No. US2005272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 231
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-231

Query Match      6.5%; Score 61.4; DB 8; Length 1825;
Beet Local Similarity 53.7%; Pred. No. 2,1e-05;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

OY 555 AACTGAGGCTTTTCTTCTACTGTCGATGCCATCCAAATGGTTTCAGAGGCGAGCATTCAA 614
Dd 597 AACTCTGGCTCGTTCCTTATTAATTGSCATCCAAATGATTTTCAGAGGAGCAAGATTCCA 656
OY 615 GTACATAGAGAACCAAGTCAAGACTAATTTT-----AATAGACATTCTACCTGATCC 668
Dd 657 ATATATTGAGGAGGAGAAATGCGCAGAAATTTAGTACAAACCGGAGATCTGACACGATCC 716
OY 669 CAAGTAATTATTTGGAGAGAGAGGCGGCAAAATCTGAGGCAATTCAGAAATGCCAA 728
Dd 717 TAGGTAATTAACCTTAGAATAGTTGGGGAGCTTTCACATGCAATTCAGAGTCTAA 776
OY 729 GAATGGGCTTTTACCACCAACCACTGAGCTAATGATGATCCAAAGTCAAGATGATAGT 788
Dd 777 CCAAGAGCCTTTGCTAGTCCAAATTCACATGCAAGACGTAATGGTTCCAAATTCAGTGT 836
OY 789 TCTTAGAGTGATCAATCAATGCTGATGTCGACATCTCCTTAAGTA 833
Dd 837 GTACAGATGATGATTAATTAATCCCTATCATAGCTTCATGATGTA 881

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OM protein - nucleic search, **using framep2n model**

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(without alignments)
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Title: US-09-978-274A-2

Perfect score: 1617
Sequence: 1 MKWLVVVTILIAVLIAPT.....VISTYYNMYNIGDLPEGF 314

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 segs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pico -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abse04
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1617	100.0	1249	15	PAPAPSRIP
3	1352	83.6	792	6	AX427704 Sequence

4	1332	82.4	786	15	AB071855	AB071855 Phytolacc
5	1307	80.8	1092	6	AX427720	AX427720 Sequence
6	1241.5	76.8	942	15	AY572976	AY572976 Phytolacc
7	1235.5	76.4	942	15	AY547315	AY547315 Phytolacc
8	1235.5	76.4	1164	15	PAPAP	X55383 P.americana
9	1235.5	76.4	1195	6	AX42103	AX42103 Sequence
10	1235.5	76.4	1195	6	I43835	I43835 Sequence 1
11	1235.5	76.4	1195	6	I55866	I55866 Sequence 1
12	1235.5	76.4	1379	6	AR009535	AR009535 Sequence
13	1235.5	76.4	1379	6	AR136704	AR136704 Sequence
14	1235.5	76.4	1379	6	AX427731	AX427731 Sequence
15	1232.5	76.2	1379	6	AR141172	AR141172 Sequence
16	1231.5	76.2	1164	15	AY049785	AY049785 Phytolacc
17	1229.5	75.0	1195	6	A36639	A36639 Sequence 1
18	1227.5	75.9	1378	6	AX427732	AX427732 Sequence
19	1227.5	75.9	1379	6	AR136705	AR136705 Sequence
20	1225	75.8	939	15	AY327475	AY327475 Phytolacc
21	1216.5	75.2	1114	15	AF533515	AF533515 Phytolacc
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24	1166.5	72.1	1052	15	AY137202	AY137202 Phytolacc
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32	1031	63.8	918	6	I89987	I89987 Sequence 1
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34	960	59.4	714	15	AF603354	AF603354 Phytolacc
35	953	58.9	711	15	AF338910	AF338910 Phytolacc
36	952	58.9	714	15	AY603352	AY603352 Phytolacc
37	947	58.6	714	15	AY603353	AY603353 Phytolacc
38	788	48.7	465	6	AX427706	AX427706 Sequence
39	703	43.5	1226	15	CAAV	X96474 C.aculeatum
40	703	43.5	1226	15	CAAV	AX427708 Sequence
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43	511	31.6	902	6	AX427733	AX427733 Sequence
44	484	29.9	902	15	AF533516	AF533516 Phytolacc
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ALIGNMENTS

RESULT 1
AX427702 945 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 1 from Patent WO0233107.
DEFINITION AX427702
ACCESSION AX427702.1 GI:21537815
VERSION
KEYWORDS
ORGANISM
SOURCE
Phytolacca americana (American pokeweed)
Phytolacca americana
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
1
Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.
AUTHORS
TITLE
JOURNAL
Patent: WO 0233107-A.1 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES
Location/Qualifiers
1. 945
/organism="Phytolacca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"
1. 24
/note="Binding site for primer PPS1BP"
misc_feature
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misc_feature
/note="Binding site for primer PSXDR"
misc_feature
736..777

Percent Similarity: 100.0%
 Best Local Similarity: 100.0%
 Query Match: 100.0%
 DB: 15
 Gaps: 0

US-09-978-274A-2 (1-314) x PAPABSRIP (1-1249)

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 DB 166 TCACCTGTGCGCAATTAATACATCACTTGTATCTGTGAATGCGACCATTAACAAATAT 225
 QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysThrGly 60
 DB 226 GCCACCTTTATGAAATCTTTCGTATTCACCGAAAGATCCAAATCTAAATGCTATGGC 285
 QY 61 IleProMetLeuProAspThrAsnSerThrProLysThrLeuLeuValLysLeuGlnGly 80
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 QY 101 SerAspProPheAsnGlyAsnLysCysArgThrIleIlePheAsnAspIleThrSerThr 120
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 QY 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerSerSerArgValAlaMetSer 140
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 QY 141 IleAsnThrAsnSerLeuLysProThrMetGluLysLysValGluValAsnSerArgAsn 160
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 QY 161 GluValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
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 QY 201 AlaAlaArgPheLysThrIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheThr 220
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 QY 281 GlyThrCysGlnThrThrThrGlnAsnAlaMetPheSerGlnValIleIleSerThrThr 300
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RESULT 3
 AX427704

LOCUS AX427704 792 bp DNA linear PAT 20-JUN-2002
 DEFINITION Sequence 3 from Patent WO023107.
 ACCSSION AX427704
 VERSION AX427704.1 GI:21537816
 KEYWORDS

ORGANISM

Phytolacca americana (American pokeweed)
 Phytolacca americana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE

1 Neelam, A., Atkinson, H. J., McPherson, M. J. and Thomas, C. J. R.
 Plant cell death system
 Patent: WO 023107-A 3 25-APR-2002;
 CAMBRIDGE ADVANCED TECH (GB)

FEATURES

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ORIGIN

Alignment Scores:

Pred. No.: 1.96e-104 Length: 792
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 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 83.6% Indels: 0
 DB: 6 Gaps: 0

US-09-978-274A-2 (1-314) x AX427704 (1-792)

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 QY 45 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysThrGlyIleProMetLeu 64
 DB 64 GAATCTCTGTAATCAAGGAAAGATCCAAATCTAATGCTATGCGCATACCAATGCTA 123
 QY 65 ProAspThrAsnSerThrProLysThrLeuLeuValLysLeuGlnGlnValAlaAsnLys 84
 DB 124 CCGATACCTAATTCGACCCCTTAAGTCTTAATTTGAAGTCCAAAGTGCAGAACTTAAA 193
 QY 85 ThrIleThrLeuMetLeuArgAsnAsnLeuLysValMetGlyThrSerThrGluArgThrAsp 104
 DB 184 ACCATTAACCTAATGCTGAGACCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 243
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 DB 244 AATGGCAATTAAGTGTGTTACCATATATTAATTAATTAATTAATTAATTAATTAATTA 303
 QY 125 ValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnThrAsn 144
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Db 364 AGTTATATCCGACCAAGAAAGAGCAAGTAATCAAGAAATCAAGTCCAAATTG 423
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LOCUS AB071855 786 bp DNA linear PLN 19-MAR-2002
DEFINITION Phytolacca americana paps2 gene for PAP-S2, partial cde.
ACCESSION AB071855
VERSION AB071855.1 GI:19570839
KEYWORDS
SOURCE Phytolacca americana (American pokeweed)
ORGANISM Phytolacca americana
Bukarjaya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
AUTHORS Honjo,E. and Watanabe,K.
TITLE Cloning of genomic DNA encoding two types of pokeweed antiviral
protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
their recombinant proteins with other PAP isoforms
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 786)
AUTHORS Watanabe,K. and Honjo,E.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2001) Keiichi Watanabe, Saga University,
Department of Applied Biological Sciences, Honjo-machi, Saga city,
Saga 840-8502, Japan (E-mail: watakei@cc.saga-u.ac.jp,
tel:81-952-28-8774, fax:81-952-28-8774)
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ORIGIN
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DB: 15 Gaps: 0
US-09-978-274a-2 (1-314) x AB071855 (1-786)
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Db 61 GAATCTCTTGATATCAAGGAAAGATCCAAACTAAATGCTATGGCATACCAATGCTTA 120
QY 65 PROAEPThRAENSEThRPROLYSTRLEULEUVALYSEUGINGIYVIAENLEULY 84
Db 121 CCGAATACATAATTCGACCCCTTAAGTACTTAATGGTTAAGCTCCAAAGTGCMAA 180
QY 85 ThRIETHRIEUEMETLEUARGARGAANAENLEUYVAIMEGIYTRSEARAPPROPE 104
Db 181 ACCAATTAATCAATATGCTGAGCAAGAAATTAATTAATTAATTAATTAATTAATTAATTA 240
QY 105 ASNGIYASNIYCYAARGTYRHAIEIIEPHEASNAPIIETHSERThRGUARThRAAP 124
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QY 125 VALGIUASNTHRIEUCYSE 144
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Db 541 AAGTACATAGAGAACCAAGTCAAGACTAATTTTAATAGCAATTCACCTGATCCCAA 600
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Db 661 GGGGCTTTACCAACCACTTGAGCTAGTGAGTCCAAAGGTACCAAGTGGATAGTTCTT 720
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QY 285 ThrThr 286
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RESULT 5
LOCUS AX427720 1092 bp DNA linear PAT 20-JUN-2002

DEFINITION Sequence 19 from Patent WO0233107.
 ACCESSION AX427720
 VERSION AX427720.1 GI:21537829
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct
 other sequences; artificial sequences.
 REFERENCE
 1 Neelam, A., Atkinson, H.J., Mcpherson, M.J. and Thomas, C.J.R.
 AUTHORS
 TITLE
 JOURNAL
 Patent: WO 0233107-A 19 25-APR-2002;
 CAMBRIDGE ADVANCED TECH (GB)
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 LOCUS
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 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 PhytoIaccia americana (American pokeweed)
 PhytoIaccia americana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; PhytoIaccaceae; PhytoIaccia.
 1 (bases 1 to 942)
 Xiao, Z.A. and Jiang, Y.
 A gene encoding the pokeweed antiviral protein in the leaf of
 PhytoIaccia americana
 Unpublished
 2 (bases 1 to 942)
 Xiao, Z.A.
 Direct Submission
 Submitted (13-MAR-2004) College of Life Sciences, Beijing Normal
 University, No. 19 Xinjiekouwai Street, Haidian District, Beijing
 100875, China
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US-09-978-274a-2 (1-314) x AY547315 (1-942)

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LOCUS PhytoIaccia americana antiviral protein gene, complete cds.
ACCESSION AY547315
VERSION AY547315.1 GI:44889055
KEYWORDS
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ORGANISM PhytoIaccia americana (American pokeweed)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; PhytoIaccaceae; PhytoIaccia.
1 (bases 1 to 942)
AUTHORS Zhao, Y., Wang, X., Zhou, G., and Li, H.
TITLE A pokeweed antiviral protein gene in roots of PhytoIaccia americana
JOURNAL Acta Virol. 48 (2), 131-132 (2004)
15462289
REFERENCE 2 (bases 1 to 942)
AUTHORS Zhao, Y., Wang, X., and Li, H.
TITLE Direct Subinjection
JOURNAL Submitted (11-FEB-2004) Plant Virology, Institute of Plant
Protection, CMAIS, No.2 Yuanmingyuan Road West, Beijing 100094, P.R.
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Query Match: 76.4% Indels: 3
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Db 1 ATGAAAGTATGCTGTGGTGAACAATTCATA-----TGGCTCATCTTGGACCAACT 54
OY 21 SerThrCysAlaIleLeuThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTy 40
Db 55 TCAACTTGGGCTGTGAATACATCATCATCATCATGTTGGAAGTACCAACCATTAGCAATAC 114
OY 41 AlaThrPheMetCysLeuLeuArgAsnGlnAlaLysAspProLysLysCysTyGly 60
Db 115 GCCACTTCTGATGATGATCTTCTGTAAGCAAGCAAGATCAAGTTTAAATCTTATGA 174
OY 61 IleProMetLeuProAspThrAsnSerThrProLysTyLeuLeuValLysLeuGlnGly 80
Db 175 ATACCAATGCTGCTCCCAATACCAATACCAATCCAAAGTCTGTTGGTGGCTCCAAAGT 234
OY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuTyValMetGlyTy 100
Db 235 TCAAAATTAATAAAACCATCACTAATGCTGAGAGCAAAACAATTGTATGTATGGGTAT 294
OY 101 SerAspProPheAsnGlnLysLysCysArgTyHisIlePheAsnAspIleThrSerThr 120
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 QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyIleSerGlyValAsp 180
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 QY 181 SerPheProValYrThrGlnValPhePheLeuLeuValIleGlnMetValSerGlu 200
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 Db 655 CCTAAATCCCAAGTAACTTAATTTGCAAGACATGGGGTAAAGATTTCACAGCAATTCAT 714
 QY 241 AsnAlaIysAsnGlyAlaLeuProLyysProLeuGlnLeuValAspAlaIysGlyThrLys 260
 Db 715 GATGCCAAGATGAGATTTCACCAACCTCTCGAGCTAGGATGCGAGTGGCCAG 774
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 QY 281 GlyThrCysGlnThrThrYr--GlnAsnAlaMetPheSerGlnValIleSerThr 299
 Db 835 GGGAGCGTCAAGCAACTTAATCAAAATGCGCATGTTCTCTCACTTAATATGCTACT 894
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 LOCUS P.americana PAP gene for anti-viral protein.
 DEFINITION X55383.1 GI:20421
 ACCESSION X55383.1 GI:20421
 VERSION anti-viral protein; cell wall protein; PAP gene; ribosome
 KEYWORDS inactivating protein.
 SOURCE Phytolacca americana (American pokeweed)
 ORGANISM Phytolacca americana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Phytolaccaceae; Phytolacca.
 1 (bases 1 to 1164)
 Lin, Q., Chen, Z. C., Antoniw, J. F. and White, R. F.
 Isolation and characterization of a cDNA clone encoding the
 anti-viral protein from Phytolacca americana
 Plant Mol. Biol. 17 (4), 609-614 (1991)
 1912488
 JOURNAL Antoniw, J. F.
 PUBLISHED 2 (bases 1 to 1164)
 REFERENCE Antoniw, J. F.
 TITLE Direct Submission
 AUTHORS Submitted (05-NOV-1990) Antoniw, J. F., AFRC Inst of Arable Crops
 JOURNAL Researched, Dept. of Plant Pathology, Rothamsted Experimental
 Station, Harpenden, Hert, AL5 2JG, UK
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 CDS

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 QY 61 IleProMetLeuProAspThrAsnSerThrProLyysTyrLeuValYsLeuGlnGly 80
 Db 176 ATACCAATGCTGCCATATACATCAATCAAAATGACGTGTGGTTCACAGGT 235
 QY 81 AlaAsnLeuYsThrIleThrLeuMetLeuArgArgAsnAsnLeuYrValMetGlyTyr 100
 Db 236 TCAATTAATAAAACCATCAACATATGCTGAGCGAAGCAAACTTTGATGATGGGTAT 295
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 QY 121 GluArgThrAspValGlnAsnThrLeuYsSerSerSerSerSerArgValAlaMetSer 140
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 QY 141 ILeasntYrAsnSerLeuYrProThrMeGlulYsValaglValaAsnSerArAsn 160
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 QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyIleSerGlyValAsp 180
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Db 836 GGGAGCTGCAGCAACTTATACCAAAATGCGATGTTCTCCTCACTTATATATGCTACT 895
Qy 300 TYRTYAsnTYMeSerAsnLeuG1YAspLeuPheG1UGlyPhe 314
Db 896 TATTATATTAATTAATGTTATCTTGGTATCTTGGTATCTTGGTATCTTGGTATCT 940
RESULT 9
LOCUS A42103 1195 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 1 from Patent EP0637591.
ACCESSION A42103
VERSION A42103.1 GI:2297595
KEYWORDS
SOURCE .
ORGANISM Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
1 (bases 1 to 1195)
REFERENCE
AUTHORS Moon, Y., Jeon, H., Choi, K., Lee, K. and Kim, W.
TITLES A novel expression vector for phytolacca antiviral protein
JOURNAL JINRO LIMITED (KR)
COMMENT
Other publication AU 662844 950914
Other publication JP 7067660 950314
Other publication CA 2102859 950103
Other publication AU 5064293 950119.
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/organism="Phytolacca americana"
/mol_type="unassigned DNA"
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Pred. No.: 1.9e-94 Length: 1195
Score: 1235.50 Matches: 239
Percent Similarity: 86.3% Conservative: 33
Best Local Similarity: 75.9% Mismatches: 40
Query Match: 76.4% Indels: 3
DB: 6 Gaps: 2
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Qy 41 AlaThrPheMetG1UeSerIeuArgAsnGlnAlaIleAspProIySleuTYSCyS1Yg1Y 60
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Qy 61 IleProMetIeuProAspThrAsnSerThrProIyTYrIleuValIleuValIleuGlnG1Y 80
Db 207 ATACCAATGCTGCGCAATACCAATCAAAATGACGTTGTTGTTGAGCTCCAAAGT 266
Qy 81 AlaAsnIleuThrIleThrIleuMetIeuArgAsnAsnIeuTYRValIleMetG1YTYR 100
Db 267 TCATAATATAAAACCATCACTATGCTGAGAGCAAAATTTGTAATGATGGGTAT 326

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Db 327 TCTGATCCCTTGAACCAATATATGCTTACATATCTTTATATGATATCTCAGGTACT 386
Qy 121 G1UArgThrAspValG1UAsnThrIeuCySerSerSerSerSerIArgValAlaMetSer 140
Db 387 GAAGCCCAAGATGTAAAGACTACTCTTGTGCCCAAAAGCCAAATCTGCTTAAATAAAC 446
Qy 141 IleAsnTYRAsnSerIeuTYRProThrMetG1UValAlaG1UValIleAsnSerArgAsn 160
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Qy 161 GlnValGlnIleuG1YIleGlnIleuSerSerAspIleG1YValIleSerG1YValAap 180
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Qy 181 SerPheProValIyThrTrpIuAlaPhePheIleuValAlaIleGlnMetValSerG1U 200
Db 567 TCATTCACTGAGAAACCGAAGCCGAATTCCTATTTGGTGGCCATTAACAAATGATACAGAG 636
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Qy 241 AsnAlaIyAsnG1YAlaIleuProIySleuG1UValIleValAspAlaArgIYThrIyS 260
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Qy 281 G1YThrCyegInThrThyTyr---GlnAaAlaMetPheSerGlnValIleIleSerThr 299
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LOCUS I43835 1195 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 5633155.
ACCESSION I43835
VERSION I43835.1 GI:2468933
KEYWORDS
SOURCE .
ORGANISM Unknown.
REFERENCE
AUTHORS Kim, M.-K., Lee, K.-H., Na, B.-K., Jeong, H.-S., Choi, K.-W., Moon, Y.-H.
and Jeon, H.-S.
TITLES Expression vector for phytolacca antiviral protein and process for
preparing transgenic plant transformed therewith
JOURNAL Patent: US 5633155-A 1 27-MAY-1997
FEATURES
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Pred. No.: 1.9e-94 Length: 1195
Score: 1235.50 Matches: 239
Percent Similarity: 86.3% Conservative: 33
Best Local Similarity: 75.9% Mismatches: 40
Query Match: 76.4% Indels: 3
DB: 6 Gaps: 2

US-09-978-274A-2 (1-314) x 143835 (1-1195)

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Db 87 TCAACTGGGCTGGTAATCAATCACTACATGTTGAGAGTACCACTTAAATGCAAAATAC 146
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Db 147 GCCACTTTCTGATGATGATCTTGGTAATGAGCGAAAGTCCAACTTAAATGCTATGGA 206
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RESULT 11

LOCUS 155866 1195 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 5648234.
ACCESSION 155866
VERSION 155866.1 GI:2476660

KEYWORDS

Unknown.

SOURCE

ORGANISM

Unknown.

Unclassified.

REFERENCE

1 (bases 1 to 1195)

ATTORNS

Moon, Y.-H., Jeon, H.-S., Choi, K.-W., Lee, K.-H. and Kim, M.-K.

TITLE

Expression vector for Phytolacca antiviral protein

JOURNAL

Patent: US 5648234-A 1 15-JUL-1997;

FEATURES

Location/Qualifiers

1..1195

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ORIGIN

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Score:	86.3%	75.9%				
Best Similarity:	76.4%					
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DB:						

US-09-978-274A-2 (1-314) x 155866 (1-1195)

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Db	807	TGGATAGTGTGAGAGTGGATGAAATCAAGCCTGTATGACACTTTAACTACCTTGCT	866
Qy	281	GIlyThrCysGIInThrTyr---GIAsnAlamEtPhsSerGInValIlleIseSerThr	299
Db	867	GCGAGCTGTCAACAACCTTATTAACCAAAATGTCATGTTTCCCAACTTATATATGTCI	926
Qy	300	TyTyrIAsenTyrMetSerAsnLeuGIAspLeuPheGIuGIyPhe	314
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Db 399 ATACCAATGCTGCCCAATACAAATACCAATCCAAAGTACGTTGTTGAGCTCCAAAGT 458
Qy 81 AlaAsnLeuIleuValIleThrLeuMetLeuArgAsnAsnLeuTyrValIleMetGlyTyr 100
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Db 879 CTTATCTCCAAAGTACTTAATTTGAGAGACATGAGGATGATGATGATGATGATGATGAT 938
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Qy 261 TrpIleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuTyrValAsn 280
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Qy 281 GlyThrCysGlnThrTyr---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
Db 1059 GGGAGCTGTCAAGACCTTATACCAAAATGCCAATGTTCTCAACTTAATATGCTACT 1118
Qy 300 TyrTyrAsnTyrMetSerAsnLeuGlyAspLeuPheGluGlyPhe 314
Db 1119 TATATATATATACATGTTAATCTTGGTATCTATTGAAGATTC 1163

RESULT 14

AX427731 1379 bp DNA linear PAT 20-JUN-2002
LOCUS AX427731
DEFINITION Sequence 30 from Patent WO0233107.
ACCESSION AX427731
VERSION AX427731.1 GI:21537838
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Garryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
AUTHORS Neelam, A., Atkinson, H.J., Mcpherson, M.J. and Thomas, C.J.R.
TITLE Plant cell death system

JOURNAL Patent: WO 0233107-A 30 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:3527"
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Score: 1235.50 Matches: 239
Percent Similarity: 86.3% Conservative: 33
Best Local Similarity: 75.9% Mismatches: 40
Query Match: 76.4% Indels: 3
DB: 6 Gaps: 2
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Qy 61 IleProMetLeuProAspThrAsnSerThrProlyTyrLeuLeuValIleLeuGlnGly 80
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Qy 81 AlaAsnLeuIleuValIleThrLeuMetLeuArgAsnAsnLeuTyrValIleMetGlyTyr 100
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Qy 101 SerAspProPheAsnGlyIleAsnLeuGlnIleuIleuTyrGlyIleValIleSerGlyVal 120
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Qy 121 GluArgThrAspValGluAsnThrIleuCysSerSerSerSerSerArgValAlaMetSer 140
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Qy 141 IleAsnTyrAsnSerLeuTyrProThrMetGluIleValAlaGluValAsnSerArgAsn 160
Db 639 ATAACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 698
Qy 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyIleValIleSerGlyValAsp 180
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Qy 181 SerPheProValIleThrGlnAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
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Qy 261 TrpIleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuTyrValAsn 280

Db 999 TGAATAGTGTGAGAGTGATGAATCAAGCTGATGACCTTAACCTGTTGCT 1058
Qy 281 GlyThrCysGlnThrThyTyr---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
Db 1059 GGAAGCTGTACAGCACTTAATCAACCAATGCCATGTTCTCTCACTTAATATGCTACT 1118
Qy 300 TyrTyrAsnTyrMetSerAsnLeuGlyAspLeuPheGluGlyPhe 314
Db 1119 TATTATTAATTAACATGGTTAATCTGTGATCTATTGTAAGGATTC 1163

RESULT 15
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LOCUS AR141172
DEFINITION Sequence 1 from patent US 6146628.
ACCESSION AR141172
VERSION AR141172.1 GI:15100689
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1379)
AUTHORS Uekun, F.M. and Turner, N.E.
TITLE Biotherapeutic agents comprising recombinant PAP and PAP mutants
JOURNAL Patent: US 6146628-A 14-NOV-2000;
FEATURES
Location/Qualifiers
1..1379
/organism="unknown"
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Alignment Scores:
Pred. No.: 4e-94 Length: 1379
Score: 1232.50 Matches: 238
Percent Similarity: 86.3% Conservative: 34
Best Local Similarity: 75.6% Mismatches: 40
Query Match: 76.2% Indels: 3
Gaps: 2

US-09-978-274A-2 (1-314) x AR141172 (1-1379)

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Qy 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLeuAspProLeuLeuLeuLeuLeuLeu 60
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Qy 61 IleProMetLeuProAspThrAsnSerThrProLeuTyrLeuLeuValLeuGlnGly 80
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Db 459 TCAAAATRAAAAAACCATCAACATATGCTGAGAGAAACAATTGTATGTATGGGTAT 518
Qy 101 SerAspProPheAsnGlyAsnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 120
Db 519 TCTGATCTCCCTTTGAAAACCAATTAATGCTTACCATATCTTTAATGATATCTCAGGTACT 578
Qy 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSer 140
Db 579 GAACGCCAAGATGTAGAGACTTACTTGTGCCAAATGCCAAATCTCGTGTAGAAAAAC 638
Qy 141 IleAsnTyrAsnSerLeuTyrProThrMetGluLeuLeuLeuLeuLeuLeuLeuLeuLeu 160
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Qy 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLeuIleSerGlyValAsp 180

Db 699 CAGGTCCAACTGGGAATTCAAAATCTCGACAGATTAATTTGGAAGAATTTCTCGAGTGATG 758
Qy 181 SerPheProValLeuThrGlnAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
Db 759 TCAATTCATGAGAAAACCCAAAGCCGAATTCCTAATGGTAGCCATACAAATGGTATCGAG 818
Qy 201 AlaAlaArgPheLeuTyrIleGluAsnGlnValLeuThrAsnPheAsnArgAlaPheTyr 220
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Qy 221 ProAspProLeuValIleAsnLeuGluLeuLeuTyrGlyLeuIleSerGlnAlaIleHis 240
Db 879 CTTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAATTTCAACAGCAATTCAT 938
Qy 241 AsnAlaLeuAsnGlyAlaLeuProLeuProLeuGlnLeuValAspAlaLeuLeuLeuLeu 260
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Qy 261 TrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLeuLeuLeuLeu 280
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Qy 281 GlyThrCysGlnThrThyTyr---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
Db 1059 GGAAGCTGTACAGCACTTAATTAACCAAAATGCGCATGTTCTCAACTTAATATGCTACT 1118
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Db 1119 TATTATTAATTAACATGGTTAATCTGTGATCTATTGTAAGGATTC 1163

Search completed: April 9, 2006, 07:31:28
Job time : 7173.98 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 9, 2006, 00:56:13 ; Search time 833.351 Seconds
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Title: US-09-978-274A-2

Perfect score: 1617
Sequence: 1 MKVWLVVVTLIAMIAPF.....VIISTYNNYMNIGDLFEFG 314

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-OUTFMT=pcr -NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abseq03h
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1352	83.6	792	6	AAD42716
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8	1233.5	76.3	1378	12	ADG76061
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ALIGNMENTS

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XX
AC AAD42715;
XX
DT 15-NOV-2002 (first entry)
XX
DE Pokeweed pro-PAP-S protein encoding DNA.
XX
KW Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KW gene; ds.
XX
OS Phytothacca americana.
XX
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XX FT /*product= "Pro-PAP-S protein"
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XX FT 1..24
XX FT /*tag= b
XX FT /bound_moiety= "Primer PPS1BF"
XX FT complement (735..776)
XX FT /*tag= c
XX FT /bound_moiety= "Primer PSXDR"
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XX      25-APR-2002.
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XX      15-OCT-2001; 2001WO-GB004593.
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XX      14-OCT-2000; 2000GB-00025217.
XX
XX      (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX      Thomas CR, Mcpherson MJ, Atkinson MJ, Neelam A;
XX      WPI; 2002-489891/52.
XX      P-PSDB; AAE55918.
XX
XX      Inducing necrotic effect in specific cells of plant by transforming plant
XX      PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX      PT which acts in response to application of specific stimulus to plant.
XX
XX      Claim 24; Page 73-74; 87pp; English.
XX
XX      The invention relates to a method of inducing a necrotic effect in
XX      CC specific cells of a plant. The method involves transforming the plant
XX      CC with a chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX      CC PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
XX      CC in response to the application of a specific stimulus to the plant so as
XX      CC to facilitate expression of the pokeweed antiviral protein in specific
XX      CC cells of the plant. The method is useful for inducing a necrotic effect
XX      CC in specific cells of a plant. The present sequence is pokeweed pro-PAP-S
XX      CC protein encoding DNA
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XX
XX      QY      21 SerThrCysAlaIleleanthrIlethrPheAspAlaGlyAsnAlaThrIleAsnlyTy 40
XX      DB      61 TCAACTGTGGCCATAATAGATCACCTTGTGATGCGAAATGCCACCATTAACAATAT 120
XX
XX      QY      41 AlaThrPheMetGlySerleuAlaGlnAlaIleAlaAspProlySleuylsGlyTgLy 60
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XX      QY      61 IleProMetleuProAspThrAsnSerThrProlySlyTleuValylSleuGlnGly 80
XX      DB      181 ATACCAATGCTACTACTAATTAATTCGACCCCTTAAGTACTTATTTGGTTAAGCTCCAAAGT 240
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XX      QY      81 AlaAsnLeuylsThrIleThrleuMetleuArgArgAsnAsnleuTyValMetGlyTy 100
XX      DB      241 GCAAAACCTAAACCAATTAACATGATGCGAGCAAAATTAATTAACGATGGGCTAT 300
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DB      421 ATTAATCAAAATGCTTATATCCGACCATGAGAAAGAAAGCAAGAAATCAAGAAAT 480
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QY      221 ProAspProlyValIleAsnleuGlnGlyTyTrpGlyValylSleuGlnAlaIleHis 240
DB      661 CCGATCCCAAAAGTAAATTAATTTGAGAGAAAGTGGGCAAAATCTCTGAGCAATTCAC 720
QY      241 AsnAlaIysAsnGlyValAlaLeuProlySProleuGluLeuValAspAlaIysGlyThrlys 260
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QY      281 GlyThrCysGlnThrThrTyTrpGlnAsnAlaMetPheSerGlnValIleIleSerThrTy 300
DB      841 GGAACCTGTCAAGCAACTTACCAAAATGCAAGTGTCTCAAGATTAATATTTCTACTTAT 900
QY      301 TyAsnTyMetSerAsnleuGlyAspLeuPheGluGlyPhe 314
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XX      RESULT 2
XX      AAD42716 standard; DNA; 792 BP.
XX      ID      AAD42716;
XX      AC      AAD42716;
XX      DT      15-NOV-2002 (first entry)
XX      DE      Pokeweed mature PAP-S protein encoding DNA.
XX      OS      Pokeweed
XX      KW      Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
XX      gene; db.
XX      XX
XX      OS      Phytolacca americana.
XX      FH      Key
XX      CDS      Location/Qualifiers
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PN	WO20023107-A2.
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25	-APR-2002.
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Pf	15-OCT-2001; 2001WO-GB004593.
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PR	14-OCT-2000; 2000GB-00025217.
PA	(ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
PI	Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;
DR	MP1: 2002-489891/52.
DR	P-PSDB; MAE25919.
XX	
PT	Inducing necrotic effect in specific cells of plant by transforming plants
PT	with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX	which acts in response to application of specific stimulus to plant.
PS	Claim 2; Page 76; 87pp; English.
XX	
CC	The invention relates to a method of inducing a necrotic effect in
CC	specific cells of a plant. The method involves transforming the plant
CC	with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC	PAP ¹ , PAP ^{II} and PAP ^S , where the gene(s) comprises a promoter which acts
CC	in response to the application of a specific stimulus to the plant so as
CC	to facilitate expression of the pokeweed antiviral protein in specific
CC	cells of the plant. The method is useful for inducing a necrotic effect
CC	in specific cells of a plant. The present sequence is pokeweed mature PAP ^S
XX	-S protein encoding DNA
SQ	
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Query Match:	83.6% Indels: 0
DB:	6 Gaps: 0
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Dd	4 ATAAATACGATCACTTTATGTCTGAATAATGCCACATTACAAATATGCCACTTATG 63
Dy	45 GluSerLeuAgAsnGlnAlaLyBaAPProLYBleuLYcCyTyrglyllepPrometLeu 64
Dd	64 GAATCTCTTCGTATCAAGCGAAAGATCCAAAATCTAAATGCATATGGCATACCAATGCTA 123
Dy	65 ProAdPThrAsnSerThrProLYsTYrleuLeuValLYleuGlnGylAlaenlleuLYs 84
Dd	124 CCTGATACCTAATTCGACCCTTAATGTCCTTATGTTAGTCCAAAGGTGCAACCTTAAA 183
Dy	85 ThrllerTrMeuLeuArgArGaenAleuLYrValMetGlyTYrSeArAPProPhe 104
Dd	184 ACCATTACCTAATGTGCTGAGACAATAATTAATTATACGTATGGGCTATTCTGATCCTTC 243
Dy	105 AsngIyaenLYcYeArGYrHisilePhenaApIlleThserThrgluaGthrAsp 124
Dd	244 AATGGCAATAAAGTGTCGTATCACTAATATTTAAGAATTAACAAGCACCGAACGCACTGAT 303
Dy	125 ValGIuaenThleucYasSerSerSerSerArValAlaMetSerilleanTYasn 144
Dd	304 GGAGGAATACCTCTTGGCTCAAGTTCTTAGTTCCTCGTGTCATATGTCATTAATCAAT 363
Dy	145 SerleuTYrProThrMetGluLYalYBaAlglValaSnSerArGaengInvalGlnleu 164
Dd	364 AGCTTATATCCAGCATYGAAAAAGAAAGCAAGATTAATCCAAAGAAATCAAGTCCAATTG 423

QY	155	GLYIILEGIIILELSESESRASPIIEGLIYLSIIIESEGLIYVAlAsPSeRPheProVal	184
Db	424	GSAAITTCANATICTGACGAGTGAACITGGAAAAATCTCTGAGAGTATTCATTCCCTGTA	493
QY	185	LYSThrGIuAlAPhePheLeuLeuValAlIIEGIInMetValSerGIuAlAlAATpHe	204
Db	484	AAAATCGAGGCGTTTTTTTCTACTGGTAGCCATCAAAATGGTTTCAGAGGCGAGCATTC	543
QY	205	LYSTYTYIIIEGLIAsnGInValIYsThrAsnPheAsnAlAlAPheTYrProAspPoloYs	224
Db	544	AAGTCAATAGAAACCAACTCAAGACTAATTTTAAATAGAGCATTCACCTGATCCCAAA	603
QY	225	VALIIIEAsnLeuGIuLyuSTpGIYLSIIIESEGLIAlAlIIEHISAsnAlAlYsAsn	244
Db	604	GTAATTAACCTTGGAGAGAGAGTGGGGCAAAATCTCTGAGGCATTCACAAATGCCAAGAT	663
QY	245	GLIAlAsnProLYsPheLeuGIuLeuValAspAlAlYsGLIYThrLYSTpIIIEValLeu	264
Db	664	GGGGCTTTTACCAACCACTGAGCTAGTGATGCCAAAGTACCAAGTGGATTAAGTTCTT	723
QY	265	ArgValAspGIuIIIEAsnArgAspValAlAlAsnLeuLYsTYrValAsnGLIYThrCY6GIn	284
Db	724	AGAGGTAGTGAATCAATCGTATGTGGCCTTTAAGTAACTTAATGAAACCTGTGAG	783
QY	285	ThrThr 286	
Db	784	ACAACT 789	
RESULT 3			
AAD42729			
ID	AAD42729	standard; DNA; 1092 BP.	
XX			
AC	AAD42729;		
XX			
DT	29-AUG-2003	(revised)	
DT	15-NOV-2002	(first entry)	
XX			
DE	Pokeweed PAP-S/TEV PCS/rice cystatin delta D86 fusion DNA.		
XX			
XX	Neurotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;		
KW	Chimeric; rice; cystatin delta D86; N1A protease cleavage site; PCS; ds.		
KW			
XX	Phytoplasma americana.		
OS	Oryza sativa.		
OS	Tobacco; Erch virus.		
OS	Chimeric.		
XX			
FH	Key	Location/Qualifiers	
FT	primer_bind	1..29	
FT		/*tag= a	
FT		/bound_moiety= "Primer PS1BP"	
FT		681..686	
FT	misc_feature	/*tag= b	
FT		/note= "Modified XbaI site"	
FT	primer_bind	complement(742..786)	
FT		/*tag= c	
FT	primer_bind	/bound_moiety= "Primer PCS-PAPSR"	
FT		766..806	
FT		/*tag= d	
FT	primer_bind	/bound_moiety= "Primer PCS-Delta86P"	
FT		766..786	
FT	misc_feature	/*tag= e	
FT		/note= "TEV N1A protease cleavage site"	
FT	primer_bind	complement(1066..1092)	
FT		/*tag= f	
FT		/bound_moiety= "Primer SYNPODELta86P"	
XX			
PN	MO20023107-A2.		
PD			
XX	25-APR-2002.		
XX			
PF	15-OCT-2001; 2001WO-GB004593.		

XX 14-OCT-2000; 2000GB-00025217.
 PR (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
 XX Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;
 XX WPI; 2002-469891/52.
 XX
 XX Inducing necrotic effect in specific cells of plant by transforming plant
 PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
 PT which acts in response to application of specific stimulus to plant.
 XX
 XX Disclosure; Page 83; 87pp; English.
 XX
 XX The invention relates to a method of inducing a necrotic effect in
 CC specific cells of a plant. The method involves transforming the plant
 CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
 CC PAP', PAP II and PAP-S, where the gene(s) comprises a promoter which acts
 CC in response to the application of a specific stimulus to the plant so as
 CC to facilitate expression of the pokeweed antiviral protein in specific
 CC cells of the plant. The method is useful for inducing a necrotic effect
 CC in specific cells of a plant. The present sequence is a fusion DNA. This
 CC sequence comprises pokeweed pro-PAP-S DNA, rice cystatin delta D86 DNA
 CC and Tobacco Etch virus (TEV) N1a protease cleavage site (PCS). (Updated
 CC on 29-AUG-2003 to standardise OS field)
 CC
 XX
 XX Sequence 1092 BP; 369 A; 195 C; 222 G; 306 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 3,86e-128 Length: 1092
 Score: 1307.00 Matches: 254
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 80.8% Indels: 0
 DB: Gaps: 0
 US-09-978-274A-2 (1-314) x AAD42729 (1-1092)
 QY 25 ILeAsnThrlleThrPheAspAlaGlyAsnAlaThrlleAsnlyrTyAlaTrnPhemec 44
 Db 4 ATAAATACGATCACTTGTGATGCTGGAATATGCCACTTAAACAAATATGCGACCTTTATG 63
 QY 45 GluSerleuArganglnAlaIyAspProlyLeuIyCystrgIyIleProMetleu 64
 Db 64 GAATCTCTCGTATACAGCGAAAGATCCAAACCTAAATAGTATGCAATCAACCAAGCTA 123
 QY 65 ProAspThrAsnSerThrProlyrTyIleuValIyIleuGlnGlyAlaAsnleuIy 84
 Db 124 CCGAATACATAATTCGACCCCTTAAGTACTTAATGCTTCAAGGTGCAAACTAATAA 183
 QY 85 ThrIleThreuleMetLeuArgAsnAsnleuTyValMetGlyTySerAspProphe 104
 Db 184 ACCATTACACTAATGCTGAGACGAATTAATTATAGCTATGCGCTATTTGATCCCTTC 243
 QY 105 AenglyAsnlyCystrgTyIleIlePheAsnAspIleThrSerThrgIuArgThrAsp 124
 Db 244 AATGGCAATTAAGTGTGATCAATATATTAATTAATTAATTAATTAATTAATTAATTAAT 303
 QY 125 ValGluAsnThreuleCySerSerSerSerSerSerSerValAlaMetSerIleAsnTy 144
 Db 304 GGGGAAATACCTTTGCTCAAGTCTAGTCTCGGTGCAATGTCCTAATTAATCAAT 363
 QY 145 SerleuTyProThreMetGlyIyValAlaGluValAsnSerArganglnValGlnleu 164
 Db 364 AGCTTATATCCGACCAATGGAAGAAAGCAAGATTAATCAAGAAATCAAGTCCATTTG 423
 QY 165 GlyIleGlnIleleuSerSerAspIleGlyIyIleSerGlyValAspSerPheProval 184
 Db 424 GGAATTCAAATACTCGACAGTGCATTTGGAATAATCTCGGAGTTGATTCATTCCTGTA 483
 QY 185 lyeThrGluAlaPhePheleuValAlaIleGlnMetValSerGluAlaAlaIaArgpne 204

Db 484 AAAACTGAGCGCTTTTCTTACTGTAGCCATCAATAGGTTCAAGAGCAGCGCATTC 543
 QY 205 lyeTyIleGluAsnGlnValIySerThraAsnPhaAsnArgAlaPheTyProAspProly 224
 Db 544 AAGTACATTAAGAGCAACCAAGTCAAGACTTAATTTAATTAAGACATTCACCTGATCCAAA 603
 QY 225 ValIleAsnleuGluGlyIyIleSerGlyValAlaIleHisAsnAlaIyAsn 244
 Db 604 GTAAATTAATCTTGAAGAGAAAGTGGGCAAAATCTCTGAGCAATTCACATGCCCAAT 663
 QY 245 GlyAlaIeupProlySerProleuGluIleuValAspAlaIyGlyThryIyTPDIIleVal 264
 Db 664 GGGGCTTTACCAACCACTTGAAGTATGATGCCAAAGTACCAAGTATGATGTTCTT 723
 QY 265 ArgValAspGluIleAsnArgAspValAlaIleuIleuTyIy 278
 Db 724 AGAGTGAATGAATCAATCGTATGTGCACTCTTAAGTAC 765
 RESULT 4
 AA245197
 ID AA245197 standard; DNA; 1379 BP.
 AC AA245197;
 DT 29-FEB-2000 (first entry)
 DE Wild-type pokeweed antiviral protein (PAP) nucleotide sequence.
 XX
 XX Pokeweed antiviral protein; PAP, PAP II; antifungal; transgenic plant;
 KW ribosome inhibiting protein; RIP; cereal crop; viral resistance; PVX;
 KM potato virus X; cucumber mosaic virus; CMV; ss;
 tomato yellow leaf curl virus.
 XX
 XX Phytolacca americana.
 FH Key Location/Qualifiers
 FT CDS 225..1166
 FT /*tag= a
 FT /product= "PAP"
 FT /note= "Pokeweed antiviral protein"
 XX
 XX MO9960843-A1.
 XX
 XX 02-DEC-1999.
 XX
 XX 21-MAY-1999; 99WC-US011301.
 XX
 XX 22-MAY-1998; 98US-0086374P.
 XX
 XX (RUTP) UNIV RUTGERS STATE NEW JERSEY.
 XX
 XX Turner NE, Wang P;
 XX WPI; 2000-062555/05.
 XX P-PADB; AAY58025.
 XX
 XX New antiviral DNA useful for generating transgenic plants resistant to
 PT viruses and/or fungi.
 PT
 PS Example; Page 4-5; 43pp; English.
 PS
 PS This is the pokeweed antiviral protein (PAP) nucleotide sequence. PAP is
 CC a type I ribosome-inhibiting protein (RIP) found in the cell walls of
 CC Phytolacca americana (pokeweed). It is a single polypeptide chain that
 CC catalytically removes a specific adenine residue from a highly conserved
 CC stem-loop structure in the 28S rRNA of eukaryotic ribosomes. The pokeweed
 CC antiviral protein II (PAP II) protein confers antiviral and/or antifungal
 CC activities to plants. A DNA molecule encoding a PAP II protein with an
 CC intact catalytic active site amino acid residue (R172) is useful for
 CC generating transgenic plants. PAP II DNA is useful for generating
 CC transgenic plants (especially cereal crops) through transforming a
 CC proplast or introducing the DNA directly into a plant part prior to
 CC regeneration. Cells and seeds which exhibit anti-viral and/or anti-fungal

CC actively thus have increased resistance to viruses and/or fungi. Viruses
 CC include potato virus X (PVX), cucumber mosaic virus (CMV), and tomato
 CC yellow leaf curl virus, and fungi include Pythium, Phytophthora,
 CC Sclerotinia and Aspergillus. PAP II proteins also confer resistance to
 CC other plants pests including insects, bacteria and nematodes. PAP II DNA
 CC is also useful for identifying a PAP II protein having reduced
 CC cytotoxicity. PAP II has a reduced cytotoxicity compared to PAP, so
 CC unlike PAP transgenic plants which are stunted and sterile, PAP II
 CC transgenic plants have a normal and fertile phenotype

SO Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,91e-120	Length:	1379
Score:	1235.50	Matches:	239
Percent Similarity:	86.3%	Conservative:	33
Best Local Similarity:	75.9%	Mismatches:	40
Query Match:	76.4%	Indels:	3
DB:	3	Gaps:	2

US-09-978-274A-2 (1-314) x AAZ5197 (1-1379)

QY 1 MetlyValMetLeuValValValThreulealATPLeuilealalProthr 20
 DB 225 ATGAAGTCGATGCTTGCGTGAACAATCAATA-----TGGCTCATTCCTGACCAACT 278
 QY 21 SerThrCysAlaIleAsnThrIleThrePheAspAlaGlyAsnAlaThrIleAsnLysThr 40
 DB 279 TCAACTGGGCTGGTAATACATCAATCAATGTTGGAATACACCATTAAGCAAAATAC 338
 QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysThrGly 60
 DB 339 GCCACTTTCTCGATGATCTTGGTATGACGAAAGATCCAAAGTTAAATGCTATGCA 398
 QY 61 IleProMetLeuPProAspThrAsnSerThrProLysThrLeuLeuValLysLeuGlnGly 80
 DB 399 ATACCAATGCTGCCCAATACCAATCAAAATCAAGTACGTTGCTTGAACCTCAAGGT 458
 QY 81 AlaAsnLeuLysThrIleThreMetLeuArgAsnAsnLeuLysValMetGlyThr 100
 DB 459 TCAATTAATAAAACATCACTATGCTGAGACGAAACAAATGTAATGATGAGTAT 518
 QY 101 SerAspProPheAsnGlyAsnLysCysArgThrHisIlePheAsnAspIleThrSerThr 120
 DB 519 TCGATCCCTTGAACCAATTAATGCTTACCATATCTTAATGATATCTCAGTACT 578
 QY 121 GluArgThrAspValGluAsnThrLeuLysSerSerSerSerSerArgValAlaMetSer 140
 DB 579 GAACGCCAAGATGAGAGACTACTCTTGGCCCAATGCAATCTCGGTAGTAAAAAC 638
 QY 141 IleAsnThrAsnSerLeuLysProThrMetGlnLysAlaGluValAsnSerArgAsn 160
 DB 639 ATAAACTTGTATGATCAATATCAACATGTGAATCAAAAGCGGAGTAAATCAAGAGT 698
 QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
 DB 699 CAGGTCAACTGGGAATTCAAATATCTGACAGTAAATTTGAAAAGATTTCGAGTATG 758
 QY 181 SerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
 DB 759 TCATTCATCTGAGAAACCGAAGCGGAATTCCTATTGAGGCAATCAATGATGATGAG 818
 QY 201 AlaAlaIlePheLysThrIleGluAsnGluValLysThrAsnPheAsnArgAlaPheThr 220
 DB 819 GCGACAAATTCAGATCAATGAGAAATCGGTGAAACTAAATTTTAAACAGGCACTCAAC 878
 QY 221 ProAspProLysValIleAsnLeuGluGluLysThrGlyLysIleSerGluAlaIleHis 240
 DB 879 CCTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAAGATTTCACAGCAATTCAT 938
 QY 241 AsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrLys 260
 DB 939 GATGCCAAGATGAGTATTACCAAACTCTCGAGCTAGTGGATGCGCAGGTGCGCAAG 998

QY 261 ThrIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysThrValAsn 280
 DB 999 TGGATAGTGTGAGAGATGATGAATACAGCTCAATGATGACCTTAAGTACGTTGGT 1058
 QY 281 GlyThrCysGlnThrThrThr---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
 DB 1059 GGGAGCTGTGACACACTTAATTAACCAAAATGCCATGTTCTCTCAACTTATATGCTACT 1118
 QY 300 TyrThrAsnThrMetSerAsnLeuGlyAspLeuPheGluGlyPhe 314
 DB 1119 TATTATATTACATGATGTTAATCTTGATGATCTATTGTAAGGATTC 1163

RESULT 5

AAZ59220 ID AAZ59220 standard; cDNA; 1379 BP.
 AAZ59220; AC AAZ59220; XX 20-APR-2000 (first entry)
 DT XX
 DE Pokeweed antiviral protein coding sequence spring leaf form.
 DE XX
 KW Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
 KW resistance; potato virus X; potato virus Y; potato leaf roll virus;
 KW tuber; ss.
 XX
 OS Phytoacca americana.
 PN US6015940-A.
 PD 18-JAN-2000.
 XX
 PP 07-APR-1992; 92US-00865169.
 XX
 PR 07-APR-1992; 92US-00865169.
 XX
 PA (MONS) MONSANTO CO.
 PI
 PI Kaniewski WK, Turner NE, Lodge JK;
 XX
 DR WPI; 2000-126326/11.
 XX
 XX
 PT Production of transgenic potato plants or tubers expressing pokeweed
 PT antiviral protein which are resistant to potato virus X or Y.
 XX
 PS Claim 6; Fig 4; 30pp; English.
 XX

CC This is the coding sequence for the spring leaf form of the pokeweed
 CC antiviral protein (PAP) which is used to generate transgenic potato
 CC plants. PAP is able to confer resistance to infection by potato virus X
 CC (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in the
 CC potato plant or tuber expressing PAP
 CC XX

SO Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,91e-120	Length:	1379
Score:	1235.50	Matches:	239
Percent Similarity:	86.3%	Conservative:	33
Best Local Similarity:	75.9%	Mismatches:	40
Query Match:	76.4%	Indels:	3
DB:	3	Gaps:	2

US-09-978-274A-2 (1-314) x AAZ59220 (1-1379)

QY 1 MetlyValMetLeuValValValThreulealATPLeuilealalProthr 20
 DB 225 ATGAAGTCGATGCTTGCGTGAACAATCAATA-----TGGCTCATTCCTGACCAACT 278
 QY 21 SerThrCysAlaIleAsnThrIleThrePheAspAlaGlyAsnAlaThrIleAsnLysThr 40
 DB 279 TCAACTGGGCTGGTAATACATCAATCAATGTTGGAATACACCATTAAGCAAAATAC 338

[illegible]

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FT      /*tag= a
FT      /note= "Mature PAP' sequence"
FN      WO200233107-A2.
PD      25-APR-2002.
PP      15-OCT-2001; 2001WO-GB004593.
PR      14-OCT-2000; 2000GB-00025217.
PA      (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
PI      Thomas CJR, Mcpherson WJ, Atkinson HJ, Neelam A;
PI      WPI; 2002-468891/52.
XX      DR
XX      PR      Inducing necrotic effect in specific cells of plant by transforming plant
XX      PT      with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX      PT      which acts in response to application of specific stimulus to plant.
XX      PS      Claim 5; Page 86; 87pp; English.
XX      CC      The invention relates to a method of inducing a necrotic effect in
XX      CC      specific cells of a plant. The method involves transforming the plant
XX      CC      with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX      CC      PAP', PAP1 and PAP-8, where the gene(s) comprises a promoter which acts
XX      CC      in response to the application of a specific stimulus to the plant so as
XX      CC      to facilitate expression of the pokeweed antiviral protein in specific
XX      CC      cells of the plant. The method is useful for inducing a necrotic effect
XX      CC      in specific cells of a plant. The present sequence is pokeweed PAP' DNA
SQ      Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      1.91e-120      Length:      1379
Score:      1235.50      Matches:      239
Percent Similariety:      86.3%      Conservative:      33
Best Local Similariety:      75.9%      Mismatches:      40
Query Match:      76.4%      Indels:      3
DB:      Gaps:      2

US-09-978-274A-2 (1-314) x AHD42738 (1-1379)
QY      1 MetLyseValMetLeuValValValThrLeuLeaAlaTrpLeuLeaAlaAlaProThr 20
Db      225 ATGAGAGCGATGGTGTGTGGTGAACAATCAATA-----TGGTCATTCTTGACCAACT 278
QY      21 SerThrCysAlaAlaLeuThrThrLeuThrLeuAlaGlyValAlaThrIleAsnLysTyr 40
Db      279 TCAACTGGGCGTGTGATCAATCAATCTCAACATGTTGGAACTACACCAATTAACCAATAC 338
QY      41 AlaThrPheMetCysLeuLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGly 60
Db      339 GCCACTTTTCTGAATGATCTTGTGTATGAGCGAAGATCCAAATTGTAATGCTATGCA 398
QY      61 IleProMetLeuProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGly 80
Db      399 ATACCAATGCTGCGCAATCAATCAATCAATCCAAATGATCGTTGGTGAAGCTCAAGGT 458
QY      81 AlaAsnLeuLysThrIleThrLeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyr 100
Db      459 TCAAAATTAATAAACCATCACTAATAGCTGAGCAACAACAATTTGATGATGGATTAT 518
QY      101 SerAspProPheAsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThr 120
Db      519 TCTGATCCCTTGAAGAACCAATTAATGTGTTACCAATATCTTAATGATATCTCAGTACT 578
QY      121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSer 140
Db      579 GAACGGCAAGATGTADAAGCTAATCTTTTGGCCCAATGCCAATTTCTCGTTAGTAACAA 638
QY      141 IleAsnTyrAsnSerLeuTyrProThrMetGluLysValAlaGluValIleAsnSerArgAsn 160

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QY 201 AAlaAlaArgPheIleuTyrlleGluAenGluValIleuThrAenPheAenArgAlaPheTyr 220
 Db 819 GCAGCAAGATTCAAGTACATAGAGAAATCAGGTGAAAACTAATTTTAAACAGACATTCAAC 878
 QY 221 ProAspProIleValIleAenLeuGluGluIleuTyrGlyIleuSerGluAlaIleHis 240
 Db 879 CCTAATCCCAAGTACTTAATTTTGCAAGACATGGGGTAAGATTTCACACAGCAATTCAT 938
 QY 241 AsnAlaIleuAenGluValAleuProIleuSerProLeuGluIleuValAspAlaIleuSerGlyThrLys 260
 Db 939 GATGCCAAGATGAGATTGTACCCAAACCTCTGAGCTAGTGAATGCCACTGGTCCAG 998
 QY 261 TrpIleValIleuArgValAspGluIleAenArgAspValAlaIleuLeuIleuSerGlyThrValAsn 280
 Db 999 TGGATAGTGTGAGAGTGAATCAAGCCCTGATGTAGCACTTAAACTACGTTGCT 1058
 QY 281 GlyThrCysGlnThrThrTyr---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
 Db 1059 GGGAGCTGTCAAGCACTTATTAACCAAAATGCCATGTTCTCTCAACTTATTAATGTCTACT 1118
 QY 300 TyrTyrAsnTyrMetSerAenLeuGluAspLeuPheGluGlyPhe 314
 Db 1119 TATTAATTAATTAATGATGTTAATCTTGGTGAATCTAATTTGAAGATTTC 1163

RESULT 8

ADG76061
 ID ADG76061 standard; DNA; 1378 BP.

AC ADG76061;

XX 11-MAR-2004 (first entry)

XX American pokeweed antiviral protein (PAP) DNA SegID 1.

XX gene; ds: pokeweed antiviral protein; PAP; HIV-1; anti-HIV; antiviral;

KM nucleoside analogue inhibitor; viral protease inhibitor; viral infection;

XX american pokeweed; retroviral.

OS Phytolacca americana.

XX WO2003106479-A2.

XX 24-DEC-2003.

XX 17-JUN-2003; 2003WO-US019141.

XX 17-JUN-2002; 2002US-0389649P.

XX (PARK-) PARKER HUGHES INST.

XX Uckun FM;

XX WPI; 2004-082156/08.

XX P-PSDB; ADG76064.

XX Novel modified pokeweed antiviral protein useful for inhibiting viral

XX replication, for inducing depurination of viral RNA, or for treating

XX viral infection in subject.

XX Example 2; SEQ ID NO 1; 62pp; English.

CC This invention relates to novel modified pokeweed antiviral proteins
 CC (PAPs). Specifically, it refers to modifications relative to wild-type
 CC PAP that confer increased activity towards viral RNA, particularly
 CC retroviral RNA such as HIV-1 and drug resistant HIV-1. Furthermore,
 CC modified PAP also exhibits decreased activity towards ribosomal RNA
 CC relative to wild-type PAP. The present invention describes a molecular
 CC model of PAP-HIV RNA interactions that have been used for the rational
 CC redesign of PAP mutants with potent anti-HIV activity, where
 CC modifications have been introduced in regions other than the active site.
 CC Accordingly, these mutants represent antiviral agents that can work as
 CC nucleoside analogues inhibitors of reverse transcriptase, as well as viral
 CC protease inhibitors that can be used for treating viral infections. As

CC such, they are useful for inhibiting viral replication and for
 CC depurinating viral RNA. This polynucleotide sequence is the DNA encoding
 CC the wild type american pokeweed antiviral protein (PAP) of the invention.
 XX

SQ Sequence 1378 BP; 487 A; 234 C; 268 G; 389 T; 0 U; 0 Other;

Alignment Scores:

	3.11e-120	Length:	1378
Pred. No.:	1233.50	Matches:	239
Score:	86.3%	Conservative:	33
Percent Similarity:	75.9%	Mismatches:	40
Best Local Similarity:	76.3%	Indels:	2
Query Match:	12	Gaps:	2

US-09-978-274A-2 (1-314) x ADG76061 (1-1378)

QY 1 MetIleValMetLeuValValValValIleThrIleAlaIleTrpLeuIleAlaIleProThr 20
 Db 224 ATGAAGTCGATGCTGTGTGGTGAACAAATATCAATA-----TGGCTCATTTCTTGACACCACT 277
 QY 21 SerThrCysAlaIleAenThrIleThrPheAspAlaGlyAsnAlaThrIleAenIleTyr 40
 Db 278 TCACTTGGGCTGTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 337
 QY 41 AlaThrPheMetGluSerLeuArgAenGluAlaIleAspProIleuSerGlyTyrGly 60
 Db 338 GCACATTTCTGATGATGATCTCTGTAATGAAGGAAGATCCAAAGTTAAATGCTATGGA 397
 QY 61 IleProMetLeuProAspThrIleAenSerThrProIleuSerGlyTyrLeuValIleuGlnGly 80
 Db 398 ATACCAATGCTGCCCAATCAAAATCAAAATCAAAATCAAAATGATGTTGATGATGATGATGAT 457
 QY 81 AlaAenIleuIleThrIleThrIleuMetLeuArgArgAsnAenIleuTyrValMetGlyTyr 100
 Db 458 TCAATTAATAAAACCATTCACACTAATGCTGAACCAAAATTTGATGTGATGATGATGAT 517
 QY 101 SerAspProPheAenGluValAenIleuSerGlyTyrIleIlePheAsnAspIleThrSerThr 120
 Db 518 TCGATCCCTTGAAGCAATTAATGCTGTAATGCTGTAATGCTGTAATGCTGTAATGCTGTAAT 577
 QY 121 GluArgThrAspValGluAenThrIleuSerSerSerSerSerSerSerSerSerSerSer 140
 Db 578 GAACGCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 637
 QY 141 IleAenTyrAsnSerIleuTyrProThrMetGluIleValAlaIleValAenSerArgAen 160
 Db 638 ATTAATCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 697
 QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyIleValIleSerGlyValAsp 180
 Db 698 CAGGTCCAACTGGGAATTCAAATTAATCGACAGTAATTAATGAAGATTCTGGAAGTATG 757
 QY 181 SerPheProValIleThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
 Db 758 TCATTCACCTGAGAAAAACCAAGCCCAATTCCTAATGGTAGCCATCAAAATGGATATCAGAG 817
 QY 201 AAlaAlaArgPheIleuTyrlleGluAenGluValIleuThrAenPheAenArgAlaPheTyr 220
 Db 818 GCAGCAAGATTCAAGTACATAGAGAAATCAGGTGAAAACTAATTTTAAACAGACATTCAAC 877
 QY 221 ProAspProIleValIleAenLeuGluGluIleuTyrGlyIleuSerGluAlaIleHis 240
 Db 878 CCTAATCCCAAGTACTTAATTTTGCAAGACATGGGGTAAGATTTCACACAGCAATTCAT 937
 QY 241 AsnAlaIleuAenGluValAleuProIleuSerProLeuGluIleuValAspAlaIleuSerGlyThrLys 260
 Db 938 GATGCCAAGATGAGATTGTACCCAAACCTCTGAGCTAGTGAATGCCACTGGTCCAG 997
 QY 261 TrpIleValIleuArgValAspGluIleAenArgAspValAlaIleuLeuIleuSerGlyThrValAsn 280
 Db 998 TGGATAGTGTGAGAGTGAATCAAGCCCTGATGTAGCACTTAAACTACGTTGCT 1057
 QY 281 GlyThrCysGlnThrThrTyr---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299

DB 1058 GGGAGCGCTGACGACCACTTATACCAAAATGCCAGTTCCTCAACTATATATCTACT 1117
Qy 300 TTTTAAATTTATTCATGTTAACTTGGATCTATTGTAAGGATTC 1162
Db 1118 TATTATTAATTAACATGTTAACTTGGATCTATTGTAAGGATTC 1162

RESULT 9
AAC87929 standard; DNA; 1379 BP.
AAC87929;
AAC87929;
06-MAR-2001 (first entry)
P. americana pokeweed antiviral protein encoding DNA SEQ ID NO:1.
Phytolacca americana; pokeweed; pokeweed antiviral protein; PAP; cancer;
KW bioterapeutic; fusion protein; immunconjugate; mutant; cytostatic;
anti-HIV; human immunodeficiency virus; AIDS; leukemia; lymphoma;
XX brain tumour; neuroblastoma; soft tissue sarcoma; osteosarcoma; SS.
OS Phytolacca americana.
XX
XX Key Location/Qualifiers
XX FT CDS 225..1166
XX FT /*tag= a
XX FT /product= "pokeweed antiviral protein (PAP)"
XX US6146628-A.
XX 14-NOV-2000.
XX 11-JUL-1995; 95US-00501253.
XX 11-JUL-1995; 95US-00501253.
XX (MIND) UNIV MINNESOTA & RUTGERS.
XX (UYNE-) UNIV STATE NEW JERSEY.
XX Uckun FM, Turner NE;
XX MPI; 2001-040422/05.
XX P-PSDB; AAB36500.
XX
XX Immunconjugates useful for treating cancer and acquired immunodeficiency
XX syndrome, comprises mutant pokeweed anti-viral protein and a targeting
XX moiety that binds a cell surface receptor.
XX
XX Disclosure; Col 47-50; 32pp; English.
XX
XX The present invention describes a fusion protein or an immunconjugate
XX (I), comprising mutant Pokeweed Anti-viral Protein (PAP) having an amino
XX acid substitution at residue 75, 97 or 176 of native PAP and a targeting
XX moiety that binds a cell surface receptor. (I) can have cytosolic and
XX anti-HIV activities, and is an inhibitor of cellular RNA or protein
XX synthesis. (I) is useful for treating AIDS and cancers including
XX leukemia, lymphoma, a brain tumour, neuroblastoma, osteosarcoma, soft
XX tissue sarcoma, breast, prostate, ovarian, testicular, melanoma, lung, or
XX colon cancer. Immunconjugates prepared using PAP mutants exhibit an
XX improved therapeutic index over immunconjugates containing either wild-
XX type PAP or variant PAP. The present sequence encodes the wild-type PAP,
XX which is given in the exemplification of the present invention
XX
XX Sequence 1379 BP; 488 A; 234 C; 268 G; 389 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 3,97e-120 Length: 1379
XX Score: 1232.50 Matches: 238
XX Percent Similarity: 86.3% Conservative: 34
XX Best Local Similarity: 75.6% Mismatches: 40
XX Query Match: 76.2% Indels: 3
XX DB: 4 Gaps: 2

US-09-978-274A-2 (1-314) x AAC87929 (1-1379)
Qy 1 MellyValMelleuValValValThleuIleAlaTrpleuIleAlaProthr 20
Db 225 ATGAAAGCGATGCTTGGTGAGCAATATCAATA-----TGGCTCATTTGGACCAACT 278
Qy 21 SerThrCysAlaIleAenThrIleThrPheAspAlaGlyAsnAlaThrIleAsnValSer 40
Db 279 TCACCTTGGGCTGGAATACATCATCTACCAAGTTGGAAGTACACCATTAAGCAATAC 338
Qy 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaIleAspProlySleuIleCysTyGly 60
Db 339 GCCACTTTCTGAATGATCTTCGTAATGAAGCGAAGATCCAGTTTAAATGCTATGCA 398
Qy 61 IleProMetLeuProAspThrAsnSerThrProlySlyLeuValIleSleuGlnGly 80
Db 399 ATACCAATGCTGCCCATACCAATACCAATCCAAAGTACGTTGGTTGAGCTCCAAAGT 458
Qy 81 AlaAsnLeuSerThrIleThrLeuMetLeuArgAsnAsnLeuTyValMetGlyTy 100
Db 459 TCACATTAATAAAACCATCACACTAATGCTGAGAGCAAAACATTTGATGATGAGGTTAT 518
Qy 101 SerAspProPheAsnGlyAsnIleCysArgTyRHisIlePheAsnAspIleThrSerThr 120
Db 519 TCTGATCCCTTTGAACCATTAATATGCTTACCATATCTTTAATGATATCTCAGTACT 578
Qy 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSer 140
Db 579 GAAGCCCAAGATGTAGAGTACTCTTGGCCCAATGCCAATTCCTCGTTAGTAAAC 638
Qy 141 IleAsnThrAsnSerLeuTyProThrMetGluIleValIleGluValAsnSerArgAsn 160
Db 639 ATAACTTGATGATGATATCCACATTCGAAATCAAAACCGGAGATTAATCAAGAGT 698
Qy 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerSerAspIleGlyIleSerGlyValAsp 180
Db 699 CAGTCCAACTGGGAATTCAAATACCTGACAGATTAATTTGGAAGATTTCTGAGTANG 758
Qy 181 SerPheProValIleThrGluAlaPhePheLeuValAlaIleGlnMetValSerGlu 200
Db 759 TCATTCACGTGAGAAACCCCAAGCCGAATTCCTATTGGTGACCATCAATAGGTATCAG 818
Qy 201 AlaAlaArgPheLeuTyRTrIleGluAsnGlnValIleThrAsnPheAsnArgAlaPheTy 220
Db 819 GCAAGCAAGATTCAGATACATGAGATCAGTGAAATCTAATTTTAAACAGACATTTAAC 878
Qy 221 ProAspProlyValIleAsnLeuGlnGluTyRTrGlyIleSerGlnAlaIleHis 240
Db 879 CTTAATCCCAAGTACTTAATTTTGCAGAGACATGGGGTAAATTTCAACAGCAATTCAT 938
Qy 241 AsnAlaIleAsnGlyAlaLeuProlyProLeuGlnLeuValAspAlaIleGlyThrLys 260
Db 939 GATGCCAAGATGAGAGTTTAACTCAAACTCTGACCTAGTGATGCAAGTGGGCAAG 998
Qy 261 TrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuTyRValAsn 280
Db 999 TGGATGTGTGAGATGTGAGTAAATCAAGCTGATGTGACATCTTAAATCAAGTGGT 1058
Qy 281 GlyThrCysGlnThrThrTyR---GlnAsnAlaMetPheSerGlnAlaIleIleSerThr 299
Db 1059 GGGAGCTGACGACCACTTATACCAAAATGCCATTTCTCACTTATTAATGCTACT 1118
Qy 300 TTTTAAATTTATTCATGTTAACTTGGATCTATTGTAAGGATTC 1162
Db 1119 TATTATTAATTAACATGTTAACTTGGATCTATTGTAAGGATTC 1162

RESULT 10
ADM74765 standard; cDNA; 1164 BP.
ID ADM74765
XX ADM74765;
XX AC
XX

DT 03-JUN-2004 (first entry)
XX HIV-1 inhibition activity related Tat cDNA.
XX
XX human immunodeficiency virus; HIV-1; tumour; plant;
KM Chinese phytoleuca leaf; trans-acting activation factor; Tat; mutant;
KM gene; ss.
XX
XX Human immunodeficiency virus 1.
XX
XX
XX Key Location/Qualifiers
XX CDS 2..943
XX /tag= a
XX /product= "Tat HIV-1 protein"
XX
XX CN1400220-A.
XX
XX 05-MAR-2003.
XX
XX 02-AUG-2001; 2001CN-00123911.
XX
XX 02-AUG-2001; 2001CN-00123911.
XX
XX (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
XX
XX Peng X, Bai L, Yin B;
XX
XX MPI; 2003-469263/45.
XX
XX P-PSDB; ADM74766.
XX
XX
XX Two kinds of cDNA with activity capable of extensively inhibiting HIV and
XX its expression, separation and purification method in protokaryon.
XX
XX Example 9; Page 11-12; 17pp; Chinese.
XX
XX The present invention relates to two kinds of cDNA which can inhibit
XX human immunodeficiency virus (HIV-1) activity, including separation clone
XX of two kinds of cDNA, external mutation, fusion expression in prokaryotes
XX and application of the cDNA in preparation of preparation for curing the
XX virus and tumours. One of the described cDNAs is obtained by separation
XX and cloned from a plant Chinese phytoleuca leaf, and one from the trans-
XX acting activation factor (Tat) mutant coded by human immunodeficiency
XX virus HIV-1 gene. This polynucleotide sequence represents the Tat cDNA
XX used in the HIV-1 inhibition activity of the invention.
XX
XX
XX Sequence 1164 BP; 403 A; 203 C; 218 G; 340 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 4.02e-120 Length: 1164
XX Score: 1231.50 Matches: 239
XX Percent Similarity: 86.3% Conservative: 33
XX Best Local Similarity: 75.9% Mismatches: 40
XX Query Match: 76.2% Indels: 3
XX DB: 11 Gaps: 2
XX
XX US-09-978-274A-2 (1-314) x ADM74765 (1-1164)
XX
XX
XX 1 MettysValMetLeuValValValTrrLeuLeuAlaTrrLeuLeuAlaAlaProtr 20
XX 2 ATGAAGTCATGCTT-----GTGGTGAACATTCATGCTTCTTCTTGAACAACT 55
XX
XX 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLys 40
XX 56 TCAACTTGGGCTGTGAATCAATCATCATCAATGTTGGAAGTACCACTTACCAATAC 115
XX
XX 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysGlyGly 60
XX 116 GGCACCTTCTTCTGTGAATATCTTGTGAATGAAAGCAAGTCAAGTTAAATGCTTATGA 175
XX
XX 61 IleProMetLeuProAspThrAsnSerThrProLysTrrLeuLeuValLysLeuGlnGly 80
XX 176 ATACCAATGTTGCCCAATACCAATCCAAATCCAAATGATGCTTGAAGTCTCAAGGT 235

QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgArgAsnLeuLysTrrValMetGlyTyr 100
DB 236 TCAATATTAATAAACAATTCACATTAATGTGAGCGAACAATTGTATGTGATGGCTAT 295
QY 101 SerAspProPheAsnGlnLysLeuLysCysGlyTrrIleIlePheAsnAspIleThrSerThr 120
DB 296 TGTGATCCCTTGTGATCCAAATATGTCGTTCACATTAATGATATCTCAAGTACT 355
QY 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerArgValAlaMetSer 140
DB 356 GAACGCCAAGATGTATAGACTACTCTTGTGCCAAATCCCAATCTCTGTGTACTATAAAC 415
QY 141 IleAsnTrrAsnSerLeuTrrProThrMetGluLysAlaGluValAsnSerArgAsn 160
DB 416 ATTAATCTATGATGATGATATCCAACTTGTGAATCAAAAGCGGAGTAAATCAAGACT 475
QY 161 GlnValGlnLeuGlnLysIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
DB 476 CAAGTTCAACTGGGAATTCAAATACCTGACAGTAATATGGAAGATTTCTGAGAGTACG 535
QY 181 SerPheProValLysThrGlnAlaPhePheLeuLeuValAlaIleGlnMetValSerGln 200
DB 536 TCATTCATCGAGAAACCGAAGCCGAATTCCTACTGTGACCATCAATATGATACAGAG 595
QY 201 AlaAlaArgPheLysTrrIleGlnAsnGlnValLysThrAsnPheAsnArgAlaPheTyr 220
DB 596 GCAGCAAGATTCAGATACATAGGGAATCAGTGAAAATTAATTTTAAAGAGACTCAAT 655
QY 221 ProAspProLysValIleAsnLeuGlnLysTrrGlyLysIleSerGlnAlaIleHis 240
DB 656 CCAATATCCCAAGATTAATTTGGAAGAGACATGGGGTAATTTCTACAGCAATTCAT 715
QY 241 AsnAlaLysAsnGlnValAlaLeuProLysProlLeuGlnLeuValAspAlaLysGlyThrLys 260
DB 716 GATGCCAAGATTCGACTTTTACCCAACTCTCGACTGTGATGATCCAGTGTGCCAG 775
QY 261 TrrIleValLeuArgValAspGlnIleAsnArgAspValAlaLeuLeuLysTrrValAsn 280
DB 776 TGGATGTGTGATGAGTGTGATATCAAGCTGATGTGACCTTTAAACTACGTTGGT 835
QY 281 GlyThrCysGlnThrTrrTyr--GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
DB 836 GGGAGCTGCAACCACTTAATACCAAAATGCAATGTTTCTCAACTTAATATGTCTACT 895
QY 300 TrrTrrAsnTrrMetSerAsnLeuGlnLysAspLeuPheGlnGlyPhe 314
DB 896 TATTATTAATTATATGCTAATCTGTGTATCTATTGTAAGGATTC 940
XX
XX
XX RESULT 11
XX AAQ56672
XX ID AAQ56672 standard; cDNA; 1195 BP.
XX AC AAQ56672;
XX
XX 16-OCT-2003 (revised)
XX 25-MAR-2003 (revised)
XX 04-SEP-1994 (first entry)
XX
XX Sequence of Phytoleuca antiviral protein (PAP) cDNA.
XX
XX Antiviral protein; PAP; virus-resistance; transgenic plant; ss.
XX
XX Phytoleuca americana; L.
XX
XX
XX Key Location/Qualifiers
XX CDS 33..974
XX /tag= a
XX
XX EP58554-A1.
XX
XX 09-MAR-1994.
XX
XX 30-JUN-1993; 93EP-00110445.
XX
XX

XX 16-AUG-1992; 92KR-00014895.
 PR (JINR-) JIN RO LTD.
 PA
 PI Kim M, Lee K, Na B, Jeong H, Choi K, Moon Y, Jeon H;
 XX WPI; 1994-076002/10.
 DR P-PSDB; AAR48548.
 XX
 PT Expression vector for phytolecta antiviral protein - used for producing
 PT transgenic virus-resistant plants and for producing the antiviral agent.
 XX
 PS Disclosure; Fig 1; 15pp; English.
 CC To isolate PAP gene, total cellular mRNA was purified from leaves of
 CC phytolecta americana L. obd. in Korea. A cDNA library was constructed.
 CC The PAP gene was selected by immunoscreening employing anti-PAP antibody.
 CC A deletion mutant was prepd. from the isolated PAP gene, and the DNA
 CC sequence of the PAP genome was determined. (Updated on 25-MAR-2003 to
 CC correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 1195 BP; 420 A; 201 C; 230 G; 344 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6,78e-120 Length: 1195
 Score: 1229.50 Matches: 238
 Percent Similarity: 86.0% Conservative: 33
 Best Local Similarity: 75.6% Mismatches: 41
 Query Match: 76.0% Indels: 3
 DB: Gaps: 2
 US-09-978-274A-2 (1-314) x AAQ56672 (1-1195)
 QY 1 MetlyValMetLeuValValValThreuleAlaTrpleuileAlaIleProthr 20
 DB 33 ATGAAGTCGATGCTTGTGGTGAATATCAATA-----TGGCTCATTTCTTGACCAACT 86
 QY 21 SerThrCysAlaIleAsnThrIleThrPheAspIleGlyAsnIleThrIleAsnIleThr 40
 DB 87 TCAACTTGGCTGTGAATACATATCATATCAATTTGAAGTACACCATTTAGCAAAATAC 146
 QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaIleAspProlySleuIleCysIleGly 60
 DB 147 GCCACTTTTCTGAATGATCTTTCGTAATGAGCGAAATCCAACTTTAAATGTAATGCA 206
 QY 61 IleProMetLeuProAspThrAsnSerThrProlySleuIleValIleGlnGly 80
 DB 207 ATACCAATGCTGCCCAATACAAATCAAAATGACGTGTTGAGTCCCAAGT 266
 QY 81 AlaAsnLeuIleThrIleThrLeuMetLeuArgAsnAsnLeuIleValMetGlyIle 100
 DB 267 TCAAAATTAATAAACAATCAATCACTATATCTGACGAAACAAATTTGATGATGGTAT 326
 QY 101 SerAspProPheAsnGlyAsnIleCysArgIleIlePheAsnAspIleThrSerThr 120
 DB 327 TCTGATCCCTTTGAAACACCAATTAATGCTTACATATCTTATATGATCTCAAGTACT 386
 QY 121 GlnArgThrAspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSer 140
 DB 387 GAACGCCAAGATATGAGATCACTCTTGGCCAAATCCCAATTCCTCGTGAAGTAAAC 446
 QY 141 IleAsnIleAsnSerLeuIleProThrMetGluIleValIleGluValIleAsnSerArgAsn 160
 DB 447 ATTAACCTTATATGTCATATCCAACTTGGAATCAAAACCGGAGTAAATCAAGAGT 506
 QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyIleSerGlyValAsp 180
 DB 507 CAAGTCCAACTGGGAATTCAAATATCTGACAGATATTTGAAAGATTTCTGGAGTANG 566
 QY 181 SerPheProValIleThrIleGluIlePhePheLeuLeuValAlaIleGlnMetValSerGlu 200
 DB 567 TCATTCACGTAGAAACCGAAGCGAATTCCTATGTGTACCAATGATATCAGAG 626

QY 201 AlaIleAsnProPheIleThrIleGluAsnGlnValIleThrAsnPheAsnArgAlaPheIle 220
 DB 627 GCAGCAAGATTCAGATGATGAGATACAGGTGAAAATTAATTTTAAACAGCAATTCAC 686
 QY 221 ProAspProIleValIleAsnLeuGluIleThrIleGlyIleSerGlnAlaIleHis 240
 DB 687 CCTAATCCCAAGATCTTAATTTTCAAGACATGGGGTAAAGATTTCACAGCAATTCAT 746
 QY 241 AsnAlaIleAsnGlnIleAlaLeuProIleProIleGluIleValIleAspAlaIleGlyIle 260
 DB 747 GATGCCAAGATGAGATTTTACCAAACTCTGAGCTAGTGAATGCGCAGTGGCCAG 806
 QY 261 ThrIleValIleAsnArgValIleAsnArgAspValAlaLeuLeuIleIleValIleAsn 280
 DB 807 TGGATGATGTTGAGAGTGAAGTGAATCAAGCTGATGTACCTTTAACTAAGTGTGT 866
 QY 281 GlyThrCysGlnThrThrIleIleGlnAsnAlaMetPheSerGlnValIleIleSerThr 299
 DB 867 GGGAGCTGTGACAACTTATATACCAAAATGCCATGTTCTCTCACTTATATATGTCTACT 926
 QY 300 TyrThrAsnIleThrMetSerAsnLeuGlyAspLeuPheGlnIlePhe 314
 DB 927 TATTATATTTACATGTTAATCTTGTGATCTATTTGAAGATTC 971
 RESULT 12
 AAD42739
 ID AAD42739 standard; DNA; 1378 BP.
 AC AAD42739;
 DT 15-NOV-2002 (first entry)
 XX
 DB Pokeweed PAP' DNA #2.
 XX
 OS Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds-
 XX
 PH Phytolecta americana.
 FT Key Location/Qualifiers
 FT misc_feature 290..1076
 FT /*tag= a
 FT /note= "Mature PAP' sequence"
 XX
 PN W0200233107-A2.
 XX
 XX 25-APR-2002.
 PD
 XX 15-OCT-2001; 2001MO-GB004593.
 PF
 PR 14-OCT-2000; 2000GB-00025217.
 XX
 PA (ADT8-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
 XX
 PI Thomas CJR, Mcpherson MJ, Atkinson HU, Neelam A;
 XX WPI; 2002-489891/52.
 DR
 PT Inducing necrotic effect in specific cells of plant by transforming plant
 PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
 PT which acts in response to application of specific stimulus to plant.
 XX
 PS Claim 5; Page 86-87; 87pp; English.
 CC The invention relates to a method of inducing a necrotic effect in
 CC specific cells of a plant. The method involves transforming the plant
 CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
 CC PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
 CC in response to the application of a specific stimulus to the plant so as
 CC to facilitate expression of the pokeweed antiviral protein in specific
 CC cells of the plant. The method is useful for inducing a necrotic effect
 CC in specific cells of a plant. The present sequence is pokeweed PAP' DNA

SQ Sequence 1378 BP; 488 A; 234 C; 269 G; 387 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,34e-119	Length:	1378
Score:	1227.50	Matches:	238
Percent Similarity:	86.0%	Conservative:	33
Best Local Similarity:	75.6%	Mismatches:	41
Query Match:	75.9%	Indels:	3
DB:	6	Gaps:	2

US-09-978-274A-2 (1-314) x AAD42739 (1-1378)

```

QY 1 MetLyvAlMeLeuValValValThrLeuIleAlaTrpLeuIleAlaAlaProthr 20
   |||||
DB 225 ATGAGTCAATGCTTGTGGTGAACAATATCAATA-----TGGCTCATTTCTTGACCAACT 278
   |||||

QY 21 SerThrCyAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTrp 40
   |||||
DB 279 TCAACTTGGGCTGTGAATCAATCATCATCAATGTTGAAGATGCCACCATTTAGCAATATC 338
   |||||

QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCyTrpGly 60
   |||||
DB 339 GCCACTTTTCGGAATGATCTTCTGTAATGAAGCCAAAGATCCAAAGTTTAAATCTATGA 398
   |||||

QY 61 IleProMetLeuProAspThrAsnSerThrProLysTrpLeuValLysLeuGlnGly 80
   |||||
DB 399 ATACCAATGCTGCCCATATCAAAATACAAATCCAAAGCAGTGTGGTGGTCCCAAGGT 458
   |||||

QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgArgAsnLeuLysTrpValMetGlyTrp 100
   |||||
DB 459 TCAAAATTAATAAAACCAATCACTAATGCTGAGAGCAAAATTTGATGTGATGGGTAT 518
   |||||

QY 101 SerAspProPheAsnGlyAsnLysCyAspGlyPheIlePheAsnAspIleThrSerThr 120
   |||||
DB 519 TCTGATCCCTTTGAACCAATATATCTCTTACCAATCTTAAATATATCTCAGTACT 578
   |||||

QY 121 GluArgThrAspValGluAsnThrLeuLysSerSerSerSerSerArgValAlaMetSer 140
   |||||
DB 579 GAACGCCAAGATGTATAGACTACTCTTGGCCAAATGCCAATCTCGTGTATTAATAAA 638
   |||||

QY 141 IleAsnTrpAsnSerLeuLysProThrMetGluLysValGluValAsnSerArgAsn 160
   |||||
DB 639 ATTAATTTGATGTGATATCCAAACATTTGGAATCAAAAGCGGAGTAAATCAAGAGT 698
   |||||

QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
   |||||
DB 699 CAGGTCAACTGGGATTCAAATACTCGACAGTAATATTTGGAAGATTTCTGAGAGTATG 758
   |||||

QY 181 SerPheProValLysThrGluAlaPhePheLeuValAlaIleGlnMetValSerGlu 200
   |||||
DB 759 TCATTCACCTGAGAAACCCAAAGCCGAATTCCTATTTGTGTAGCCATACAAATGATACAG 818
   |||||

QY 201 AlaAlaArgPheLysTrpIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTrp 220
   |||||
DB 819 GCGAGCAAGATTCAGATCAATAGAGATCAGGTGAAAACTAATTTTAAACAGAGATTCAC 878
   |||||

QY 221 ProAspProLysValIleAsnLeuGlnGluLysTrpGlyLysIleSerGluAlaIleHis 240
   |||||
DB 879 CCTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAAGTTTCAACAGCAATTCAT 938
   |||||

QY 241 AsnAlaLysAsnGlyAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyTrpLys 260
   |||||
DB 939 GATGCCAAGATGAGAGTTTACCCTCAAACTCTGAGCTAGTGATGCCAGTGGTGCAGAG 998
   |||||

QY 261 TrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTrpValAsn 280
   |||||
DB 999 TGAATAGTGTGAGAGTGAATCAACCTGAGTGAAGCACTTTAAACATACGTTGAT 1058
   |||||

QY 281 GlyThrCyAsnGlnThrThrTrp---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
   |||||
DB 1059 GGGAGCTGTCAGACCAACTTATACCAAAATGCGATTTTCTCACTTATATAGTCTACT 1118
   |||||

QY 300 TyrTrpAsnTrpMetSerAsnLeuGlyAspLeuPheGluGlyPhe 314

```

DB 1119 TATTATATATACATGCTTAATCTGTGATCTATTTGAAGATTC 1163

RESULT 13

AAZ59221 standard, cDNA; 1379 BP.

XX AAZ59221,
AC
XX
XX 20-APR-2000 (first entry)

DE Variant pokeweed antiviral protein spring leaf form coding sequence.
XX
XX Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
KM resistance; potato virus X; potato virus Y; potato leaf roll virus;
KM tuber; ss.

OS Phytolacca americana.

XX US6015940-A.

XX 18-JAN-2000.

XX 07-APR-1992; 92US-00865169.

XX 07-APR-1992; 92US-00865169.

XX (MONS) MONSANTO CO.

XX Kaniowski WK, Turner NE, Lodge JK;

XX WPI; 2000-126326/11.

PT Production of transgenic potato plants or tubers expressing pokeweed
XX antiviral protein which are resistant to potato virus X or Y.

XX Claim 7; Fig 5; 30pp; English.

CC This is the coding sequence for a variant spring leaf form of the
CC pokeweed antiviral protein (PAP) which is used to generate transgenic
CC potato plants. PAP is able to confer resistance to infection by potato
CC virus X (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in
CC the potato plant or tuber expressing PAP. PAP varies from PAP
CC (AAZ59220) by mutations L20R and Y49H

SQ Sequence 1379 BP; 489 A; 234 C; 269 G; 387 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,34e-119	Length:	1379
Score:	1227.50	Matches:	238
Percent Similarity:	86.0%	Conservative:	33
Best Local Similarity:	75.6%	Mismatches:	41
Query Match:	75.9%	Indels:	3
DB:	3	Gaps:	2

US-09-978-274A-2 (1-314) x AAZ59221 (1-1379)

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DB 225 ATGAGTCAATGCTTGTGGTGAACAATATCAATA-----TGGCTCATTTCTTGACCAACT 278
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QY 21 SerThrCyAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTrp 40
   |||||
DB 279 TCAACTTGGGCTGTGAATCAATCATCATATGTTGAAGATCCACCATTTAGCAATATC 338
   |||||

QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCyTrpGly 60
   |||||
DB 339 GCCACTTTTCGGAATGATCTTCTGTAATGAAGCCAAAGATCCAAAGTTTAAATGCTATGA 398
   |||||

QY 61 IleProMetLeuProAspThrAsnSerThrProLysTrpLeuValLysLeuGlnGly 80
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DB 399 ATACCAATGCTGCCCATATCAAAATACAAATCCAAAGCAGTGTGGTGGTCCCAAGGT 458
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QY 81 AlaAsnLeuYsrThrlleThrLeuMetLeuArgArgAsnLeuYrValMetGlyTyr 100
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 QY 101 SerAspProPheAsnGlyAsnLeuYrCyArGlyrHisIlePheAsnAspIleThrSerThr 120
 DB 519 TCGATCCCTTTGAAACCAATMAATGTCGTACATATCTTAAATGATATCTCAGACT 578
 QY 121 GluArgThrAspValGluAsnThrLeuCySerSerSerSerSerArgValAlaMetSer 140
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 DB 639 ATAAACTTGTATGATCATATCCAACTTGGAATCAAAAGCGGAGTAAATCAAGACT 698
 QY 161 GluValGluLeuGlyIleGlnIleLeuSerSerAspIleGlyValIleSerGlyValAsp 180
 DB 699 CAGGTCCAACTGGGAATTCAAATCTCGACGATATGTGAAAGATTTCTGGAGTATG 758
 QY 181 SerPheProValIleYsrThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
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 QY 201 AlaAlaArgPheYrYrIleGluAsnGlnValIleYsrThrAsnPheAsnArgAlaPheTyr 220
 DB 819 GCAGCAAGATTCAGATGATCATAGAGATCAGGTGAAACTATTTAAACAGCATTTCAAC 878
 QY 221 ProAspProIleValIleAsnLeuGluGluYrTyrGlyYrIleSerGluAlaIleHis 240
 DB 879 CCAATCCCAAGACTTAATTTGCAAGACACATGGGGTAAAGATTTCAACGCAATTCAT 938
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 DB 939 GATGCCAAGATGAGCTTTTACCCAACTCTCGAGCTAGAGATGCCAGTGGCCAG 998
 QY 261 TyrIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuYrYrValAsn 280
 DB 999 TGGATAGTGTGAGAGTGGATGAAATCAAGCTGATAGACCTTAACTACGTTGGT 1058
 QY 281 GlyThrCyArgIleThrThrTyr--GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
 DB 1059 GGGAGCTGTCAGCAACTTATTAACCAAAATGCCATGTTCTCTCAACTATATATGCTACT 1118
 QY 300 TyrTyraAsnTyraMetSerAsnLeuGlyAspLeuPheGluGlyPhe 314
 DB 1119 TATTATATTAATCAATGCTTAATCTTGGATCTATTTGAAGGATTC 1163
 RESULT 14
 ID AAQ81457 standard; cDNA; 1195 BP.
 AC AAQ81457;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-AUG-1995 (first entry)
 XX
 DB Phytolacca antiviral protein (PAP) cDNA.
 XX
 KM Antiviral protein; vector pMJ12; KCCM 10037; PAP; ss.
 XX
 OS Phytolacca americana; L.
 XX
 PN AU9350642-A.
 PD 19-JAN-1995.
 XX
 PF 11-NOV-1993; 93AU-00050642.
 PR 02-JUL-1993; 93KR-00012360.
 XX
 PA (JINR-) JIN RO LTD.
 XX

PI Lee K, Choi K, Jeon H, Kim M, Moon Y;
 XX
 DR WP1; 1995-067518/10.
 XX
 PT Recombinant vector for producing Phytolacca anti-viral protein - and
 PT transformed E. coli useful for making immunconjugates for treatment of
 PT AIDS.
 XX
 PS Claim 1; Fig 1; 27p; English.
 XX
 CC Total cellular mRNA from leaves of *P. americana* was used to produce a
 CC cDNA library and this screened with anti-PAP antibody raised in rabbits
 CC against purified PAP. Inserts were isolated from 2 clones and sequenced
 CC to identify a 1195 ORF (AAQ81457) that encodes a 313 AA PAP including a
 CC 22 AA signal peptide. The mature PAP gene was subjected to PCR
 CC amplification using primers AAQ81458 and AAQ81459. The amplification
 CC product was cut with Hind III and inserted into the commercial FLAG (RTW)
 CC vector cut with the same enzyme to form pMJ12. pMJ12 is deposited with
 CC the Korean Collection of Culture and Microorganism (KCCM), an
 CC International Depository Authority, on June 30 1993, ad deposition No.
 CC KCCM 10037, and claimed. (Updated on 16-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 1195 BP; 420 A; 203 C; 229 G; 343 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 7, 73e-119 Length: 1195
 Score: 1219.50 Matches: 237
 Percent Similarity: 85.7% Conservative: 33
 Best Local Similarity: 75.2% Mismatches: 42
 Query Match: 75.4% Indels: 3
 DB: 2 Gaps: 2
 US-09-978-274A-2 (1-314) x AAQ81457 (1-1195)
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 DB 33 ATGAAGTCGATGCTTGGTGGTGAACATATCAATA-----TGGCTCATTTCTGGACCAACT 86
 QY 21 SerThrCyArgAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLeuYrTyr 40
 DB 87 TCAACTGGGCTGTGATATCAATCATCATCAATGTTGGAAGTCCACCATTAGCAATATAC 146
 QY 41 AlThrPheMetGluSerLeuArgAsnGlnAlaIleAspProIleLeuYrCyTyrGly 60
 DB 147 GCCACTTTTCTGATGATGATCTTCTGTAATGAAGCCAAAGATCAAGTTAAATCTTATGCA 206
 QY 61 IleProMetLeuProAspThrAsnSerThrProIleYrLeuLeuValIleLeuGlnGly 80
 DB 207 ATACCAATGCTGCCAATACAAATACAAATCCAAAGTAGCGTGTGAGCTCCAAAGT 266
 QY 81 AlaAsnLeuYsrThrlleThrLeuMetLeuArgArgAsnLeuYrValMetGlyTyr 100
 DB 267 TCAATATATAAAACCATCACTATGCTGAGACGAAACAAATTGTATGATGGTTAT 326
 QY 101 SerAspProPheAsnGlyAsnLeuYrCyArGlyrHisIlePheAsnAspIleThrSerThr 120
 DB 327 TCTGATCCCTTTGAAACCACTAATATGCTTACCATATCTTATATGATATCTCAGACT 386
 QY 121 GluArgThrAspValGluAsnThrLeuCySerSerSerSerSerArgValAlaMetSer 140
 DB 387 GAAGCCCAAGATGAGAGACTACTCTTGCCCAATGCAATCTCGTGTATGATAAAAC 446
 QY 141 IleAsnTyraAsnSerLeuYrProThrMetGluYrValGluValAsnSerArgAsn 160
 DB 447 ATAACTTGTATGATGATATCCAACTTGGAATCAAAAGCGGAGTAAATCAAGACT 506
 QY 161 GluValGluLeuGlyIleGlnIleLeuSerSerAspIleGlyValIleSerGlyValAsp 180
 DB 507 CAGGTCCAACTGGGAATTCAAATCTCGACGATATGTGAAAGATTTCTGGAGTATG 566
 QY 181 SerPheProValIleYsrThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
 DB 567 TCATTCACTGAGAAACCGAAGCCGAATTCCTATTGGTAGCCATACAAATGGTATCAGAG 626


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Db      1788  AAGTGGATAGTGTGAGAGTGGATGATGGAACCTGATGTGGAGCTCCTTAAGTATGTT 1847
Qy      280  AsnGlyThrCysGlnThrThrTyGlnAsnAlaMetPheSerGlnValIleIleSerThr 299
Db      1848  AATGGGACCTGCCGCGCACTTACCAAGGCCATGTTCCCTCACCCT-ATAATGCTTACT 1906
Qy      300  TyrTyrAsnTyrMetSerAsnLeuGlyAsp-LeuPheGluGlyPhe 314
Db      1907  TATTATATATTACATGCGCTAATCTTGTGACTCTATTGAGGATTTC 1952

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Search completed: April 9, 2006, 02:22:19
 Job time : 842.351 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: April 9, 2006, 01:41:02 ; Search time 5706.88 Seconds
(without alignments)
2574.284 Million cell updates/sec

Title: US-09-978-274A-2
Perfect score: 1617
Sequence: 1 MKYVVLVVVTLIAWLAAPF.....VISTYYNYSNGLDFEGF 314

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 41078325 segs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-UNITS-bits -START=1 -END=1 -MATRIX=blomum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abses07
-USBR=US09978274.@CEN_1_1.9564.@runat_07042006_173034_28424 -NCP=6 -ICPU=3
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
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8: gb_est7:*
9: gb_gsa1:*
10: gb_gsa2:*
11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	345.5	21.4	829	7	CN782289 EST00385
2	281.5	17.4	1021	2	BE036639 MP03B03 M
3	266.5	16.5	993	2	BE035039
4	263.5	16.3	1033	2	BE036541
5	256.5	15.9	816	2	BE035038
6	251.5	15.6	639	2	BE037217
7	251.5	15.6	903	7	CO103587

8	248.5	15.4	837	1	AM053634
9	245	15.2	649	6	CA838757
10	245	15.2	649	6	CA839330
11	245	15.2	661	6	CA835532
12	245	15.2	671	6	CA839511
13	245	15.2	689	6	CA833333
14	245	15.2	689	6	CA833383
15	239	14.8	639	7	CO121195
16	225	13.9	639	6	CA835855
17	222	13.7	1038	2	BE033546
18	208.5	12.9	438	2	BE130330
19	198	12.2	662	6	CF227047
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22	187.5	11.6	811	2	BE034055
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25	154	9.5	671	7	CN846973
26	151	9.3	405	8	T24255
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28	150	9.3	678	6	CA840373
29	149.5	9.2	665	6	CF227084
30	148.5	9.2	603	5	BO590856
31	148	9.2	667	6	CA838446
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37	134	8.3	546	5	BO588856
38	134	8.3	601	6	CA198032
39	132	8.2	621	7	CV052755
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ALIGNMENTS

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LOCUS
DEFINITION
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antiviral ribosome-inactivating protein CAP30B [Chenopodium album],
mRNA sequence.
CN782289
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BET.
Chenopodium quinoa (quinoa)
Chenopodium quinoa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Chenopodium.
1 (bases 1 to 829)
Cole,N.D., Coleman,C.E., Christensen,S.A., Jellen,E.N.,
Stevens,M.R., Bonfaccio,A., Rojas-Beltran,J.A., Fairbanks,D.J. and
Maughan,P.J.
Development and use of an expressed sequenced tag library in quinoa
(Chenopodium quinoa Willd.) for the discovery of single nucleotide
polymorphisms
Plant Sci. 168 (2), 439-447 (2005)
Contact: Coleman, Craig E.
Department of Plant and Animal Sciences
Brigham Young University
275 WIDB, Brigham Young University, Provo, UT 84602, USA
Tel: (801) 422-5145
Fax: (801) 422-0008
Email: craig_coleman@byu.edu
Plate: 02 row: J column: 22
Seq primer: M13 Forward

High quality sequence stop: 829.
Location/Qualifiers

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ORIGIN

Alignment Scores:

Pred. No.:	1,22e-31	Length:	829
Score:	345.50	Matches:	97
Percent Similarity:	52.0%	Conservative:	46
Best Local Similarity:	35.3%	Mismatches:	109
Query Match:	21.4%	Indels:	23
DB:	7	Gaps:	10

US-09-978-274A-2 (1-314) x CN782289 (1-829)

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Db 92 gatgtaaccttcaactcgaaaccaaactcagacagatgacttataaacaccttctgcga 151
Qy 46 serleuarasnglnalalyasapprolyleuileucyetyrslylepromeleupro 65
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Qy 66 aapthraserthrprolytyrleuileuvallyleuglnglyalaaenleulythr 85
Db 212 ccacacacacacacacacacacacacacacacacacacacacacacacacacacacac 271
Qy 86 -----ilethrleuileuargagaaenleulytyrlametclytyrserap 102
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Qy 238 alallehisbnalalyasnglyalaleuaprolyleuileuglualeuvalaaleaala--- 256
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RESULT 2
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MP03B03 MP Mesembryanthemum crystallinum cDNA 5' similar to
ribosome-inactivating protein gelonin, mRNA sequence.

ACCESSION
BE036639
VERSION
BE036639.1 GI:8331648
KEYWORDS
SOURCE
ORGANISM
Mesembryanthemum crystallinum (common iceplant)

REFERENCE
AUTHORS
Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
Ferreira, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: chm@u.arizona.edu

TITLE
JOURNAL
COMMENT
An open reading frame exists.
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Location/Qualifiers
1..1021

FEATURES
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1. 1021
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Query Match: 17.4% Indels: 42
DB: 2 Gaps: 13

US-09-978-274A-2 (1-314) x BE036639 (1-1021)
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Qy 16 llealaalprothser-----thrCysala 24
Db 156 tatgtgcacacatcatcaac 215
Qy 25 lleasnthrilethrphespalalegynalaatrleasnlytyrlarthrphemet 44
Db 216 ttaacacacgcttcaacatcaac 269
Qy 45 gluserleuarasnglnalalyasapprolyleuileucyetyrslylepromeleupro 64
Db 270 acatctctccagcgtcaactctctgac---acacacacatgt-----caaatc 314
Qy 65 proasppthraserthr-----prolytyrleuileuvallyleuglngly 80

Df 315 CCGGAGACACGGTCAACCGCACCGGATCTCCACAGATTGTCTTGTCGACTCGAACAACA 374

Gy 81 A1aaenLeuYerThrIleThreUetleuaArgArGaAsnLeuTyValMetGlYTr 100
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Df 375 ACCGCGCAAAAMAGCATCACCCTGCCAATCGACGATGCAGACMAGCGTCTATCTCGTAGCCATAC 434

Gy 101 SerAPProPhaenGlyAsnLysCySaGrYrThSilePheAsnApplleThSerThr 120
435 CCGGACAMAGCTT--GGCGAAAAGAACCCTGCCAATCTCTTAGGAATGCTCCACGCTC 491

Df 121 GluArgThrAspValGluSenThrIeuCySerSerSerSerSerArgValAlaMetSer 140
492 GCTAG-----AACCACTCTTCAAGGCGCAGCGCTTCCG-----AAC 530

Gy 141 l1eaenTyraSnserleutyProThrMetGluLySLyalaGluValaSnSerArgAn 160
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Df 531 ATTGCGTTCCGAGGAGGTATACATAGCCTTAGAGMAAGCGCTGCAAAG---CAAGCCGAAT 587

Gy 161 GluValGlnLeuGlylleglnlleSeuSerSerApplleglyLyaleSerGlyValap 180
588 GCMAATAgMTTGGGGGTGATTAACATAGATTGGCATTCGAGTCGATTTTGGTAG-AAC 646

Df 181 SerPheProvallygThrgluabPhePheleuValAlalleGMeVaSerlu 200
647 CCGATTAAATGGGCATGTTAGGCCCCAAATCTTGATGTGATACAGATGTTTTCTAA 706

Gy 201 AlaalAargPheyletyrlllegluangin---VallystAsnPhaasnArgalabe 219
707 GGAGCACGGTTTAATATATTTGAAGTAGTCACCCAAAGCGTTACATGCTCGTTCA 766

Df 220 TyrProAbpProLyevailleaenleuglugulystrPgilyLysleSer---GluAla 238
767 AACCCCGACCCGAAAAGTGTGAGTTTGGGAGAACATTTGGGAGAAATTCCGACAAAT 826

Gy 239 lleHisaenAlalyasndylAlaleuProlys-----ProleugluValaspala 256
827 ATAAGACAGTGTCCGGAATACTGTTGTC-AAATATTCACCGCGCATCTTCCAAATGC 885

Df 257 LysglYthrlystrPillevallseuArgVal 266
::: :::: :::: :::: :::: ::::

Df 886 TGATGTTACATGAGAGTGATTAAGGTG 915

RESULT 3
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LOCUS M002A03 MM Mesembryanthemum crystallinum cDNA 5' similar to
DEFINITION antitrital protein, mRNA sequence.

ACCESSION BE035039
VERSION BE035039.1 GI:8330048
KEYWORDS EST.

SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Asteroaceae; Mesembryanthemum.
1 (bases 1 to 993)

REFERENCE Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
Petrea, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu
Insert Length: 1 Std Error: 0.00.
Location/Qualifiers
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/mol_type="mRNA"

FEATURES
SOURCE

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XhoI; Plants stressed 6 weeks in 500mM NaCl"

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Query Match:	16.5%	Indels:	13
DB:	2	Gaps:	4

US-09-978-274A-2 (1-314) x BE035039 (1-993)

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Db	746	GAHAACCTCTTTTAAAGGAGCGACCCGTTCCAAACATTTCCATTGGTGTAACATACATGCG	687
Qy	145	rLeuTYrProThrMetGluIuYelYalAgiValAsnSerzrAgnAgnValGlnLeuG1	165
Db	686	TCTG-----GAGAAAGCTGCCGCGTCAAGACGAAACAGATATTGAGTTGGG	642
Qy	165	YlLeGlnlleLeuSerSerAepIleGlyLysIleSerGlyValAspSerPheProVally	185
Db	641	GCTTGCTAAACTTAAGAGTTTGCCATCGAGTCGATTTATGGTAAAAAAACGATCGATGGGA	582
Qy	185	sThGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPheLy	205
Db	581	ACTGAGGCGCCAAATCTTCTACGTATGCCATCCAGATGGTTCCAGAGACGACGCGTTCCA	522
Qy	205	sTYrIleGluAsnGlnVal--LysThrAsnPheAsnArgAlaPheTYrProAepProLy	224
Db	521	TTATATCGAGACTAAGGTGACCGGAAGTGGGTCAATGAGTCTTCAAAACCGATCCGAA	462
Qy	224	sValIleAsnLeuGlnGlnLysTYrTPGilyLysIleSerGluAlaIleHisAsnAlaLysAs	244
Db	461	AGATATTAACTTGGAGAAACAATGGGAGAAAGATTCCGATGAGATTCATTAAGTCAATTAC	402
Qy	244	nGlyAlaLeuPro-----LysProLeuGlnLeuValAspAlaLys	257
Db	401	GTCGAACAACACCTCTCTAATTGTACGAACATTTCCCGCATTAACCTTAATCAATGCTGA	342
Qy	257	sGlyThrLysTYrIleValLeuArgValAspGlnIleAsnArgAspValAlaLeuLeuLy	277
Db	341	TGGTACACAATGGAAGGTGATAGATTGCCACATATAAACCTGACTTGGGAGATCTCAA	282
Qy	277	sTYr 278	
Db	281	GTTC 278	
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DEFINITION		ME01B07 MP Mesembryanthemum crystallinum cDNA 5' similar to	
ACCESSION		BE036541	
VERSION		BE036541.1	
KEYWORDS		GI:8331550	
SOURCE		EST.	
ORGANISM		Mesembryanthemum crystallinum (common iceplant)	
REFERENCE		Mesembryanthemum crystallinum	
AUTHORS		Bukartec, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.	
		1 (Bases 1 to 1033)	
		Bohner, H., Borchert, C., Brazille, S., Brooke, J., Baton, M., Parnet, H., Kawasaki, S., McColough, A., Michalowski, C.B., Palacio, C., Scara, G., Wheeler, M. and Zepeda, C.R.	
TITLE		Functional Genomics of Plant Stress Tolerance	
JOURNAL		Unpublished (2000)	

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Db	330	AGAAAAGAGCGCAATTGATATTAGTAAGCTAATAATAGTTTCATATAAAAAACAGCGATAAA	379
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Db	360	ATGAATGAAGAAGCATGAGGCTACATTTCTTCTAGCTTCGATTCGAAAGGTTTGAGAGCTT	439
Qy	202	AlaArgPheIySTyTleGluAsnGluValIySThrAsnPheAsnArgAlaPhe-TyPPr	221
Db	440	GCACGGTTCTCTTTCATACATACAGAGAAAGGTTA---GCCAGCATTTGACGAAAAATTTCAAGGCGC	496
Qy	221	oAsPProIySTyValIleAsnLeuGluGluIySTyPgly-----	233
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Qy	234	---LyeIleSerGluAlaIleHisAsn	241
Db	557	ACCAAGGTGACACCTTCGATCCACCAT	584
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DEFINITION	COI03587	903 bp	mRNA
ACCESSION	GR_EB0032EB01.r	GR_Eb	Goesypium raimondii cDNA clone GR_EB0032EB01
VERSION	COI03587		
KEYWORDS	COI03587.1	GI:48902273	
SOURCE	EST		
ORGANISM	Goesypium raimondii		
REFERENCE	Goesypium raimondii		
AUTHORS	Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and Wing,R.A.		
TITLE	Global assembly of Cotton ESTs		
JOURNAL	Unpublished (2004)		
COMMENT	Contact: Rod A. Wing Arizona Genomics Institute The University of Arizona Forbes Building Room 303, Tucson, AZ, 85721-0036, USA Tel: 520 626 9595 Fax: 520 621 1259 Email: twing@genome.arizona.edu Plate: 0032 row: E column: 01. Location/Qualifiers		
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	/tissue_type="floral"		
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	/lab_host="DH10B"		
	/clone_id="GR_Eb"		
	/note="Vector: pCMV.SPORT-6.1; site_1: NotI; site_2: EcoRV; library made by invitrogen with RNA supplied by Wendle lab. Directional clones into NotI-EV. Colonies plated/picked by AGI. More glycerol clones held in -80."		
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Alignment Scores:			
Pred. No.:	6,49e-20	Length:	903
Score:	251.50	Matches:	80
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Best Local Similarity:	28.2%	Mismatches:	110
Query Match:	15.6%	Indels:	45
Db:	7	Gaps:	11
US-09-978-274A-2 (1-314) x	COI03587 (1-903)		
Qy	1	MctIySTyValMetLeu---ValValValValThLeuIleAlaTrPLeuIleAlaIleAlaPro	19

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Db      67 ATGAAGGTGGATTGCTGTGATTGATTATCATAGGCGCTTATGGATATCATAGTGAA 126
Qy      20 ThreSerThrCys-----AlaIleAsnThrIleThr 29
Db      127 CCATCGCTGCTGATGCTGTATACAGAAATGACACAGCTCAAGATTACACAGTGA 186
Qy      30 PheAspAlaGlyAsnAlaThrIleAsnLysThrIleThrPheMetGlySerAspAsn 49
Db      187 TTCACCACTGAAGACCAAGACCAAGACTTATCTGATGTTATGAAAGATCTGTACAT 246
Qy      50 GluAlaIleAspProLysLeuLysCysThrGlyIleProMetLeuProAspThrAsnSer 69
Db      247 GCATTGACAGAGGCTGCAGATAGAGCGAGACATGCCGATTTGCTCCCGCATGCA 306
Qy      70 ThrPro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLysThr 85
Db      307 CAGCTTACTGATCCTCGCAATATGTTCTGTAGAGCTTCAAT---GGTTACCAACT 363
Qy      86 IleThrLeuMetLeuAlaGlyAsnAsnLeuTyrValMetGlyTyrSerAspProPheAsn 105
Db      364 GTCACTATGACCTTGCATGTACGTAATGTATCTTGAGGTATCTGCAAGTGGCGGC 423
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Db      424 TCC-----TATTTCTTACGGATGTCCAGAC-----GATGTA 456
Qy      126 GluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTyrAsnSer 145
Db      457 CGTATGCTTTGTTGTTCCAGACAGTACT-----GCCCTAACCTTTACAGGC 501
Qy      146 LeuTyrProThrMetGlyLysLysLysLysLysLysLysLysLysLysLysLys 165
Db      502 AGATATGGGGGACCTTGAGGGTGTCTGCGGAGTAGATGACAGGAAGGAATCCCTCGGA 561
Qy      166 IleGlnIleLeuSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 181
Db      562 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 621
Qy      182 PheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAla 201
Db      622 GCCCTTATC-----GCAAGAGCCCTCATAGTTGATTCAGATGTTTCCGAACT 672
Qy      202 AlaArgPheLysTyrIleGluAsnGlnVal-----LysThrAsn 214
Db      673 GCCCGATGAGAAACATCCAGCAAAATCTTGCAGTTGCAGAGCTTCACGGCGATGA 732
Qy      215 PheAsnArgAlaPheTyrProAspProLysValIleAsnLeuGlnGlyLys 234
Db      733 ACTTATGGAACGTTTATATCCAGATGGCTTATATGATGAGTACGAAACACAGCTGGAGAC 792
Qy      235 IleSerGluAlaIleHisAsnAlaLysAsnGlyAlaLeuProLysProLeuGlnLeuVal 254
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RESULT 8
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LOCUS     130-1401T3 Ice plant lambda Uni-Zap XR expression library, 30 hours
DEFINITION
NACL treatment Mesembryanthemum crystallinum cDNA clone L30-1401
5', mRNA sequence.
ACCESSION
AM053634
VERSION   AM053634.1 GI:5916827
KEYWORDS  EST.
SOURCE     Mesembryanthemum crystallinum (common iceplant)
ORGANISM  Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Astaceae; Mesembryanthemum.
REFERENCE
1 (bases 1 to 837)

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AUTHORS  Cushman, J. C.
TITLE     An expressed sequence tag database for the common ice plant,
          Mesembryanthemum crystallinum
JOURNAL   Unpublished (1997)
COMMENT   Contact: Cushman JC
          Department of Biochemistry
          University of Nevada
          MS200, Reno, NV 89557-0014, USA
          Tel: 775-784-1918
          Fax: 775-784-1650
          Email: jcushman@unr.edu
          Poly(A) tail, 10 nt: 838. .847
          PCR Primers
          FORWARD: T7
          BACKWARD: T3
          Insert length: 847 Std Error: 5.00
          Plate: L30-15 Row: A Column: 5
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               /dev_stage="Six week old"
               /clone_lib="Ice plant lambda Uni-Zap XR expression
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               /note="Vector: lambda Uni-Zap XR, Bluescript SK-, Site_1:
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Score: 248.50 Matches: 76
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Best Local Similarity: 35.3% Mismatches: 84
Query Match: 15.4% Indels: 20
DB: 1 Gaps: 8
US-09-978-274A-2 (1-314) x AM053634 (1-837)

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Qy      58 CysTyrGlyIleProMetLeuProAspThrAsnSerThr-----ProLysTyr 73
Db      62 TGT-----CAATCCCCCGTGCAGACCGTCAACCGCATCTCAACGATTC 109
Qy      74 LeuLeuValLysLeuGlnGlyAlaAsnLeuLysThrIleThrLeuMetLeuArgAsn 93
Db      110 GTCTGTGTCGACCTCAAAACACCTCTGCAAAAGACCATCTCCGATCGACGTGACA 169
Qy      94 AsnLeuTyrValMetGlyTyrSerAspProPheAsnGlyAsnLysCysArgTyrHisIle 113
Db      170 AGCGTCTATGTCGTGCGCTACCGCGACAGCTT---GGCGAABAAGACCGTGCACCTTC 226
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Db 383 GAGTCGGTTTGGTAAGAACCCGATTAATGGCAGGTGAGCCAAATTCCTGCTANT 442

Qy 194 AAlaIleGlnMetValSerGluAlaAlaArgPheIleTyrIleGluAngln---ValLys 212

Db 443 GCTATACAGAGTTTCTGAAGACGACGCTTAAGTATTAAGTAAGGAGCCAA 502

Qy 213 ThrAsnGlnAsnArgAlaPheTyrProAspProLysValIleAsnLeuGluLysTyr 232

Db 503 AGTCGGTTACATGGGTTGGTCAACCCGACCCGAAGTG-CYGAATTTGGAGAACATAGG 561

Qy 233 GilyValIleSerGluAlaIleHisAsnAlaLysAnglnAlaLeu 247

Db 562 GGAAGATTCCAGAGATCATAGACAGTTCGGCGCAAAACCGCTTG 606

RESULT 9
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LOCUS DEFINITION MCT020B02.167445 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT020B02 5, mRNA sequence.

ACCESSION CA838757 GI:26566522
VERSION CA838757.1
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Bukayofa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 649)
Cushman, J.C.
An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL COMMENT Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRIMERS FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 020 row: B column: 02
Seq primer: T3 20mer
High quality sequence stop: 649.
Location/Qualifiers 1. .649

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/dev_stage="five-week-old"
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/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

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Score: 245.00 Matches: 62
Percent Similarity: 53.4% Conservative: 24
Best Local Similarity: 38.5% Mismatches: 61
Query Match: 15.2% Indels: 14
DB: Gaps: 4

US-09-978-274a-2 (1-314) x CA838757 (1-649)

Qy 126 GluAsnThrIleuCySerSerSerSerArgValAlaMetSerIleAsnTyrAsnSer 145

Db 25 GAGAGATCTTTTACATGAGACACGTTCCGAAACCTTGCTTCAAGGACTTACACATCC 84

Qy 146 LeuTyrProThrMetGluLysValGluValAsnSerArgAsnGlnValGlnLeuGly 165

Db 85 TTA-----GAGATGCTGCAACCAACGACGAGAGACCATAGATTAGGG 129

Qy 166 IleGlnIleuSerSerArgPheIleGlyLysIleSerGlyValAspSerPheProValLys 185

Db 130 GTGATTAACCTAGAGTTGGCATCGAGTCCGTTTATGTGAACATCGACAGACAGAGA 189

Qy 186 ThrGluAlaPhePheLeuValAlaIleGlnMetValSerGluAlaAlaArgPheLys 205

Db 190 AATGAGGCCAAATCTTGCTGATTGCCATACAGATGTTCTGAAGACGAGGTTCAAG 249

Qy 206 TyrIleGluAsnGlnValLysThrAsnPhe-----AsnArgAlaPheTyrProAspPro 223

Db 250 TATATTAGAGTAAAGTGAGCAACCAAGTCGTTAGATTATGATCGTTCTTACCGACCG 309

Qy 224 LysValIleAsnLeuGluLysTyrGlyLysIleSerGluAlaIleHisAsnAlaLys 243

Db 310 AAAATGCTGCTTTTGGAGACCAATGGGGAGATTTCGACGAGATTCATGAGAGTCT 369

Qy 244 AsnGlyValAlaLeuPro-----LysProLeuGluLeuValAlaPheLys 257

Db 370 ---GGGGCGAAACCTGCTGTATGAATCTTCACTCCGATTCCTGTTAAAGAACCAAT 426

Qy 258 GlyThrLysTyrPheLysValLeuArgValAspGluIleAsnArgAspValAlaLeuLys 277

Db 427 GTGATCCATGACGACGCTGATTAAGTTGACACATTTAGACTGAATGGGATATCTCAG 486

Qy 278 Tyr 278

Db 487 TTC 489

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CA839330 649 bp mRNA linear EST 12-DEC-2002
LOCUS DEFINITION MCT026C11.171755 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT026C11 5, mRNA sequence.

ACCESSION CA839330
VERSION CA839330.1 GI:26567095
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Bukayofa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 649)
Cushman, J.C.
An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL COMMENT Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRIMERS FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 026 row: C column: 11
Seq primer: T3 20mer
High quality sequence stop: 649.
Location/Qualifiers 1. .649

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1. .649
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Db	438	GGTATTCACATGACCGGTGATTAAGGTTCACATATTAGACCTGAATGGGGATACCAAG	497
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CA839511.1 GI:26567276			
EST.			
Mesembryanthemum crystallinum (common iceplant)			
Mesembryanthemum crystallinum			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;			
Caryophyllales; Alzooceae; Mesembryanthemum.			
1 (bases 1 to 671)			
Cushman, J.C.			
An expressed sequence tag database for the common ice plant,			
Mesembryanthemum crystallinum			
Unpublished (1997)			
Contact: Cushman JC			
Department of Biochemistry			
University of Nevada			
MS200, Reno, NV 89557-0014, USA			
Tel: 775-784-1918			
Fax: 775-784-1650			
Email: jcushman@unr.edu			
PCR Primers			
FORWARD: T3 20mer			
BACKWARD: T7 21mer			
Plate: 028 row: D column: 04			
Seq primer: T3 20mer			
High quality sequence stop: 671.			
Location/Qualifiers			
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library, 5 days 0.5 M NaCl treatment, Crasulacean acid			
metabolism, phase IV (5:30 PM)."			
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:			
Score; Site_2: XhoI; Library construction has been performed			
according to Stratagene's recommended protocol for the			
lambda UniZapXR vector and cDNA synthesis kit."			
ORIGIN			
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Pred. No.: 2,666-19 Length: 671			
Score: 245.00 Matches: 62			
Percent Similarity: 53.4% Conservative: 24			
Best Local Similarity: 38.5% Mismatches: 61			
Query Match: 15.2% Indels: 14			
DB: 6 Gaps: 4			
US-09-978-274A-2 (1-314) x CA839511 (1-671)			
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Db	25	GAGATCTCTTTCATCGAGCAACAGTTCGGAACCTTTCGCTTCAAGGACCTTACACATCC	84

QY	146	LeuYrProTrMetGluLysLysAlaGluValAsnSerAArgAsnGlnValGlnLeuGly	165
Db	85	TTA-----GAGAAATCTCCAAACCAACGACGACGAAAGCCATAGAGTTAGG	129
QY	166	lIeGlnIleuSerSerAspIleGlyLysIleSerGlyValAspSerPheProValLys	185
Db	130	GTGGATAAACTAGAGTTTGCATCGAGCGGTTTATGGTAAAGCATCGAACATGACAGA	189
QY	186	ThrGlnAlaPhePheLeuLeuValAlaAlaGlnMetValSerGlnValAlaAlaArgPheLys	205
Db	190	AATAGAGGCCAAATCTTGCTGATTGATCCCATACAGATGGTTCTGTGAAGCAGCAAGGTTCAAG	249
QY	206	TyrIleGlnAsnGlnValLysThrAsnPhe-----AsnArgAlaPheTyrProAspPro	223
Db	250	TAATTTAGAGATTAAGGTGAACCAAGTCGCTTAATATATGAATGCTTTACCCGACCCG	309
QY	224	LysValIleLeuLeuGlnGluLysTyrGlyLysIleSerGlnValAlaIleHisAsnAlaLys	243
Db	310	AAATATGCTGCTTTGGAGAACCAATTGGGGGAGATTTCGACGAGAGATTCAATGAGAGTCT	369
QY	244	AsnGlyAlaLeuPro-----LysProLeuGlnGluLeuValAspAlaLys	257
Db	370	---GGGGGGAACCTGCTTGTATGAATCTTACCTCGATTCGCTTAAGAAACCAAT	426
QY	258	GlyThrLysTyrPileValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLys	277
Db	427	GGTATCATCATGACGGTGTGATTAAGGTTGACACTTATAGACCTGAAATGGGAGATCTCAAG	486
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ACCESSION	CA833333		
VERSION	CA833333.1	GI:26561098	
KEYWORDS	EST.		
SOURCE	Mesembryanthemum crystallinum (common iceplant)		
ORGANISM	Mesembryanthemum crystallinum		
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.		
AUTHORS	1 (bases 1 to 689)		
TITLE	Cushman, J.C.		
JOURNAL	An expressed sequence tag database for the common ice plant.		
COMMENT	Mesembryanthemum crystallinum		
COMMENT	Unpublished (1997)		
COMMENT	Contact: Cushman JC		
COMMENT	Department of Biochemistry		
COMMENT	University of Nevada		
COMMENT	MS200, Reno, NV 89557-0014, USA		
COMMENT	Tel: 775-784-1918		
COMMENT	Fax: 775-784-1650		
COMMENT	Email: jcushman@unr.edu		
COMMENT	PCR Primers		
COMMENT	FORWARD: T3 20mer		
COMMENT	BACKWARD: T7 21mer		
COMMENT	Plate: 021 row: A column: 09		
COMMENT	Seq primer: T3 20mer		
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/dev stage="five-week-old"
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BcoRI; site 2: XhoI; library construction was performed
according to Stratagene's recommended protocol for the
lambda UniZapR vector and cDNA synthesis kit."

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ORIGIN

Alignment Scores:

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Percent Similarity:	53.4%	Conservative:	24
Best Local Similarity:	38.5%	Mismatches:	61
Query Match:	15.2%	Indels:	14
DB:	6	Gaps:	4

US-09-978-274A-2 (1-314) x CA833333 (1-689)

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Qy	146	LeuTrYProThmEgUubYbYbAlaGluValaAemSerArgAaNgInValGInLeuGly	165
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Qy	166	ILeGInLeUeUSeRserAapLleGlyLySILeSerGlyValaAapSeRPhaProValbys	185
Db	141	GTGATTAACATAAGATTGGCGATCGATCGCTTTATGTGAAGACATCAACAGTCAAGAA	200
Qy	186	ThrGluAlaPhePheUeuUeuValAlaILeGInMetValSerGluAlaAlaArgPheUys	205
Db	201	AATGAGGCCAAATTTCTTGGCTGATGTCGATACAGATGGTTTTCGAAGCAGCAAGTTCAAG	260
Qy	206	TyrILleGluAaNgInValLystrAaPhe-----AaMArgAlaPheTrYProAapPro	222
Db	261	TATATTGAGGTAAAGGTGAACCAAACTGGCTTAGATTGAATCGTTTACCCGACCCG	320
Qy	224	LyEValILleAaMLeuGluGluLystrPGLyLySILeSerGluAlaILeHIAaMAlaUys	243
Db	321	AAATATGCTGCTTTTGGAGACCAATTCGGGGAAAGATTTGGCAGAGATTCAGAGAGTCT	380
Qy	244	AaNgLyValaLeuPro-----LyPProLeuGluLeuValaAapAlaUys	257
Db	381	---GGGGCGAAACCTCTCTTGATGAATCTTTACCTCCGATTCCTGTTAAAGAAACCAAT	437
Qy	258	GLYThrLystrPILleValaLeuArgValaAapGluILeAaMArgAapAlaILeUeuUys	277
Db	438	GGGATCCATCGACGGTGGATTAAGTGTGACATATTAGACCTCGAAATGGGATACTCAAG	497
Qy	278	Tyr 278	
Db	498	TTC 500	

RESULT 14	CA833383	
LOCUS	CA833383	689 bp mRNA linear EST 12-DEC-2002
DEFINITION	MCS021F04.152044 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Cressnolaccan acid metabolism, phase I (2AM). Mesembryanthemum crystallinum cDNA clone MCS021F04 5', mRNA sequence.	
ACCESSION	CA833383	
VERSION	CA833383.1	GI:26561148
KEYWORDS	EST.	
SOURCE	Mesembryanthemum crystallinum (common iceplant)	
ORGANISM	Mesembryanthemum crystallinum	
REFERENCE	Eukaryotes: Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.	
AUTHORS	1 (bases 1 to 689) Cushman, J.C.	

TITLE	an expressed sequence tag database for the common ice plant, <i>Mesembryanthemum crystallinum</i>
JOURNAL	Unpublished (1997)
COMMENT	Contact: Cushman JC

FEATURES

Source

1.689

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library" E. coli M169 host
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ORIGIN

Alignment Scores:

Pred. No.:	2, 77e-19	Length:	68
Score:	245.0	Matches:	62
Percent Similarity:	53.4%	Conservative:	24
Best local Similarity:	38.5%	Mismatches:	61
Query Match:	15.2%	Indels:	14
DB:	6	Gaps:	4

US-09-978-274A-2 (1-314) X CA833383 (1-689)

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Qy      126  GUAATThrLeuCySerSerSerSerSerhArgAlaMetSerLleAmTyAAsnSer  145
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Db      36  GGAATCTCTTTCATGAGACCAACACTTGGAACTTGCGTTCAAAAGGACTTAACATCC  95

Qy      146  LeuTyProThrMetGluLysLeuValAsnSerArgAsnGlnLeuGly  165
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Qy      166  IleglnlleuSerSerAspIleGlyLysIleSerGlyValAspSerPheProVallys  185
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Db      141  GGGATAAACTAGAGATTGGCATCGACGCGGTTATAGTAAAGATGACAGCAAGTCAAGA  200

Qy      186  ThrGlnAlaPhePheLeuLeuValAlaIleGlnMetValSerGlnAlaAlaArgPheLys  205
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Db      201  AATGAGGCCCAATCTTGCTGATTCCTCATACAGATGGTTCTGAAGCAGCAAGGTTCAAG  260

Qy      206  TyrIleGluAsnGlnValLysThrAsnPhe-----AsnArgAlaPheTyProAspPro  223
      |||||
Db      261  TATATTGAGAGTAAAGTGAACCAAAATGCGTTAGATTATAGAAATCGTTCTTACCCGACCCG  320

Qy      224  LysValAlaAsnLeuGluGluLysTrpGlyLysIleSerGlnAlaIleHisAsnAlaLys  243
      |||||
Db      321  AAAATCGTCCTTTTGGAGACCAATTTGGGGGAAAGATTTGCGAGAGATTCTAGAGAGCT  380

Qy      244  AsnGlyAlaLeuPro-----LysProLeuGluLeuValAspAlaLys  257
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Db      381  ---GGGGCAAAACCTGCTTGATGAAATTTTCAACCTCGAATCCGTTAAAGAAACCAAAAT  437

Qy      258  GlyThrLysTrpIleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuLys  277
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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 8, 2006, 13:04:24 ; Search time 342.749 Seconds
(without alignments)
1628.463 Million cell updates/sec

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Sequence: 1 MKWLVVVVTLIAWLIAPF.....VISTYNNYNSLGLDFEGF 314

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1
US-08-373-858-1
; Sequence 1, Application US/08373858
; Patent No. 5633155
GENERAL INFORMATION:
APPLICANT: Kim, Man-Keun
APPLICANT: Lee, Kwan-Ho
APPLICANT: Na, Byeong-Kook
APPLICANT: Jeong, Han-Seung
APPLICANT: Choi, Kyu-Whan
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
TITLE OF INVENTION: Expression Vector for Phytoacta
TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
TITLE OF INVENTION: Plant Transformed Thereof.
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Darby & Darby
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373.858
FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/17986-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7770
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: cDNA to mRNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Phytolacca americana*
US-08-373-858-1

Alignment Scores:

Pred. No.:	2,598-139	Length:	1195
Score:	1235.50	Matches:	239
Percent Similarity:	86.3%	Conservative:	33
Best Local Similarity:	75.9%	Mismatches:	40
Query Match:	76.4%	Indels:	3
DB:	2	Gaps:	2

US-09-978-274a-2 (1-314) x US-08-373-858-1 (1-1195)

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RESULT 2

US-08-342-786B-1

Sequence 1, Application US/08342786B

Patent No. 5648234

GENERAL INFORMATION:

APPLICANT: Moon, Young-Ho

APPLICANT: Jeon, Hong-Seob

APPLICANT: Choi, Kyu-Wan

APPLICANT: Lee, Kwan-Ho

APPLICANT: Kim, Man-Keun

TITLE OF INVENTION: A No. 5648234e1 Expression Vector for *Phytolacca*

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSES: Darby & Darby

STREET: 805 Third Ave.

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/342,786B

FILING DATE: 21-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/147,024

FILING DATE: 01-NOV-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, S. Peter

REGISTRATION NUMBER: 25,351

REFERENCE/DOCKET NUMBER: 0136/08862-US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)527-7700

TELEFAX: (212)753-6237

TELEX: 236687

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1195 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: cDNA to mRNA

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: *Phytolacca americana* L.

IMMEDIATE SOURCE:

CLONE: PAP
US-08-342-786B-1

Alignment Scores:

Pred. No.:	2.59e-139	Length:	1195
Score:	1235.50	Matches:	239
Percent Similarity:	86.3%	Conservative:	33
Best Local Similarity:	75.9%	Mismatches:	40
Query Match:	76.4%	Indels:	3
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US-09-978-274A-2 (1-314) x US-08-342-786B-1 (1-1195)

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Db 627 GCAGCAAGATTCAAGTACATAGAAATCAAGTGAATCTAATTTTACAGCATTCAC 686
Qy 221 ProAspProLysValIleAsnLeuGlnGluLysTrpGlyLysIleSerGlnAlaIleHis 240
Db 687 CCTAATCCCAAGATCTTAATTTGCAAGACATGCGGTGATGATTCAACGCAATTCAT 746
Qy 241 AsnAlaLysAsnGlyAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLys 260
Db 747 GATGCCAAGATGAGCTTTTACCCAACTCTGAGCTTAGTGAGATGCAAGTGGGCCAG 806
Qy 261 TrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyValAsn 280
Db 807 TGGATAGTGTGAGAGTGAATGAAATCAAGCGTATGACACTTTAACTAGCTTGTGT 866
Qy 281 GlnThrCysGlnThrThrTy--GlnAsnAlaMetSerGlnValIleIleSerThr 299
Db 867 GGGAGCTGTCAAGCACTTATTAACAAATGCCATGTTTCTCAACTTAATTAATGTTACT 926
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Qy 300 TyrThrAsnTyMetSerAsnLeuGlyAspLeuPheGlnGlyPhe 314
Db 927 TATTAATAATACATGTTAATCTTGTGATCTTATTTGAAGGATTC 971
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RESULT 3

US-08-500-611-1
Sequence 1, Application US/08500611Patent No. 5756322
GENERAL INFORMATION:APPLICANT: Turner, Nigun E.
TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants
NUMBER OF SEQUENCES: 2CORRESPONDENCE ADDRESS:
ADDRESSER: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: WestfieldSTATE: NJ
COUNTRY: USA
ZIP: 07090-1497COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOSSOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,611
FILING DATE: 11-JUL-1995
CLASSIFICATION: 435ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linearFEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
NAME/KEY: mutation
LOCATION: replace(233, "a")FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
NAME/KEY: mutation
LOCATION: replace(435, "c")

US-08-500-611-1

Alignment Scores:

Pred. No.:	3.25e-139	Length:	1379
Score:	1235.50	Matches:	239
Percent Similarity:	86.3%	Conservative:	33
Best Local Similarity:	75.9%	Mismatches:	40
Query Match:	76.4%	Indels:	3
DB:	2	Gaps:	2

US-09-978-274A-2 (1-314) x US-08-500-611-1 (1-1379)

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Qy 1 MetlyValMetleuValValValThreulea1aTripleu1lea1aProthr 20
Db 225 ATGAAGCGATGCTTGTGGTACATATCAATA-----TGGCTCATTTCTTGACACCAACT 278
Qy 21 SerThrCysAlaIleAnthrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTy 40
Db 279 TCAACTGGGCTGGAATACATCATCTCAATGTGGAAGTACCAACATTAGCAATATAC 338
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QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaIleAspProlySLeuIysCysTyrGly 60
DB 339 GCCACCTTTCTGAATGATCTTGGTAATGAAAGCGAAGATCCAGATTAAATCTAATGCA 398
QY 61 IleProMetLeuProAspThrAsnSerThrProlySLeuLeuValIleLeuGlnGly 80
DB 399 ATACCAATGCTGCCAATCAATCAAAATCCAAAGACTGTTGGTGTGAGCTCCAAAGT 458
QY 81 AlaAsnLeuIleThrIleThrLeuMetLeuArgAsnAsnLeuTyrValIleMetGlyTyr 100
DB 459 TCMAATTAATAAAACCATTCACACTAATGCTGAGACGAAACCAATTGTATGTGATGGGTTAT 518
QY 101 SerAspProPheAsnGlnIleAsnIysCysArgTyrHisIlePheAsnAspIleThrSerThr 120
DB 519 TCTGATCCCTTTGAAACCAATAAATGTCGTACCATATCTTTATGATATCTCAGGACT 578
QY 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSer 140
DB 579 GAACGCCAAGATGTAGAGACTACTCTTGGCCAAATGCCAAATTCGTGTGTAGTAAAAAC 638
QY 141 IleAsnTyrAsnSerLeuTyrProThrMetGluLeuIleValIleGluValIleAsnSerArgAsn 160
DB 639 ATAACTTTGATGTGATGATATCCAACTTGGAAATCCAAACCGGAGATAAATCAGAGAGT 698
QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyIleSergIleValIleAsp 180
DB 699 CAGGTCCAACTGGGAATTCMAATATCTCGACAGTAATATTCGAAAGATTCCTGAGAGTATG 758
QY 181 SerPheProValIleSthrGluAlaPhePheLeuValAlaIleGlnMetValSergIle 200
DB 759 TCATTCCTGAGAGAAACCGAAGCCGAATTCCTATGTTGGTCCCAATCAAAATGATATCAGAG 818
QY 201 AlaAlaArgPheIleTyrIleGluAsnGlnValIleThrAsnPheAsnArgAlaPheTyr 220
DB 819 GCAGCAGATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 878
QY 221 ProAspProlyValIleAsnLeuGlnGluIleTyrGlyIleSergIleValIleAsn 240
DB 879 CCTAATCCCAAGTACTTATATTCGAAAGACATGAGGATGATGATGATGATGATGATGATGAT 938
QY 241 AsnAlaIleAsnGlnIleAlaLeuProlyPheProleuGlnLeuValIleAspAlaIleSthr 260
DB 939 GATGCCAAGATGTAGAGTCTTAACTCCAAACCTCTGAGCTGTGATGATGATGATGATGATGAT 998
QY 261 TrpIleValIleLeuArgValAspGluIleAsnArgAspValAlaLeuLeuIysTyrValAsn 280
DB 999 TGGATAGTGTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1058
QY 281 GlyThrCysGlnThrThrTyr---GlnAsnAlaMetPheSergIleValIleIleSergThr 299
DB 1059 GGGAGCTGTGACGACATTAATACCAAAATGCCATGTTCTCTCACTATATATGATGATGATGAT 1118
QY 300 TyrTyrAsnTyrMetSerAsnLeuGlnIleAspLeuPheGlnGlyPhe 314
DB 1119 TATTATTAATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1163

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RESULT 4

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US-08-500-694-1
; Sequence 1, Application US/08500694
; Patent No. 5880329
; GENERAL INFORMATION:
; APPLICANT: Turner, Nilgun E.
; TITLE OF INVENTION: DNA Encoding Pokeweed Antiviral Protein
; TITLE OF INVENTION: Mutants
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Lerner, David, Littenberg, Krumholz & Mentlik
; STREET: 600 South Avenue West
; CITY: Westfield
; STATE: NJ
; COUNTRY: USA
; ZIP: 07090-1497

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 11-JUL-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Foley, Shawn P.
; REFERENCE/DOCKET NUMBER: OCTRS 3.0-039
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-654-5000
; TELEFAX: 908-654-7866
; TELEX: 139-125
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1379 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 225..1163
;
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(233, "a")
;
; FEATURE:
; NAME/KEY: mutation
; LOCATION: replace(349, "g")
;
; NAME/KEY:
; LOCATION:
;
; NAME/KEY: mutation
; LOCATION: replace(435, "c")
;
US-08-500-694-1
;
Alignment Scores:
Pred. No.: 3,25e-139 Length: 1379
Score: 1235.50 Matches: 239
Percent Similarity: 86.3% Conservative: 33
Best Local Similarity: 75.9% Mismatches: 40
Query Match: 76.4% Indels: 3
DB: 2 Gaps: 2
US-09-978-274A-2 (1-314) x US-08-500-694-1 (1-1379)
QY 1 MetIleValMetLeuValValValIleThrLeuIleAlaTrpLeuIleAlaIleProThr 20
DB 225 ATGAAGTCAGATGCTGTGTGTGTGACAAATATCAATATCAATATCAATATCAATATCAATATCA 278
QY 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnIysTyr 40
DB 279 TCAACTTGGGCTGTGAAATCAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 338
QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaIleAspProlySLeuIysCysTyrGly 60
DB 339 GCCACCTTTCTGAATGATCTTGGTAATGAAAGCGAAGATCCAGATTAAATCTAATGCA 398
QY 61 IleProMetLeuProAspThrAsnSerThrProlySLeuLeuValIleLeuGlnGly 80
DB 399 ATACCAATGCTGCCAATCAATCAAAATCCAAAGACTGTTGGTGTGAGCTCCAAAGT 458
QY 81 AlaAsnLeuIleThrIleThrLeuMetLeuArgAsnAsnLeuTyrValIleMetGlyTyr 100
DB 459 TCMAATTAATAAAACCATTCACACTAATGCTGAGACGAAACCAATTGTATGTGATGGGTTAT 518
QY 101 SerAspProPheAsnGlnIleAsnIysCysArgTyrHisIlePheAsnAspIleThrSerThr 120
DB 519 TCTGATCCCTTTGAAACCAATAAATGTCGTACCATATCTTTATGATATCTCAGGACT 578
QY 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSer 140
DB 579 GAACGCCAAGATGTAGAGACTACTCTTGGCCAAATGCCAAATTCGTGTGTAGTAAAAAC 638

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0Y 141 |||leAenTyraenSerleuTyProthmetGlySylrBaIaGluValAsnSerKrgasn 160
Db 639 ATAAACTTGAGTCGATTCGATTCGAACATTGGATCAAAAGCGGAGTAAATCAAGAAAGT 698
0Y 161 GlnValGlnleuGlyIleGlnIleleuSerSerAspIleGlyLysIleSerGlyValAsp 180
Db 699 CAGGTCCAACTCGGAATTCAAATAATCCGACAGTATATTGGAAAGATTTCTGAGTATG 758
0Y 181 SerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
Db 759 TCATTCACTGAGAAAAACCGAACCCGAATTCCTATTGGTAGCCATTCGAATGGTATCAGAG 818
0Y 201 ALAAlaATGPhelLysTyrIleGlnleuGlnValLysThrAsnPheAsnArgAlaPheTyr 220
Db 819 GCAGCAATTCAGATTCAGTACAGATTCAGTGAATCAGTGAATCTAATTTTAAACAGGACATTCAAC 878
0Y 221 ProAspProLysValIleAsnleuGlnGluLysTyrGlyLysIleSerGluValAlaIleHis 240
Db 879 CCTAATCCCAAGTACTTAATTTGCAAGACATGGGGTAAAGATTTCGAACGCAATTCAT 938
0Y 241 AsnAlaLysAsnGlyValAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLys 260
Db 939 GATGCCAAGAATGGAGTTTAAACCCAACTCTCGACTGAGTGAAGACCAAGTGCTGCCAAG 998
0Y 261 TrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsn 280
Db 999 TCGATAGTGTGAGAGTCGATGAATGAATCAAGCCTGATGTAGACCTTTAAACTACGCTTGGT 1058
0Y 281 GlyThrCysGlnThrThrTyr---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
Db 1059 GGGAGCTGTCAAGACACTTATATACCAAAATGCAATGTTTCCCAACTATATATGCTACT 1118
0Y 300 TyrTyrAsnTyrMetSerAsnleuGlyAspLeuPheGluGlyPhe 314
Db 1119 TATTATATATACATGTTTAACTTGCTGATCTATTATTTGAAGATTC 1163

RESULT 5
US-07-865-169-1
; Sequence 1, Application US/07865169
; Patent No. 6015940
; GENERAL INFORMATION:
; APPLICANT: Tumer, Nilgun E.
; APPLICANT: Lodge, Jennifer K.
; APPLICANT: Kaniewski, Wojciech K.
; TITLE OF INVENTION: Virus Resistant Potato Plants
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
; STREET: 700 Chesterfield Parkway No. 6015940ch
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/865,169
; FILING DATE: 19920407
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10547)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1379 base pairs
;

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	TYPE:	NUCLEIC ACID
	STRANDEDNESS:	single
	TOPOLOGY:	linear
	MOLECULE TYPE:	CDNA
	US-07-865-169-1	
Alignment Scores:		
Pred. No.:	3,256-139	1,379
Score:	1,235.50	239
Percent Similarity:	86.3%	33
Best Local Similarity:	75.9%	40
Query Match:	76.4%	3
DB:	Gaps:	2
US-09-978-274A-2 (1-314) x US-07-865-169-1 (1-1379)		
QY	1	MetyrsVlMclleuValValValThrluLeuLeaATPleuLleAlaAlaPProthr 20
DB	225	ATGAAGTCGAAGCTTGTGGTGAACAATCAAAV-----TGGCTCAATTCGTGACCAACT 278
QY	21	SeThrCySaIleAeSnThrIleThrPheApAlaGlyAsnAlaThrIleAenlySTYr 40
DB	279	TCAACTTGGCGCTGGAATACATCTCTACAAATGTGGAAAGTACCAACTTACCAATAC 338
QY	41	AlaThrPheMetGluSerLeuArgAnGlnAlaAlaAspProLyLeuLyScYrGly 60
DB	339	GCCACTTTTCGAATGATCTTCGTATGAAGGAAAGATCCAAAGTTTAAATGCTATGGA 398
QY	61	IleProMetLeuPProAspThrAsnSerThrProLySTYrLeuLeuValLySleuGngly 80
DB	399	ATACCAATGCTGCGCCAAATCAAAATCAATCCAAAGTACGTGTGGTTGAGCTCCAAAGT 458
QY	81	AlaAsnLeuLySThrlIleThrLeuMetLeuArgArgAsnLeuTyTValMetGlyTYr 100
DB	459	TCAATATAAAAACCATCACTACATACTGAGACGAAACAATTGTGATGGGTAT 518
QY	101	SerAspProPheAsnGlyAsnLyScYArgTYrHisIlePheAsnAspIleThrSerThr 120
DB	519	TCTATATCCCTTGGAAACCAATTAATGTGTTACCAATCTTAAATGATATCTCAGTACT 578
QY	121	GluArgThrAspValGluAsnThrIleuCySerSerSerSerSerArgValAlaMetSer 140
DB	579	GAAAGCCCAAGATGAGAGACTACTCTTTGGCCCAATGCCAATCTCGATGTAGTAAAC 638
QY	141	IleAsnTyraSnSerLeuTyTProThrMetGluLySlySaIleGluValAsnSerArgaen 160
DB	639	ATAAATCTTGTATGTCATCTCAATCCAAATTTGAAATCAAAAGCGGAGTAAATCAAGAAGT 698
QY	161	GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLySlyIleSerGlyValaAp 180
DB	699	CAGGTCCCAACTGGGAATTCAAATCTCAACAGTAATATTGGAAACATTTCTGAGAGATG 758
QY	181	SerPheProValLySThrlGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
DB	759	TCAATTCACGTAGAAAACCGGAAGCGGAATTCCTATTTGGTAGCATCAAAATGTATCAGAG 818
QY	201	AlaAlaArgPheLySTYrIleGlnAsnGlnValLySThraenPheAsnArgAlaPheTYr 220
DB	819	GCACCAAGATTCAAGTACATAGAGATCAGGTGAAACATAATTTTAAACAGAGCAATTCAC 878
QY	221	ProAspProLyValIleAsnLeuGlnGluLySTPGLySlyIleSerGlnAlaIleHis 240
DB	879	CTTAATCCCAAGTACTTAATTTTGCMAAGACATGGGGTAAAGATTTCACAGCAATTCAT 938
QY	241	AsnAlaLyBaGnglyAlaLeuProLySTProLeuGlnLeuValaAspAlaLySlyTYrHis 260
DB	939	GATCCCAAGATGAGATTTTACCAAACTCTCGAGCTAGAGATGCGAGTGGTCCAAAG 998
QY	261	ThrIleValLeuArgValaAspGlnIleAsnArgAspValaIleuLeuLySTYrValAsn 280
DB	999	TGGATAGTGTTGAGAGTGAGTAATCAAGCCTATGTAGCATCTTTAAATCAATCGTTGCT 1058
QY	281	GlyThrCySglnThrTYr---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299

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Db      1059 GGGAGCTGTGCACGACTATATACCAAAATGCGATTTCGCCAACCTATATATGCTTACT 1118
Oy      300 TTTTYYAANTTYMetSerAsnLeuLysApIlePheGluGlyPhe 314
          |||||
Db      1119 TATTATAATTACATGTTATATCTTGTAATCTTATTTGAAGAATTC 1163

RESULT 6
US-09-005-273-1
; Sequence 1, Application us/09005273
; Patent No. 6137030
; GENERAL INFORMATION:
; APPLICANT: Turner, Nilgun E.
; TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
; TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
; ADDRESSEE: MENTILIK
; STREET: 600 South, Avenue West
; CITY: Westfield
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07090
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,273
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,611
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,694
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/11546
; FILING DATE: 11-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Foley, Shawn P.
; REGISTRATION NUMBER: 33,071
; REFERENCE/DOCKET NUMBER: OCFRS 3.3-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-654-5000
; TELEFAX: 908-654-7866
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1379 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 225..1163
; /
; NAME/KEY: sig_peptide
; LOCATION: 225..290
; /
; US-09-005-273-1

Alignment Scores:
Pred. No.:           3,25e-139             Length:         1379
Score:              1235.50                 Matches:         239
Percent Similarity: 86.3%                  Conservative:    33
Best Local Similarity: 75.9%                Mismatches:     40
Query Match:        76.4%                   Indels:         3
DB:                 3                       Gaps:           2

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QY	1	MctyvsVAlmctleuValValValThleuilealATPleuileAlAProthr	20
Db	225	ATGAAGTCGAGCTGTGTGTGACAAATACATA-----TGGCTCATCTTCCGACCAACT	278
QY	21	SerThrCyValAlleAenthrlleThrPheAplAglYAsnAlaThrIleAsnlyeTy	40
Db	279	TCAACTTGGCGTGGTAATACATCATCTCAATGTGGAAAGTACCACTATGCAATATAC	338
QY	41	AlaThrPheMetGluSerLeuArgAsnGlnAlaIysAspProlybLeuLyCyetrGly	60
Db	339	GCACATTTCTGAAATGATCTTCGTAAATGACGAAAGATCCAACTTTAAATGCTATGGA	398
QY	61	IleProMetLeuProAspThrAsnSerThrProlyeTyrlleuLeuValIleLeuGlnIy	80
Db	399	ATACCAATGCTGCCCAATACAAATACAAATCCAAAGTACGCTGTGTGTGAGCTCCAGST	458
QY	81	AlaAsnleuLystrIleThrLeuMetLeuArgAsnAsnleuTyValMetGlyTy	100
Db	459	TCAATATAAAAAACCATCACTAATATGCTGAGAGAAACAATTTGTATGTATGGGTAT	518
QY	101	SerAspProPheAsnGlyAsnLyCyetrGlyThrllePheAsnAspIleThSerThr	120
Db	519	TCTGATCCCTTGAACCAATAAATGCTGTACATATCTTAATGATATCTCAGTACT	578
QY	121	GluArgThrAspValGluAenthThLeuCySerSerSerSerSerATGValAMetSer	140
Db	579	GAAAGCCCAAGATGATGAGACTACTCTTGTCCCAATGCCAATCTCGTGTATGTAATAAC	638
QY	141	IleAsnTyraAsnSerLeuTyProThrMetGlnLyAlaIysAlaGluValAsnSerArgAsn	160
Db	639	ATTAACCTTGTATGTCATATCCAACTTGGAAATCAAAAGCGGAGTAAATCAAGAAGT	698
QY	161	GlnAlaGlnleuGlyIleGlnIleLeuSerSerAspIleGlyIysIleSerGlyValAsp	180
Db	699	CAGGTCCACTGGGAATTCAAATCTGACAGATATATGGAAGAATTTCTGAGTATG	758
QY	181	SerPheProValIystrGlnAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu	200
Db	759	TCATTTCACTGAGAAACCGAAGCCGAATTCCTATGTGATGACATACAAATGATATCAGAG	818
QY	201	AlaAlaArgPheLystrIleGlnAsnGlnValIystrAsnPheAsnArgAlaPheTy	220
Db	819	GCACCAAGATTCAGTACATGAGAAATCAGGTGAAACTTAATTTTACAGAGCATTCAC	878
QY	221	ProAspProLyAsValIleAsnLeuGlnGlybTrpGlyIysIleSerGluAlaIleHis	240
Db	879	CTTAATCCCAAGATCAATTAATTTGCAAGAGACATGGGGTAAAGATTTCAACGCAATTCAT	938
QY	241	AsnAlaIysAsnGlyAlaLeuProLyProLeuGlnleuValAspAlaIySgLyThLyse	260
Db	939	GATGCCAAGATGAGATTTTACCCAAACCTCTCGAGCTAGTACATGCCAGTGGGCCAAG	998
QY	261	TrpIleValleuArgValAspGlnIleAsnArgAspValAlaLeuLeuLystrValAsn	280
Db	999	TGGATAGTGTGAGAGGATGAAATCAACCTGATATACACTTAAACTAGCGTGTGT	1058
QY	281	GlyThrCySglnThrTrpTyrlleGlnAsnAlaMetPheSerGlnValIleIleSerThr	299
Db	1059	GGGAGCTGTACAGAACTTATTAACCAAAAGGCCATGTTCTCTCAACTTATTAATGTCTACT	1118
QY	300	TyTyTyAsnTyrmecSerAsnleuGlyAspLeuPheGlnIyPhe	314
Db	1119	TATATATATTAACATGTTAATCTTGGTGAATCTATTTGAAAGATTC	1163
RESULT 7			
PCT-US96-11546-1			
Sequence 1, Application PC/TUS9611546			
GENERAL INFORMATION:			
APPLICANT: Tumet, Nilgun E.			
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein			
TITLE OF INVENTION: Mutants			
NUMBER OF SEQUENCES: 2			

;;
CORRESPONDENCE ADDRESS:
ADDRESSER: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
PCT-US96-11546-1
Alignment Scores:
Pred. No.: 3.25e-139 Length: 1379
Score: 1235.50 Matches: 239
Percent Similarity: 86.3% Conservative: 33
Best Local Similarity: 75.9% Mismatches: 40
Query Match: 76.4% Indels: 3
DB: Gaps: 2
US-09-978-274A-2 (1-314) x PCT-US96-11546-1 (1-1379)
QY 1 MetLysValMetLeuValValValThrlleuLeaLarThrlleuLeaLarProthr 20
DB 225 ATGAGTCGATGCTTGCGTGAACAATACATA-----TGGCTCATCTTGGACCACT 278
QY 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyr 40
DB 279 TCAACTTGGGCTGGATACATCATCATACATGTTGGAGTACCACTTAGCAATAC 338
QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGly 60
DB 339 GCCACTTTCGTGAATCTTCGTGAATGAGCGAAGATCCAACTTAAATGCTATGGA 398
QY 61 ILPEKmetLeuProAspThrAsnSerThrProLysTyrLeuValLysLeuGlnGly 80
DB 399 ATACCAATGCTGCCAATACAAATACAAATCCAAAGTACGTTGGTGAAGCTCAAGGT 458
QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyr 100

DB 459 TCMAATAAAAAACCATCACATCACTGATCTGAGACGAACAATTGTATGTCATGGTTAT 518
QY 101 SerAspProPheAsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThr 120
DB 519 TCTGATCCCTTGGAAACCAATTAATGCTGTACCATATCTTATGATATCTCAGTACT 578
QY 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSer 140
DB 579 GAACGCCAAGATGAGAGACTACTCTTGGCCAAATCCAAATCTCGTGTAGTAAAG 638
QY 141 IleAsnTyrAsnSerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAsn 160
DB 639 ATAACTTGTATGATGATATTCACACATTGGAAATCAAAACCGGAGTAAATCAAGACT 698
QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
DB 699 CAGGTCCAACTGGGAATTCAAATTCGACAGTAAATTTGGAAAGATTCTCGAGGTATG 758
QY 181 SerPheProValLysThrGlnAlaPhePheLeuValAlaIleGlnMetValSerGlu 200
DB 759 TCATTCACTGAGAAACCGAAGCCGAATTCCTATGTGTACCCATACAAATGTATCAGAG 818
QY 201 AlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyr 220
DB 819 GCAGCAAGATTCAAGTACATAGAGAAATCAGGTGAAAATTAATTTACAGAGCTTCAAC 878
QY 221 ProAspProLysValIleAsnLeuGluGluLysTyrGlyLysIleSerGluAlaIleHis 240
DB 879 CCTAATCCCAAGACTTAATTTGCAAGACATGGGGTAAAGTTTCACACGCAATTCAT 938
QY 241 AsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrLys 260
DB 939 GATGCCAAGATGAGCTTTTACCCAACTCTGAGCTAGAGATGCAAGTGGCCAG 998
QY 261 TrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsn 280
DB 999 TGGATAGTGTGAGAGTGATGAATCAACCTGATGATGATGATGATGATGATGATGAT 1058
QY 281 GlyThrCysGlnThrThrTyr---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
DB 1059 GGGAGCTGTGACGACACTTATTAACAAAGCCATGTTCTCACTATTAATGATGATCT 1118
QY 300 TyrTrpAsnTyrMetSerLeuLeuGlyAspLeuPheGluGlyPhe 314
DB 1119 TATTATATTAATCAATGTTAATCTTGGATGATTAATTTGAAGATTC 1163
RESULT 8
US-08-501-253A-1
Sequence 1, Application US/08501253A
Patent No. 6146628
GENERAL INFORMATION:
APPLICANT: Tumor, Patih
TITLE OF INVENTION: Biotherapeutic Agents Comprising
TITLE OF INVENTION: Recombinant PAP and PAP Mutants
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 6146628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: US
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,253A
FILING DATE: 11-JUL-1995
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Kettieberger, Denise M.
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 600.323US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
US-08-501-253A-1

Alignment Scores:

Pred. No.:	7.49e-139	Length:	1379
Score:	1232.50	Matches:	238
Percent Similarity:	86.3%	Conservative:	34
Best Local Similarity:	75.6%	Mismatches:	40
Query Match:	76.2%	Indels:	3
DB:	3	Gaps:	2

US-09-978-274A-2 (1-314) x US-08-501-253A-1 (1-1379)

QY 1 MetLyValMetLeuValValValThrLeuLeaIaTrpLeuLeaIaIaIaProThr 20
DB 225 ATGAAATCGATGGCTTGTGGAGCAATATCAATA-----TGGCTCATCTTGGACCAACT 278
QY 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTy 40
DB 279 TCAACTTGGCTCTGATACATCATCATCATGTTGGAGTACCACTTACCAATAC 338
QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyGly 60
DB 339 GCCACTTTCTGATGATCTTCTGTAATGAAGCAAGATCCAAAGTTTAAATCTATGGA 398
QY 61 IleProMetLeuProAspThrAsnSerThrProLysTyIleuLeuValLysLeuGlnGly 80
DB 399 ATACCAATGCTGCCAATACAAATACAAATCCAAAGTACGTTGTTGAGCTCCAAAGT 458
QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuTyValMetGlyTy 100
DB 459 TCBAATTAATAAAACCATTCACATATGCTGAGACGAACAATTGTATGATGGTTAT 518
QY 101 SerAspProPheAsnGlnLysAsnLysCysArgTyHisIlePheAsnAspIleThrSerThr 120
DB 519 TCTGATCCCTTTGMAACCAATAATATGCTTACCATATCTTTAATGATATCTCAGGTACT 578
QY 121 GlnArgThrAspValGlnAsnThrLeuLysSerSerSerSerSerArgValAlaMetSer 140
DB 579 GAACGCCAAGATGTAAAGACTACTCTTGTGCCAAAGCCCAATCTCGTGTATGATAAACA 638
QY 141 IleAsnTyAsnSerLeuTyProThrMetGlnLysLeuAlaIleGlnMetValSerGln 160
DB 639 ATTAATTTGATGTGATATTCACATTCGAAATCCAAACCGGAGTAAATCAAGACT 698
QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
DB 699 CAGGTCCAACTGGAATTCATAATATCTGACAGTAATATGGAAGAATTTCTGGAGTGATG 758
QY 181 SerPheProValLysThrGlnAlaPhePheLeuLeuValAlaIleGlnMetValSerGln 200
DB 759 TCATTTACTGAGAAACCCAGCGCAATTCCTATTTGGTACCCATCAAAATGCTATCAGAG 818
QY 201 AlaAlaArgPheLeuTyTrpIleGlnAsnGlnValLysThrAsnPheAsnArgAlaPheTy 220
DB 819 GCGACGAAGTTCAAGTACATAGAGATCAGGTGAAAACCTAATTTTAAACAGAGATTCAC 878

QY 221 ProAspProLysValIleAsnLeuGlnGlyTyTrpGlyLysIleSerGlnAlaIleHis 240
DB 879 CTAATCCCAAGTACTTATTTGCAAGAGACATGGGGTAAATTTCACACGCAATTCAT 938
QY 241 AsnAlaLysAsnGlnLysAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLys 260
DB 939 GATGCCAAGATAGTAACTTTTACCAAACTCTCGACCTGATGATCCAGTGTGCCAAG 998
QY 261 TrpIleValLeuArgValAspGlnIleAsnArgAspValAlaLeuLeuLysTyValAsn 280
DB 999 TGATATGCTTGGATGATGATGATCAACCCGATGTAGCACTTTAAACTGCTGGT 1058
QY 281 GlyThrCysGlnThrThrTy---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
DB 1059 GGGAGCTTCAGACCACTTATATACCAAAATGCCATGTTCTCTCACTTATATATGCTACT 1118
QY 300 TyrTrpAsnTyTrpMetSerAsnLeuGlyAspLeuPheGlnGlyPhe 314
DB 1119 TATTATTAATTAATCAATGTTAATCTTGGTATCTTATTTGAAGATTC 1163

RESULT 9

US-07-865-169-2
Sequence 2, Application US/07865169
Patent No. 6015940
GENERAL INFORMATION:
APPLICANT: Turner, Nigun E.
APPLICANT: Lodge, Jennifer K.
APPLICANT: Kaniewski, Wojciech K.
TITLE OR INVENTION: Virus Resistant Potato Plants
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. B84F
STREET: 700 Chesterfield Parkway No. 6015940ch
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865.169
FILING DATE: 19920407
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10547)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-865-169-2

Alignment Scores:

Pred. No.:	3.01e-138	Length:	1379
Score:	1227.50	Matches:	238
Percent Similarity:	86.0%	Conservative:	33
Best Local Similarity:	75.9%	Mismatches:	41
Query Match:	75.9%	Indels:	3
DB:	3	Gaps:	2

US-09-978-274A-2 (1-314) x US-07-865-169-2 (1-1379)

QY 1 MetLyValMetLeuValValValThrLeuLeaIaTrpLeuLeaIaIaIaProThr 20

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||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 225 ATGAAGCAATGCTTGAGTGAATATCAATA-----TGGCTCATTTCTTGACCAACT 278
Qy 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaIleThrIleAsnLeuTyr 40
Db 279 TCAACTGGGCTGGAAATACATCATCTACATGTTGGAAGTACACCATTAAGCAATATAC 338
Qy 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaIleAspProlySLeuLeuCysTyrGly 60
Db 339 GCCACTTTTGGGAATGATCTTGTAATGAAGCAAGTATCCAACTTTAAATGCTATGGA 398
Qy 61 IleProMetLeuPheAspThrAsnSerThrProlySLeuLeuValLeuLeuGlnGly 80
Db 399 ATACCAATGCTGCCCAATACAAATCAAAATCCAAAGCAGGTGGTGGTGAAGCTCCAAGT 458
Qy 81 AlaAsnLeuSyrThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyr 100
Db 459 TCAATATTAATAAACATCACTAATAGCTGAGAGCAAAATTTGTATGTATGATGGTAT 518
Qy 101 SerAspProPheAsnGlyAsnLeuCysArgTyrHisIlePheAsnAspIleThrSerThr 120
Db 519 TCTGATCCCTTTGAACCAATATATGCTTACCATATCTTATGATATCTCAGTACT 578
Qy 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSer 140
Db 579 GAAGCCCAAGTGTAGAGACTACTCTTGCCCAATGCCAATCTCGGTAGTAAATAC 638
Qy 141 IleAsnTyrAsnSerLeuTyrProThrMetGlnLeuSyrAlaGluValAsnSerArgAsn 160
Db 639 ATAACTTTTATGATCATATTCATATCCAAATGTGAACAAAGGGAGTAAATCAAGAAGT 698
Qy 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlySyrIleSerGlyValAsp 180
Db 699 CAGGTCCAATCGGAATTCATAATCTGACAGTAAATTTGGAAGATTTCTGGAGTATG 758
Qy 181 SerPheProVallySyrThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
Db 759 TCATTCACGTAGAAAACCGAAGCGAATTCCTATTGGTAGCATCAAAATGTATCAGAG 818
Qy 201 AlaAlaArgPheLeuSyrTyrIleGlnAsnGlnVallySyrAsnPheAsnArgAlaPheTyr 220
Db 819 GCGACCAAGATTCAGATCATAGAGAAATCAGGTGAAATCTAATTTTAAACAGGCACTTAC 878
Qy 221 ProAspProlySyrAlaIleAsnLeuGlnGluLeuSyrGlySyrIleSerGlnAlaIleHis 240
Db 879 CTTAATCCCAAGTACTTAATTTGCAAGACATGGGGTAAAGATTTCAACGCAATTCAT 938
Qy 241 AsnAlaIleAsnGlyAlaLeuProlySyrProLeuGlnLeuValAspAlaIleSyrThrLys 260
Db 939 GATGCCAAGATGAGATTTTAAACCAACTCTCGAGCTAGTGAATGCCAGTGGTGCAG 998
Qy 261 ThrIleValLeuArgValAspGlnIleAsnArgAspValAlaLeuLeuSyrTyrValAsn 280
Db 999 TGAATAGTGTGAGAGTGAATGAATCAAGCTGATATCAACTCTTAAACTAGCTGTGT 1058
Qy 281 GlyThrCysGlnThrTyrTyr---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
Db 1059 GGAAGCTGTGACACATTAATACCAAAATGCCAATGTTTCTCACTATTAATGTCTACT 1118
Qy 300 TyrTyrAsnTyrMetSerAsnLeuGlyAspLeuPheGlnGlyPhe 314
Db 1119 TATATATATTAACATGTTAATCTTGATGATCTAATTTGAAGATTC 1163

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RESULT 10

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US-09-005-273-3
; Sequence 3, Application US/09005273
; Patent No. 6137030
; GENERAL INFORMATION:
; APPLICANT: Tumor, Nilgun E.
; TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
; TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
; ADDRESSER: MENTILIK
; STREET: 600 South, Avenue West
; CITY: Westfield
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07090
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,273
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,611
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,694
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/11546
; FILING DATE: 11-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Foley, Shawn P.
; REGISTRATION NUMBER: 33,071
; REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-654-5000
; TELEFAX: 908-654-7866
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1379 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 225..1163
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 225..290
; US-09-005-273-3
; Alignment Scores:
; Pred. No.: 3,01e-138 Length: 1379
; Score: 1227.50 Matches: 238
; Percent Similarity: 86.0% Conservative: 33
; Best Local Similarity: 75.6% Mismatches: 41
; Query Match: 75.9% Indels: 3
; DB: Gaps: 2
; US-09-978-274a-2 (1-314) x US-09-005-273-3 (1-1379)
; Qy 1 MetIleValMetLeuValValValIleThrLeuIleAlaTrpLeuIleAlaIleAspThr 20
; Db 225 ATGAATCAATGCTTGAGTGAATATCAATA-----TGGCTCATTTCTTGACCAACT 278
; Qy 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaIleThrIleAsnLeuTyr 40
; Db 279 TCAACTGGGCTGGAAATACATCATCTACATGTTGGAAGTACACCATTAAGCAATATAC 338
; Qy 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaIleAspProlySLeuLeuCysTyrGly 60
; Db 339 GCCACTTTTGGGAATGATCTTGTAATGAAGCAAGTATCCAACTTTAAATGCTATGGA 398
; Qy 61 IleProMetLeuPheAspThrAsnSerThrProlySLeuLeuValLeuLeuGlnGly 80
; Db 399 ATACCAATGCTGCCCAATACAAATCAAAATCCAAAGCAGGTGGTGGTGAAGCTCCAAGT 458

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QY 81 ALaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyr 100
Db 459 TCAAAATATAAAAAACCACTACACTAATGCTGAGACGAAACCAATTGATGATGAGGGTAT 518
QY 101 SerAspProPheAsnGlnLysGlySerThrHisGlePheAsnAspIleThrSerThr 120
Db 519 TCTGATCCCTTTAAACCAATTAATGCTGTACCAATCTTTATATGATATCTCAGGTACT 578
QY 121 GluArgThrAspValGluAsnThrLeuCySerSerSerSerSerArgValAlaMetSer 140
Db 579 GAACGCCAAGATTAAGAGACTACTCTTGCCCAATGCCAATCTCGTGTAGTAAAAAC 638
QY 141 IleAsnTyrAsnSerLeuTyrProThrMetGluLysValGluValAsnSerArgAsn 160
Db 639 ATAACTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 698
QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyTyrIleSerGlyValAsp 180
Db 699 CAGGTCCAACTGGGAATTCAAATACCTGACAGATTAATGGAAGAATTTCTGAGAGTATG 758
QY 181 SerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
Db 759 TCATTACATGAGAAAACCGAACCGAATCTCTATTGCTGACCAATCAATGATGATGACAG 818
QY 201 AlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnAsnAsnArgAlaPheTyr 220
Db 819 GCAGCAAGATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 878
QY 221 ProAspProLysValIleAsnLeuGluGluLysTyrGlyIleSerGluAlaIleHis 240
Db 879 CCTAAATCCCAATACTTAATTTGCAAGACAGATGGGGTAAGATTTTCAACAGCAATTCAT 938
QY 241 AsnAlaLysAsnGlyAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLys 260
Db 939 GATGCCAAGATGAGATTTTACCCAAACCTCTGAGTATGATGATGATGATGATGATGATG 998
QY 261 TrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsn 280
Db 999 TGGATAGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1058
QY 281 GlyThrCysGlnThrThrTyr---GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
Db 1059 GGAAGCTGTCAGCACTTAATAACCAAAATGCCATGTTCTCACTTAATAATGCTACT 1118
QY 300 TyrTyrAsnTyrMetSerAsnLeuGlyAspLeuPheGluGlyPhe 314
Db 1119 TATTATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1163

RESULT 11
US-08-138-636-1
Sequence 1, Application US/08138636
Patent No. 534865
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seon
APPLICANT: Choi, Kyu-Whan
APPLICANT: Lee, Kwan Ho
APPLICANT: Kim, Man Keun
TITLE OF INVENTION: No. 534865el Genome Coding PhytoIacca Antiviral
TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 THIRD AVE.
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,636
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/08818
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: PhytoIacca insularis
CLONE: antiviral protein (PIP)
US-08-138-636-1

Alignment Scores:
Pred. No.: 918-115 length: 918
Score: 1031.00 Matches: 210
Percent Similarity: 80.3% Conservative: 39
Best Local Similarity: 67.7% Mismatches: 56
Query Match: 63.8% Indels: 7
DB: 2 Gaps: 4

US-09-978-274a-2 (1-314) x US-08-138-636-1 (1-918)

QY 1 MetLysValMetLeuValValIleThrLeuIleAlaTrpLeuIleAlaProThr 20
Db 1 ATGAAATGATGCTT-----GTGGGACAAATATCATGATGCTCATCTTCCGACCAACA 54
QY 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyr 40
Db 55 TCTACTTGGCCGCTGAATACCATCATCTACATGTTGGAAGTACCAACCATTAAGACTAT 114
QY 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGly 60
Db 115 GCAACTTTTG---ATACTCTGTAAGGCGAAGATCCAA--GTATGTGCTAATGGA 168
QY 61 IleProMetLeuProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGly 80
Db 169 ATACCAATCTGCGCCCAATATGATGATCAATTCAAAATACATATGTTGATGATGATGAT 228
QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyr 100
Db 229 TCAAAATGAAGAGGCGATTCACCTTAATGCTAAGACGAAACCAATTTATATGATGATGAT 288
QY 101 SerAspProPheAsnGlnLysAsnLysCysArgTyrHisGlePheAsnAspIleThrSerThr 120
Db 289 TCTGATCCCTTACAC---AATAGGTGCTGTTCACTTCAATGAGGCTATCTCAAGTACT 345
QY 121 GluArgThrAspValGluAsnThrLeuCySerSerSerSerSerArgValAlaMetSer 140
Db 346 GAACGCCAAGATGATGAGACTACTCTTGCCCAATGCCAATCTCGTGTAGTAAAAAC 405
QY 141 IleAsnTyrAsnSerLeuTyrProThrMetGluLysValGluValAsnSerArgAsn 160
Db 406 ATAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 465
QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyTyrIleSerGlyValAsp 180
Db 466 CAGGTCCAACTGGGAATTCAGATTAATGGAAGAATTTCTGAGAGTATG 525


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Qy      281 G|YTHrCvqGLthrhThrTyr---GlnaenAlAmetPheserqInvalIleIeserThr 239
Db      826 GGAGAGTGCAGAGAACTTATTAACCAAAATGCCATGTTTCTCACTTATTAATGCTTACT 885
Qy      300 T|T|YrAsn|YrImetSerAsnLeuG|YAsp 309
Db      886 TATTTATTAATTACATGGCTAATCTTGATGAT 915

RESULT 13
US-08-471-564-1
/ Sequence 1, Application US/08471564
/ Patent No. 5723326
/ GENERAL INFORMATION:
/ APPLICANT: Moon, Young-Ho
/ APPLICANT: Jeon, Hong-Seoh
/ APPLICANT: Choi, Kyu-Whan
/ APPLICANT: Lee, Kwan Ho
/ APPLICANT: Kim, Man Keun
/ TITLE OF INVENTION: No. 5723326el Genome Coding PhytoIacca Antiviral
/ TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: DARBY & DARBY
/ STREET: 805 THIRD AVE.
/ CITY: NEW YORK
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10022
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/471,564
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/210,396
/ FILING DATE:
/ APPLICATION NUMBER: US 08/138,636
/ FILING DATE: 15-OCT-1993
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ludwig, S. Peter
/ REGISTRATION NUMBER: 25,351
/ REFERENCE/DOCKET NUMBER: 0136/18818US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 527-7700
/ TELEFAX: (212) 753-6237
/ TELEX: 236687
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 918 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: PhytoIacca insularis
/ IMMEDIATE SOURCE:
/ CLONE: antiviral protein (PIP)
/ US-08-471-564-1

Alignment Scores:
Pred. No.:          9.1e-115          length:          918
Score:              1031.00           Matches:          310
Percent Similarity: 80.3%             Conservative:     39
Query Similarity:   67.7%             Mismatches:       56
Best Match:         63.8%             Indels:           7

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DB: 2 Gaps: 4

US-09-978-274A-2 (1-314) x US-08-471-564-1 (1-918)

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QY 41 AlaThrPheMetGlySerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTrpGly 60

Db 115 GCAACTTTTGG---ATACTTGTAAGAGCGAAGATCCAA--GTATATGCTATGCA 168

QY 61 IleProMetLeuProAspThrAsnSerThrProLysTrpLeuValLysLeuGlnGly 80

Db 169 ATACCAATGCTCCCAATATTCGATCACTCAATCCAAATATACATATTTGGTGGAGCTCCAAAGT 228

QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgArgAsnAsnLeuTrpValMetGlyTr 100

Db 229 TCAATATGAAGAAGCGCATCACCTAATGCTAAGACGAAACAAATTTATATGATGAGGCTAT 288

QY 101 SerAspProPheAsnGlyAsnLysCysArgTrpHisIlePheAsnAspIleThrSerThr 120

Db 289 TCTGATCCCTACAAAC---AATAGGTGTGTTCCATCTCTTTAAGGCTATCTCAGGATCT 345

QY 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerArgValAlaMetSer 140

Db 346 GAACCGCAAGAGTGAAGACTACTCTTTGGCCCAAAATGCGCAATTCCTGTGTGGTAAAC 405

QY 141 IleAsnTrpAsnSerLeuTrpProThrMetGluLysLysAlaGluValAsnSerArgAsn 160

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QY 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180

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QY 261 TrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTrpValAsn 280

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Db 886 TATTATATATTCATGCTGATATCTTGGTAT 915

RESULT 14

US-08-356-161-7

; Sequence 7, Application US/08356161

; Patent No. 5916772

; GENERAL INFORMATION:

APPLICANT: Lappi, Douglas A.
APPLICANT: Barthelemy, Isabel
APPLICANT: Baird, J. Andrew
APPLICANT: Sosnowski, Barbara A.
TITLE OF INVENTION: RECOMBINANT PRODUCTION OF
TITLE OF INVENTION: SAPORIN-CONTAINING PROTEINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED AND BERRY LLP
STREET: 701 Fifth Avenue, 6300 Columbia Center
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,161
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,161
FILING DATE: 13-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: No. 5916772tenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.404US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..804
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..804
OTHER INFORMATION: /note= "Nucleotide sequence
OTHER INFORMATION: corresponding to the clone M13 mp18-69 in Example 1.B.2."
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 46..804
OTHER INFORMATION: /product= "Saporin"
US-08-356-161-7
Alignment Scores:
Pred. No.: 6,51e-34 Length: 804
Score: 361.50 Matches: 100
Percent Similarity: 56.1% Conservative: 56
Best Local Similarity: 36.0% Mismatches: 97
Query Match: 22.4% Indels: 25
DB: 2 Gaps: 11
US-09-978-274A-2 (1-314) x US-08-356-161-7 (1-804)
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DB 1 GCATGATCCTGCTTCATTTTCAGTCGACAACTGATGCGGTCACTCATCAACA 60
QY 30 PheAspAlaGlyAsnAlaThrIleAsnLysThrAlaThrPheMetGluSerLeuArgAsn 49
DB 61 TTAGATTTAGTAAATCCGACCGCGGTCAATACTCATCTTTTGTGATTAATCCGAAC 120
QY 50 GlnAlaLysAspProLysLeuLysCysGlyGlyIleProMet---LeuProAspThrAsn 68

DB 121 AACGTAAAGATCCAAACCTGAAATACCGGTGTACCGACATACCGCCGATAGGCCCACT 180
QY 69 SerThrProLysThrLeuLeuValLysLeuGlnGlyAlaAsnLeuLysThrIleThrLeu 88
DB 181 TCTAAAGAAAAATTCCTTAGAATTAATTCCTCAAGATCCCGA---GGAAAGGTCTCACTT 237
QY 89 MetLeuArgAsnAsnLeuLysThrValMetGlyTyr-----SerAspProPheAsnGly 106
DB 238 GGCCTAAACGCGATTAATCTGTATGTGTGCGGTATCTGCATGTGAATGATTAACCAATGTT 297
QY 107 AsnLysCysArgThrIlePheAsnAspIleThrSerThrGlnArgThrAspValGlu 126
DB 298 AATCGGCA---TATTACTCAGATCAGAAATTAATCTCCCGCATTAAC-----345
QY 127 AsnThrLeuCysSerSerSerSerSerValAlaMetSerIleAsnThrAsnSerLeu 146
DB 346 ---GCCCTTTCCAGAGCCACAACTGCAATCAGAAACCTTAGAATACACAGAGAT 402
QY 147 TyrProThrMetGluLysLysAlaGluVal-----AsnSerArgAsnGlnVal 162
DB 403 TATCAGTCGATGAAAGAAATGCCAGATACACAGAGATCAAAAGTAAAGAAATC 462
QY 163 GlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPhe 182
DB 463 GGGTTGGGATGTACTTACTTCAAGCTCCATGGAACATGAAC---AAGAAGCAAGT 519
QY 183 ProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAla 202
DB 520 GTGGTTTAAAGACCAAGCTAGATTCCTTATGCTATTCAGATGACGGCTGAGGACGG 579
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QY 223 ProLysValIleAsnLeuGlnGluLysThrGlyLysIleSerGluAlaIleHis---Asn 241
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DB 700 GCCAAAAACGGCGTGTATTAATAAGATTATGATTCGCGTTTGAAAA-----747
QY 262 IleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysThrVal 279
DB 748 ---GTAGGACAGGTGAAGACTTG-----CAATGGGACTCTTATGATTTG 792
RESULT 15
US-08-718-904-23
Sequence 23, Application US/08718904
Patent No. 6037329
GENERAL INFORMATION:
APPLICANT: Baird, J. Andrew
APPLICANT: Chandler, Lois Ann
APPLICANT: Sosnowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996
CLASSIFICATION: 424

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ATTORNEY/AGENT INFORMATION:
NAME: No. 6037329tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.415c1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..804
NAME/KEY: misc feature
LOCATION: 1..804
OTHER INFORMATION: /note= "Nucleotide sequence
OTHER INFORMATION: corresponding to the clone M13 mp18-G9 in Example I.B.2."
FEATURE:
NAME/KEY: mat peptide
LOCATION: 46..804
OTHER INFORMATION: /product= "Saporin"
US-08-718-904-23
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Alignment Scores:
Pred. No.: 6,51e-34 Length: 804
Score: 361.50 Matches: 100
Percent Similarity: 56.1% Conservative: 56
Best Local Similarity: 36.0% Mismatches: 97
Query Match: 22.4% Indels: 25
DB: 3 Gaps: 11
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US-09-978-274a-2 (1-314) x US-08-718-904-23 (1-804)

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Db 1 GCATGATCTCCTGCTTCAATTTTCAGCTTGGAACAACACTGATCGGTCACATCAACACA 60
QY 30 PheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGluSerLeuArgAsn 49
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QY 50 GluAlaLysAspProLysLeuLysCysTyrGlyIlePromet---LeuProAspThrAsn 68
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QY 89 MetLeuArgArgAsnAsnLeuTyrValMetGlyTyr-----SerAspProPheAsnGly 106
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Db 238 GGCCTAAACGCGATACCTGTATGTGTCGCGCTATCTTGCAATGATTAACGAATGTT 297
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Db 580 CGATTAGGATCACTAACAAACCTGTATCAAGAACTTCCCAACAAAGTTCAACTCGGAA 639
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Job time : 351.749 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocollaboration Ltd.

OM nucleic - nucleic search, using bw model

Run on: April 9, 2006, 00:06:24 ; Search time 4658.27 Seconds
(without alignments)
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Title: US-09-978-274A-3

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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2: gb_in:*
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14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	792	100.0	792	6	AX427704 Sequence
2	786.4	99.3	945	6	AX427702 Sequence
3	783.2	98.9	1249	15	PAPAPSRIP
4	768.4	97.0	786	15	AB071855
5	766	96.7	1092	6	AX427720 Sequence
6	582.8	73.6	783	15	AB071854
7	539	68.1	1114	15	AF533515
8	535	67.6	882	6	A67183
9	534.2	67.4	942	15	AY572976
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11	534.2	67.4	1164	15	AY049785
12	534.2	67.4	1195	6	A42103
13	534.2	67.4	1195	6	I43835
14	534.2	67.4	1195	6	I55866
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19	531	67.0	1195	6	A36639	A36639 Sequence 1
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33	462	58.2	465	6	AX427708	AX427708
34	461	58.2	1113	15	AY071928	AY071928
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42	155	19.6	1180	15	MCU80072	U80072 Mesembryant
43	101	12.8	934	6	AX427733	AX427733
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45	99.2	12.5	902	15	AF533516	AF533516

ALIGNMENTS

RESULT 1	AX427704	792 bp	DNA	linear	PAT 20-JUN-2002
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DEFINITION	AX427704	AX427704.1	GI:21537816		
ACCESSION	AX427704				
VERSION	AX427704.1	GI:21537816			
KEYWORDS					
SOURCE					
ORGANISM					
Phytolacca americana (American pokeweed)					
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;					
Caryophyllales; Phytolaccaceae; Phytolacca.					
REFERENCE					
1	Neelam, A., Atkinson, H.J., Mcpherson, M.J. and Thomas, C.J.R.				
AUTHORS					
TITLE					
JOURNAL					
PATENT: WO 0233107-A 3 25-APR-2002;					
CAMBRIDGE ADVANCED TECH (GB)					
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ORIGIN					
Query Match					
100.0%; Score 792; DB 6; Length 792;					

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DB 793 AGAGTGGATGAATCAATCGTATGTCACCTCTTAAGTACGTTAATGAACTGTGAC 852
QY 784 ACAACTTA 791
DB 853 ACAACTTA 860

RESULT 3
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LOCUS P.americana mRNA for pokeweed antiviral protein.
DEFINITION X98079
ACCESSION X98079.1 GI:1707648
VERSION PAP-S gene; pokeweed antiviral protein (PAP); ribosome-inactivating
KEYWORDS protein.
SOURCE Phytolacca americana (American pokeweed)
ORGANISM Phytolacca americana
Phytolacca americana; Streptophyta; Embryophyta; Tracheophyta;
Bakaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE 1
AUTHORS Poyet, J.L. and Hoeveler, A.
TITL CNA cloning and expression of pokeweed antiviral protein from
in vitro seeds in Escherichia coli and its inhibition of protein synthesis
JOURNAL PBRS Lett. 406 (1-2), 97-100 (1997)
PUBMED 9109394
REFERENCE 2 (bases 1 to 1249)
AUTHORS Poyet, J.L.
TITL Direct Submission
JOURNAL Submitted (22-MAY-1996) J.L. Poyet, Laboratoire de
Biochimie-Biologie Molculaire, UFR Sciences et Techniques, 16
route de Gray, 25030 Besancon Cedex, FRANCE
REMARK Revisé by author 20-SEP-1996
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Best Local Similarity 99.6%; Pred. No. 5e-175;

Matches 785; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 ATAAATGATCACTTTGATGCTGGAATGCGCAATTAACAAATATGCCACTTATG 63
DB 178 ATAAATGATCACTTTGATGCTGGAATGCGCAATTAACAAATATGCCACTTATG 237
QY 64 GAATCTCTGTAATCAAGGAAAGATCCAAAATTAATATGTCATACCAATGTA 123
DB 238 GAATCTCTGTAATCAAGGAAAGATCCAAAATTAATATGTCATACCAATGTA 297
QY 124 CTGATACATAATTCAGCCCTTAAGTACTTAATGTTAGTCCAAAGTGCAAACTAAA 183
DB 298 CTTGATACATAATTCAGCCCTTAAGTACTTAATGTTAGTCCAAAGTGCAAACTAAA 357
QY 184 ACCATTACATAATGCTGAGACGAAATTAATTAATGATGATGAGCTATTTGATCCCTTC 243
DB 358 ACCATTACATAATGCTGAGACGAAATTAATTAATGATGATGAGCTATTTGATCCCTTC 417
QY 244 AATGCAATAGTGTGCTTACCATATATTTAATGATATTTCAAGCACGGAACGACTGAT 303
DB 418 AATGCAATAGTGTGCTTACCATATATTTAATGATATTTCAAGCACGGAACGACTGAT 477
QY 304 GTGAGAAATACCTTTGCTCAAGTTCTAGTTCTGTGTCATGTCATTAACATCAAT 363
DB 478 GTGAGAAATACCTTTGCTCAAGTTCTAGTTCTGTGTCATGTCATTAACATCAAT 537
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DB 718 AAGTACATTAAGAACCAAGTCAATTAATTTAATGACATTTTCCCTGATCCCAA 777
QY 604 GTAATTAATTTGAGAGGAGGAGGCAATATCTGAGGCAATTCACATGCAAGAT 663
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QY 664 GGGGCTTTACCAACCACTTGAAGTGAATGCCAAGGTAACAATGATAGTCTT 723
DB 838 GGGGCTTTACCAACCACTTGAAGTGAATGCCAAGGTAACAATGATAGTCTT 897
QY 724 AGAGTGGATGAATCAATCGTATGTCACCTCTTAAGTACGTTAATGAACTGTGAC 783
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QY 784 ACAACTTA 791
DB 958 ACAACTTA 965

RESULT 4
AB071855 786 bp DNA linear PLN 19-MAR-2002
LOCUS Phytolacca americana pap2 gene for PAP-82, partial cds.
DEFINITION AB071855
ACCESSION AB071855
VERSION AB071855.1 GI:19570839
KEYWORDS
SOURCE Phytolacca americana (American pokeweed)
ORGANISM Phytolacca americana
Phytolacca americana; Streptophyta; Embryophyta; Tracheophyta;
Bakaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE 1
AUTHORS Honjo, E. and Watanabe, K.

TITLE Cloning of genomic DNA encoding two types of pokeweed antiviral protein in seeds, PAP-S1 and PAP-S2, and functional comparison of their recombinant proteins with other PAP isoforms

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 786)

AUTHORS Watanabe,K. and Honjo,E.

JOURNAL Direct Submission

TITLE Submitted (19-SEP-2001) Keiichi Watanabe, Saga University, Department of Applied Biological Sciences, Honjo-machi, Saga city, Saga 840-8502, Japan (E-mail:watakei@saga-u.ac.jp, Tel:81-952-28-8774, Fax:81-952-28-8774)

FEATURES

source

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ORIGIN

Query Match 97.0%; Score 768.4; DB 15; Length 786;

Best Local Similarity 98.6%; Pred. No.1.8e-171;

Matches 775; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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64 GAATCTCTTGTATCAAGGAAAGATCCAAATCTAATAATGCTATGACCAATGCTTA 123

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124 CCGATATCAATTCGACCCCTTAAGTATTTGCTTAACTCCAAAGTGCATACTAAA 183

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244 AATGCAATAGTGTGCTTACCATATTAATTAATGCTATTAACAAGCCGAAGCAGCTGAT 303

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304 GTGAGAAATACCTTTGCTCAAGTCTAAGTCTCGTGTGCAATGTCATTAACTAACAT 363

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Db 601 GTAATTAATCTTGGAGAGAAAGTGGCCAAATCTCTGAGCAATTCACATGCGCAAT 660

Qy 664 GGGGCTTATCCCAACCACTTGAAGTATGAGATGCCAAAGTACCAAGTGAATGTTCTT 723

Db 661 GGGGCTTATCCCAACCACTTGAAGTATGAGATGCCAAAGTACCAAGTGAATGTTCTT 720

Qy 724 AAGTGAATCAATCAATGCTATGAGCACTCTTAAGTACCTTAATGGAACCTGTGAG 783

Db 721 AAGTGAATCAATCAATGCTATGAGCACTCTTAAGTACCTTAATGGAACCTGTGAG 780

Qy 784 ACAACT 789

Db 781 GCCACT 786

RESULT 5

AX427720 1092 bp DNA linear PAT 20-JUN-2002

LOCUS AX427720

DEFINITION Sequence 19 from Patent WO0233107.

ACCESSION AX427720

VERSION AX427720.1 GI:21537829

KEYWORDS

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1

AUTHORS Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.

TITLE Plant cell death system

JOURNAL Patent: WO 0233107-A 19 25-APR-2002;

CAMBRIDGE ADVANCED TECH (GB)

FEATURES

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/note="complement(742..786)"

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complement(1066..1092)

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Query Match 96.7%; Score 766; DB 6; Length 1092;

Best Local Similarity 100.0%; Pred. No.6.1e-171;

Matches 766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 ATGGAATCTCTTGTATCAAGGAAAGATCCAAATCTAATAATGCTATGAGCAATGCA 120

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121 CTACCTGATACATTAATTCGACCCCTTAAGTACTTAATGCTTAACTCCAAAGTGAACCTTA 180

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Db 181 AAAACATTAACCTAATGCTGAGACGAAATTAATTATAGTGATGGCTATTGTGATCC 240
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RESULT 6
LOCUS AB071854 783 bp DNA linear PLN 19-MAR-2002
DEFINITION Phytolacca americana paps1 gene for PAP-S1, partial cds.
ACCESSION AB071854
VERSION AB071854.1 GI:19570837
KEYWORDS
SOURCE Phytolacca americana (American pokeweed)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS Honjo, E. and Watanabe, K.
TITLE Cloning of genomic DNA encoding two types of pokeweed antiviral
protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
their recombinant proteins with other PAP isoforms
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 783)
Watanabe, K. and Honjo, E.
JOURNAL Direct Submission
TITLE Submitted (19-SEP-2001) Keiichi Watanabe, Saga University,
Department of Applied Biological Sciences, Honjo-machi, Saga city,
Saga 840-8502, Japan (E-mail: watanake@cc.saga-u.ac.jp,
Tel: 81-952-28-8774, Fax: 81-952-28-8774)

FEATURES
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Query Match 73.6%; Score 582.8; DB 15; Length 783;
Best Local Similarity 84.7%; Pred. No. 1.7e-127;
Matches 666; Conservative 0; Mismatches 117; Indels 3; Gaps 1;

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Db 1 ATCAATACGATAGTTCGACGTGAAATGCAACATTAACAATATGCTTATG 60
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Qy 124 CCTGATCTAATTCGACCCCTTATGCTATTTGTTAGCTCAAGTGCAACCTTAA 183
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Qy 244 AATGCAATAGTGTCTGTACATATTTATATATATTTACAGACCGAAGCACTGAT 303
Db 239 -ACGACATATAGTGTCTGTACATATTTATATATATTTAAAGCACGATATACAGTAT 297
Qy 304 GTGAGAAATCTCTTGTCTCAAGTTCTGATCTGTGTGATGATGCAATTAATCAAT 363
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Qy 784 ACAACT 789
Db 778 GCCACT 783

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RESULT 7
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LOCUS AF533515 1114 bp mRNA linear PLN 01-AUG-2005
DEFINITION Phytolacca octandra anti-viral protein (pap) mRNA, partial cds.
ACCESSION AF533515
VERSION AF533515.1 GI:33329822
KEYWORDS
SOURCE
ORGANISM
Phytolacca octandra
Phytolacca octandra
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
SpERMatoophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
1 (bases 1 to 1114)
Lin, J. S. and McNally, K. P.
Direct Submission
Submitted (29-JUL-2002) Reproductive Technologies, AgResearch
Wallaceville, Ward Street, Upper Hut, Wellington, New Zealand
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ORIGIN

Query Match 68.1%; Score 539; DB 15; Length 1114;

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Matches 632; Conservative 0; Mismatches 155; Indels 0; Gaps 0;
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Db 106 ATGATCTTCGTAATGAAGCGAAGATCCAAATTAAATGCTATGGAATACCAATGCTGC 165

QY 125 CTGATACTAATTCGACCCCTAAGTACTTATTGGTTAAGCTCCAAGTGCMAACCTAAAA 184

Db 166 CCATACAAATCCAGATCCAAGTACGTGTGTTGAGCTCCAAGGTTCAATAAAAAA 225

QY 185 CCATTACACTAATGCTGAGACGAATACTTATACGTGATGGCTATTCTGATCCCTTCA 244

Db 226 CCATCACACTAATGCTGAGACGAACAATTGTATGTGATGGCTATTCTGATCCCTTG 285

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Db 286 ATACCAATAGTGTGCTTACCATATCTTAATGATATCTCAGTACTGACGCCAAGATG 345

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Db 346 TAGAGACTACTCTTTGGCCCAATCCCAATTCTCGTGTATTAAACAATAAATATGATA 405

365 GCTTATATCCGACCATGGAAAGACGAGAGTAACTCAGGAATCAAGTCCAATTGG 424

Db 406 GTGATATCCAACATTGGAATCAAAAGCGGAGTAAATCAAGAAGTCAAGTCCAACCTGG 465

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Qy	545	AGTACATGAG	AGCAAGTCAAG	CTAATTTTAATAG	CAATTCTTAC	CTTGATCCCAAG	604	
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Qy	725	GAGTGAT	GAAATCA	TGATGTG	ATGCGACTCTT	AAATAGTAC	GTTAATGAACTGTG	784
Db	766	GAGTGAT	GAAATCA	AACTGAT	GTAGCACTT	AAACTA	CGTGAGTGGA	825
Qy	785	CAACTTA	791					
Db	826	CAACTTA	832					

RESULT 8				
A67183	A67183	882 bp	DNA	linear
LOCUS	Sequence 1 from Patent EP0808502.			
DISRUPTION				
ACCESSION	A67183			
VERSION	A67183.1	GI:4756167		
KEYWORDS				
SOURCE	Phytolacca insularis			
ORGANISM	Phytolacca insularis			

CONCLUSION

Caryophyllales; Phytolaccaceae; Phytolacca.

AUTHORS Moon, Y., Choi, J., Yun, Y., Jin, J., Hong, E., Lee, J., Choi, K., Lee, J.,

TITLE Novel genes encoding antiviral proteins of *Phytolacca insularis*

JOURNAL Patent: EP 0808902-A 1 26-NOV-1997;

COMMENT
Other publication JP 9308489 19971202

Other publication AU 6570696 19971127.

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Best Local Similarity 79.8%; Pred. No. 3.6e-116;

A vertical ruler with markings from 1 to 10 centimeters. The markings are in centimeters, with millimeter increments indicated between the centimeter numbers. The ruler is oriented vertically, with the 1 cm mark at the top and the 10 cm mark at the bottom.

䷗ ䷖ ䷕ ䷔ ䷓ ䷒ ䷑ ䷐ ䷏ ䷎ ䷍ ䷌ ䷋ ䷊ ䷉ ䷈ ䷇ ䷆ ䷅ ䷄ ䷃ ䷂ ䷁ ䷀

A vertical ruler with markings from 0 to 10 centimeters. The markings are in millimeters, with numbers every centimeter. The ruler is oriented vertically with the 0 mark at the top.

QY 181 AAAACATTACCTAATGCTGAGAGAAATACTATACGTATGAGGCTATTGATCCC 240
DB 181 AAAACATTACCTAATGCTGAGAGAAATACTATACGTATGAGGCTATTGATCCC 240
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QY 361 AATAGCTTATATCCGACATGAGAAAGAAAGCAAGATTAATCTAGAAATCAAGTCCAA 420
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QY 421 TTGGGAATTCGAATCTCAGACATGACATTTGGAATAATCTCTGAGTTGATTCCTTCCCT 480
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QY 481 GTAAAACTGAGGCTTTTCTTCTAGTGTGAGCCATCCAAATGTTTGAAGGCGAGCGCA 540
DB 481 GAGAAAGTCCAGAGTGAATCTTCTAGTGTGAGCCATCCAAATGTTTGAAGGCGAGCGCA 540
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DB 661 AATGGGCTTTTACCCAAACCACTTGTAGCTAGTGTGAGCCAAAGTATGATAGT 720
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DB 721 TTGAGAGTGTAGTATCAAGCGCTGATGTAGCACTCTTAAGTACGTTAAATGCAACCTGT 780
QY 781 CAGACCACTTA 791
DB 781 CAAACCAATTA 791

RESULT 9
AY572976 942 bp mRNA linear PLN 05-APR-2004
LOCUS Phytolacca americana antiviral protein (PAP) mRNA, complete cds.
DEFINITION AY572976
ACCESSION AY572976
VERSION AY572976.1 GI:45826466
KEYWORDS
SOURCE Phytolacca americana (American pokeweed)
ORGANISM Phytolacca americana
Bukayocsa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
1 (bases 1 to 942)
Xiao,Z.A. and Jiang,Y.
A gene encoding the pokeweed antiviral protein in the leaf of
Phytolacca americana
Unpublished
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
JOURNAL
Submitted (13-MAR-2004) College of Life Sciences, Beijing Normal
University, No. 19 Xinjiekouwai Street, Haidian District, Beijing
100875, China
location/Qualifiers
1..942
/organism="Phytolacca americana"
/mol_type="mRNA"
/db_xref="taxon:3527"

gene 1..942
/gene="PAP"
1..942
CDS /gene="PAP"
/codon_start=1
/product="antiviral protein"
/protein_id="AA577872.1"
/db_xref="GI:45826467"
/translation="MRVYLVTSTISLILAPSTMAVNTIYNVGSSTISKATPLND
LRNADPSLICKTGITPMLEPTNTNPTVLTVELGSKNTITLKRNLTVMSIDPF
ENKCRVYHIFNDISGERODVETTLCPNNSRVSKNINPSRPTLSKAGVSRGV
OLGIQILDSTNIGTSGVMSFTKEKTBALFLVALIOMVSEARFPIENOVNTNRAFN
PNKRVNLQSTWTKISTAIHDAKNGVLPRLIVDVSAGAKMIVLRDEIKPVALINY
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ORIGIN

Query Match 67.4%; Score 534.2; DB 15; Length 942;
Best Local Similarity 79.9%; Pred. No. 5.5e-116;
Matches 629; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 5 TAATACGATCACCCTTGTGATGCTGGAATGCCCAATTAACAATATGCACTTTATG 64
DB 68 TGAATCAATCATCTCAATGTTGAGAGTACCACTATGCAAAATAGCCACTTTCTGA 127
QY 65 AATCTCTGTATCAAGCAAGATCCAAATCTAAATGCTATGCAATCAATGCTAC 124
DB 128 ATGATCTTGTATGAGCAAGATCCAAATGCTATGAAATCAATGCTG 187
QY 125 CTGATCTAATTCGACCCCTAAGTACTTATGTTAAGTCCAAAGTGCAAACCTAAAA 184
DB 188 CCAATCAATTAACAATTCAAAGTACGTTGTTGAGTCCAAAGTTCAAATTAATAA 247
QY 185 CCAATCAATTAACAATTCAAAGTACGTTGTTGAGTCCAAAGTTCAAATTAATAA 244
DB 248 CCAATCAATTAACAATTCAAAGTACGTTGTTGAGTCCAAAGTTCAAATTAATAA 307
QY 245 ATGCAATTAAGTGTGCTTACATATATTAATGATATTAACAAGCAAGCAAGTATG 304
DB 308 AAACCAATTAATGCTTACATATCTTTATGATATCTCAGTATCGAAAGCAAGTATG 367
QY 305 TGGAGAAATCTCTTGTCTCAAGTCTAGTGTCTGCTGTGCAATGTCATTAATCAATA 364
DB 368 TAGAGACTACTCTTGTCTCAAGTCTAGTGTCTGCTGTGCAATGTCATTAATCAATA 427
QY 365 GCTTATATCCGACATGAGAAAGAAAGCAAGTATTAATCAAGTATCAAGTATG 424
DB 428 GTGATATCCCAATGGAATCAAAAGCGGAGTAAATCAAGATCAAGTCAACTG 487
QY 425 GAATCAAAATCTCAGACATGACATTTGAAAAATCTCTGAGTGTATTCATCCGTGA 484
DB 488 GAATCAAAATCTCAGACATGACATTTGAAAAATCTCTGAGTGTATTCATTCAGAGA 547
QY 485 AAACGAGGCTTTTCTAATGAGCAATCCAAATGTTTCAAGGCGAGCGCATTC 544
DB 548 AAACGAGGCGCAATCTTATGAGTGTGCAATCAATGATCAAGGCGAGCAAGTTC 607
QY 545 AGTACATTAAGAAACAAGTCAAGTATTTTATAGAGATTTCACTCTGATCCCAAG 604
DB 608 AGTACATTAAGAAACAAGTCAAGTATTTTATAGAGATTTCACTCTGATCCCAAG 667
QY 605 TAATTAATCTGAGAGAGAGTGGGCAAAATCTCTGAGCAATTCGAATGCAAGTATG 664
DB 668 TAATTAATCTGAGAGAGAGTGGGCAAAATCTCTGAGCAATTCGAATGCAAGTATG 727
QY 665 GAGCTTTACCCAAACCACTTGAATGAGTGTGCAAGTATGCAAGTATGATTTCTTA 724
DB 728 GAGTTTACCCAAACCACTTGAATGAGTGTGCAAGTATGCAAGTATGATTTCTTA 787
QY 725 GAGTGTATTAATCAATGATGATGAGTGTGCACTCTTAAGTATGAAATGCACTGTCAG 784
DB 788 GAGTGTATTAATCAATGATGATGAGTGTGCACTCTTAAGTATGAAATGCACTGTCAG 847
QY 785 CAACCTTA 791

DB	LOCUS	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
DB	848	CAACTTA	854							
RESULT 10	AY049785	1164 bp	mRNA	linear	PLN 23-OCT-2001					
LOCUS	AY049785	1164 bp	mRNA	linear	PLN 23-OCT-2001					
ACCESSION	AY049785	1164 bp	mRNA	linear	PLN 23-OCT-2001					
VERSION	AY049785.1	GI:16356654								
KEYWORDS										
SOURCE										
ORGANISM										
REFERENCE										
AUTHORS										
TITLE										
JOURNAL										
FEATURES										
source										
gene										
CDS										
Query Match	67.4%	Score 534.2	DB 15	Length 1164						
Best Local Similarity	79.9%	Prod. No. 5.2e-116								
Matches	629	Conservative	0	Mismatches 158	Indels 0	Gaps 0				
5	TAAATACATCACTTGTGATCTGGAAATGCGACCATTAACAAATATSCACCTTTATGG	64								
69	TGAATACATCATCTACCAATGTGTGAAATACCAATTCGAAATGCGCACTTTCTGG	128								
65	AATCTTCTGTAATCAAGCGAAAGATCCAAACTAAATGCTATGGATCAATGCTAC	124								
129	ATAATCTTCGTAATGAAAGCGAAAGATCCAAAGTTAAATGCTATGAAATACCAATGTTGC	188								
125	CTGATACATTAATTCGACCCCTTAAGTACTTATGTTAGCTCGAAGGTGCAAACTTAATAA	184								
189	CCAAATACAAATCCAAATCCAAATGAGTGGTGGTGAAGCTCCAAAGTTCAATTAATAA	248								
185	CCATTACACTATGCTGAGAGGAAATTAATTAATGATGAGGCTATTCGATCCCTTCA	244								
249	CCATCACACTATGCTGAGAGGAAATTAATTAATGATGAGGCTATTCGATCCCTTGG	308								
245	ATGGCAATAGTGTGTTACCAATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	304								
309	ATACCAATAGTGTGTTACCAATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	368								
305	TGAGAAATCTCTTGTGCTCAAGTTCTAGTCTCGTGTGCAATGCTCCATTAATTAATTA	364								
369	TAGAGACTACTCTTGTGCTCAAGTTCTAGTCTCGTGTGCAATGCTCCATTAATTAATTA	428								
365	GCTATATCCAGCATGGAAGGAAAGGAGTAATTAATTAATTAATTAATTAATTAATTAAT	424								

[illegible]

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QLGQILDSNIGKISGWSSTRTKTRAPFLVALIOMSEBARFKIENQVTRRAN
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Query Match 67.4%; Score 534.2; DB 15; Length 1164;

Best Local Similarity 79.9%; Pred. No. 5.2e-116; Matches 629; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

5 TAAATACGATCACCTTGTGATGCGAAATGCGACCAATTAACAATATGCGACCTTTATG 64
69 TGAATACATCATCTACATGTTGGAAGTACCACTTAGCAAAATAGCGCCCTTTCTGA 128
65 AATCTCTTGTATCAAGCGAAATGCTAAATGCTATGCGATACCAATGCTAC 124
129 ATGATCTTGTAAAGAGCGAAATGCTAAATGCTATGGAATACCAATGCTGC 188
125 CTGATCAATATGACCCCTTAAGTATGTTAGTCCAGGTCGAAACCTTAATA 184
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245 ATGCGAATTAAGTGTGTTACCAATTAATTAATTAATTAATTAATTAATTA 304
309 AAACCAATTAATGCTGTTACCAATTAATTAATTAATTAATTAATTAATTA 368
305 TGAGATTAATGCTGTTACCAATTAATTAATTAATTAATTAATTAATTAATTA 364
369 TAGAGTACTCTTGTGCGCAATTAATTAATTAATTAATTAATTAATTAATTA 428
365 GCTTAATTAATGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 424
429 GTGATTAATTAATGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 488
425 GAATTAATTAATGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 484
489 GAATTAATTAATGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 548
485 AAATGAGGCTTTTCTGCTGATGCGCAATTAATTAATTAATTAATTAATTAATTA 544
549 AAACCGAAGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 608
545 AGTACATAGAGAACCAAGTCAAGTAAATTAATTAATTAATTAATTAATTAATTA 604
609 AGTACATAGAGAACCAAGTCAAGTAAATTAATTAATTAATTAATTAATTAATTA 668
605 TAAATTAATTAATGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 664
669 TAAATTAATTAATGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 728
665 GGGCTTAATTAATGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 724
729 GAGTTTAATTAATGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 788
725 GAGTGAATTAATTAATGCGCAATTAATTAATTAATTAATTAATTAATTAATTA 784
789 GAGTGAATTAATTAATGCGCAATTAATTAATTAATTAATTAATTAATTAATTA 848
QY 785 CAACTTA 791
DB 849 CAACTTA 855

RESULT 12
A42103 1195 bp DNA Linear PAT 05-MAR-1997
LOCUS Sequence 1 from Patent EP0637591.

ACCESSION

A42103
A42103.1 GI:2297595

KEYWORDS

Phytolacca americana (American pokeweed)

SOURCE

Phytolacca americana

ORGANISM

Phytolacca americana

REFERENCE

1 (bases 1 to 1195)

Moon, Y., Jeon, H., Choi, K., Lee, K. and Kim, M.

A novel expression vector for phytolacca antiviral protein

Patent: EP 0637591-A 1 08-FEB-1995;

JINRO LIMITED (KR)

Other publication AU 662844 950914

Other publication JP 706760 950314

Other publication CA 2102859 950103

Other publication AU 5064293 950119.

Location/Qualifiers

1. 1195

/organism="Phytolacca americana"

/mol_type="unassigned DNA"

/db_xref="taxon:3327"

ORIGIN

Query Match 67.4%; Score 534.2; DB 6; Length 1195;

Best Local Similarity 79.9%; Pred. No. 5.2e-116; Matches 629; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

5 TAAATACGATCACCTTGTGATGCGAAATGCGACCAATTAACAATATGCGACCTTTATG 64
100 TGAATACATCATCTACATGTTGGAAGTACCACTTAGCAAAATAGCGCCCTTTCTGA 159
65 AATCTCTTGTATCAAGCGAAATGCTAAATGCTATGCGATACCAATGCTAC 124
160 ATGATCTTGTAAAGAGCGAAATGCTAAATGCTATGGAATACCAATGCTGC 219
125 CTGATTAATTAATGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 184
220 CCAATACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 219
185 CCAATACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 244
280 CCAATACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 339
245 ATGCGAATTAAGTGTGTTACCAATTAATTAATTAATTAATTAATTAATTAATTA 304
340 AAACCAATTAATGCTGTTACCAATTAATTAATTAATTAATTAATTAATTAATTA 399
305 TGAGAATTAATGCTGTTACCAATTAATTAATTAATTAATTAATTAATTAATTA 364
400 TAGAGTACTCTTGTGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 459
365 GCTTAATTAATGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 424
460 GTGATTAATTAATGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 519
425 GAATTAATTAATGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 484
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605 TAAATTAATTAATGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 664
700 TAAATTAATTAATGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 759
665 GGGCTTAATTAATGCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 724

Db	760	GAGTTTACCCAAACCTTCGAGCTGAGTGAATGCCAGTGGTCCAGTGGATAGTGTGGA	819
Cy	725	GAGTGGATGAATCAATCATGCTGTGATGTGGCACTTCCTTAAGTAGCTTAATGAACCTGTGGA	784
Db	820	GAGTGAATGAATCAAGCCTGATGTAGACCTTTAACTAGGTTGTGTGGAGCTGTGAGA	879
Cy	785	CAACTTA 791	
Db	880	CAACTTA 886	
RESULT 13			
LOCUS	I43835	1195 bp	DNA
DEFINITION	Sequence 1 from patent US 5633155.	linear	PAT 07-OCT-1997
ACCESSION	I43835		
VERSION	I43835.1	GI:2468933	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1195)		
	Kim,M.-K., Lee,K.-H., Na,B.-K., Jeong,H.-S., Choi,K.-W., Moon,Y.-H.		
	and Jeon,H.-S.		
TITLE	Expression vector for phytoelase antiviral protein and process for		
JOURNAL	preparing transgenic plant transformed therewith		
FEATURES	Patent: US 5633155-A 1 27-MAY-1997;		
	Location/Qualifiers		
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Query Match	67.4%; Score 534.2; DB 6; Length 1195;
Best Local Similarity	79.9%; Pred. No. 5.2e-116;
Matches 629;	Conservative 0; Mismatches 150; Indels 0; Gaps 0;
QY	5 TAAATACGATACCTTTGATGCTGGAAATGGCACCATTAACAAATATGCCACCTTTATGG 64
Db	100 TGAATACAAATATATCACAATGTGGAAATACACCATTAAGAAATATGCCACTTTCTGA 159
QY	65 AATCTCTTCGTATCAAGCGAAAGATCCAAACTAAATGCTATGGCATCAATAGCTAC 124
Db	160 ATGATCTTCGTATGAGAACGAAAGATCCAACTTTAAATGCTATGGAATACCAATGCTGC 219
QY	125 CTGATACTAATTCCACCCCTTAAGTCTTATTTGGTTAAAGCTCCAAAGTCGAAACCTAAAA 184
Db	220 CCAATACAAATACAAATCCAAAGTACGGTGTGGTGAAGCTCAAGGTTCAATATAAAAAA 279
QY	185 CCATTAACCTAATGCTGAGCGAAATACCTTATACGAGATGGGCTATTCGATCCCTTCA 244
Db	280 CCATTCACCTAATGCTGAGCGAAACAAATTTGATGATGAGTATTCGATCCCTTGG 339
QY	245 ATGGCAATAAAGTGTGTTACCATATATTTAATGATATTAACAAGACCGAAGCATGATG 304
Db	340 AAACCAATAAATGTGTTACCATATCTTTAATGATATCTCAGGATCGAAGCGCAAGATG 399
QY	305 TGGAGAATACTCTTTGCTCAAGTTCTAAGTTCTCGTGTTCGAATGTCCATTAACTACATA 364
Db	400 TAGAGACTACTCTTTGCCCAATATCCAAATCTCGTGTTAAGTAAAAACATTAACCTTGATA 459
QY	365 GCTTATATCCGACCATGGAAAAAGAGAGAAAGTAACTCAAGAAATCAAGTCCAAATGG 424
Db	460 GTCAATATCCAACTGGAAATCAAAAGCGGAGTAAATCAAGAAATCAAGTCCAACTGG 519
QY	425 GAATTCAAATATCTGACAGATGACATTTGGAAAAATCTCGAGTGTATTCATTCCTGTAA 484
Db	520 GAATTCAAATATCTGACAGATGATTTGGAAAAATTTCTGAGATATGATCATTTCACTAGA 579
QY	485 AAATCGAGGCTTTTTTTCTACTGATGACATCCAAATGATTTCAAGAGCGAGCGGATTC 544
Db	580 AAACCGAAGCGAATTCCTATTTGGTACATACAAATGGTATCGAAGCGCAAGATTC 639

Qy	545	AGTACATGAGAACCAAGTCAAGACTTAATTTTAATGAGCATCTCCCTGATCCCAAG	604
Db	640	AGTACATGAGAAATCAGGTGAAAATCTTAATTTTACAGAGCATTCAAACCTTAATCCCAAG	699
Qy	605	TAATTAACCTTGAGAGAGAGTGGGCAAAATCTCTGAGGCCAATTCACAATGCCAAGATG	664
Db	700	TACTTAATTTGGCAAGACATGGGGTAAATATTCAACACCAATTCAATGATGCCAAGATG	755
Qy	665	GGGCTTTATCCCAACCACTTGAGCTAGTGGATGCCCAGAGTACCAAGTGGATGTTCTTA	724
Db	760	GAGTTTATCCCAACTCTCGAGCTAGTGGATGCCAGTGTGCCAAGTGGATATGTTTGA	819
Qy	725	GAGTGGATGAATTCATCTGTGATGTGGCACTCCTTAAGTACGTTAAATGCAACCTGTGAGA	784
Db	820	GAGTGGATGAATTCAGACCTGTGATGTAGCACTCTTAATTAACGTTGGTGGAGCTGTTCAGA	879
Qy	785	CAACTTA 791	
Db	880	CAACTTA 886	

RESULT 14			
155866			
LOCUS	155866	1195 bp	
DEFINITION	Sequence 1 from patent US 5648234.	DNA	linear
ACCESSION	155866		
VERSION	155866.1	GI:2476660	
KEYWORDS	.		
SOURCE	unknown.		
ORGANISM	unknown.		
REFERENCE	unclassified.		
AUTHORS	1 (bases 1 to 1195)		
TITLE	Moon,Y.-H., Jeon,H.-S., Choi,K.-W., Lee,K.-H. and Kim,M.-K.		
JOURNAL	Expression vector for <i>Physolacca</i> antiviral protein		
FEATURES	Patent: US 5648234-A 1 15-JUN-1997;		
source	location/Qualifiers		
	1..1195		
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	/mol_type="unassigned DNA"		
ORIGIN			

Query Match	67.4%	Score 534.2	DB 6	Length 1195
Best Local Similarity	79.9%	Pred. No. 5.2e-116		
Matches 629	Conservative	0	Mismatches 158	Indels 0
			Gaps	0
Qy	5	TAAATACGATCACTTTGATGCTGGAAATGCCACCTTAACAACATATGCCACTTTATG	64	
Db	100	TGAATACATCATCTACATATGTTGAGAGTACCACCTTAGCAATATGCCACTTTTCTGA	159	
Qy	65	AATCTTTCTGTAATCGAAGCGAAAGATCCAAACTAAATGCTATGGCATACCAATGCTAC	124	
Db	160	ATGATCTTCTGTAATGAGCGAAAGATCCAAAGTTTAAATGCTATGGAAATACCAATGCTG	219	
Qy	125	CTGATCTAATATTCGACCCCTTAAGTACTTATGTTAAGCTCCAAAGGTGCAAACTTAAAA	184	
Db	220	CCAAATACAAATACAAATCCAAAGTACGCTTGTTGAGCTCCAAAGTTCAATTAATAAAAA	279	
Qy	185	CCATTACACTATGCTGAGACGAAATPAACTTATACGTATGGGCTATTCTGATCCCTTCA	244	
Db	280	CCATCACACTATGCTGAGACGAAACAAATTTGTATGATGGGTTATCTGATCCCTTGG	339	
Qy	245	ATGGCAATPAAAGTGCTTACCATATATTTAATGATATTAACAAGCCGAACCGACGTGAT	304	
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Qy	305	TGAGAAATACTCTTGTCTCAAGTTCTAGTCTTCGCTGTTGCAATGTCCTATTAACTACAATA	364	
Db	400	TAGAGACTACTCTTTGGCCCAATGCGCAATTCCTCGATTAAGTAAAAAACAATACTTTGATAT	459	
Qy	365	GCTTATATCCGACCATGGAAAAAGAAAGCAAGTAACTCAAGAAATCAAGTCCAAATGG	424	
Db	460	GTCGATATCCCAATGGAAATCAAAAGGGGAGTAAATTCAGAAAGTCAAGTCCAACTGG	519	

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2006, 23:57:17 ; Search time 477.387 Seconds
(without alignments)
11056.934 Million cell updates/sec

Title: US-09-978-274A-3

Perfect score: 792
Sequence: 1 atgataatacagatcacctt.....gaacctgcagacaacttaa 792

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001s:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
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- 8: geneseqn2003as:*
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- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	792	100.0	792	6 AAD42716	Aad42716 Pokeweed
2	786.4	99.3	945	6 AAD42715	Aad42715 Pokeweed
3	766	96.7	1092	6 AAD42729	Aad42729 Pokeweed
4	535	67.6	882	2 AAT99556	Aat99556 Pokeweed
5	532.6	67.2	1164	11 ADM74751	Adm74751 PhytoIacc
6	532.6	67.2	1164	11 ADM74765	Adm74765 HIV-1 inh
7	532.6	67.2	1378	12 ADG76061	Adg76061 American
8	532.6	67.2	1379	3 AAZ45197	Aaz45197 Wild-type
9	532.6	67.2	1379	3 AAZ59220	Aaz59220 Pokeweed
10	532.6	67.2	1379	6 AAD42738	Aad42738 Pokeweed
11	532.6	67.2	1379	10 ADI05787	Adi05787 DNA encod
12	531	67.0	1195	2 AAQ56672	Aaq56672 Sequence
13	531	67.0	1379	4 AAC87929	Aac87929 P. ameri
14	530.2	66.9	2472	2 AAQ43967	Aaq43967 Pokeweed
15	529.4	66.8	1195	2 AAQ81457	Aaq81457 PhytoIacc
16	529.4	66.8	1378	6 AAD42739	Aad42739 Pokeweed
17	529.4	66.8	1379	3 AAZ59221	Aaz59221 Variant P
18	493	62.2	2369	2 AAT99557	Aat99557 PhytoIacc
19	493	62.2	2369	2 ABA96543	Aba96543 PhytoIacc

20	462	58.3	465	6 AAD42717	Aad42717 Pokeweed
21	460.6	58.2	918	2 AAQ64893	Aaq64893 Antiviral
22	460.6	58.2	918	2 AAT04782	Aat04782 DNA pMVC2
23	328.4	41.5	333	6 AAD42718	Aad42718 Pokeweed
24	101	12.8	934	3 AAZ45198	Aaz45198 Wild-type
25	101	12.8	934	6 AAD42740	Aad42740 Pokeweed
26	97.8	12.3	600	2 ABA96716	Aba96716 Cloning v
27	97.8	12.3	603	2 ABA96547	Aba96547 Cloning v
28	88.2	11.1	774	2 AAQ22981	Aaq22981 Gelonin t
29	86.4	10.9	765	3 AAZ61131	Aaz61131 DNA encod
30	86.4	10.9	984	3 AAZ61125	Aaz61125 DNA encod
31	86.4	10.9	993	3 AAZ61128	Aaz61128 DNA encod
32	86.4	10.9	999	3 AAZ61122	Aaz61122 DNA encod
33	86.4	10.9	999	3 AAZ61119	Aaz61119 DNA encod
34	84.2	10.6	864	1 AAN91504	Aan91504 DNA of r1
35	82	10.4	1233	2 AAT43997	Aat43997 E. coli c
36	82	10.4	1233	3 AAA12896	Aaa12896 Bacteri
37	82	10.4	1233	9 ACD27613	Acd27613 Bacteri
38	82	10.4	1233	10 ADC34646	Adc34646 B. coli c
39	82	10.4	1233	10 ADH92070	Adh92070 Fibroblas
40	81	10.2	804	2 AAQ53895	Aaq53895 Saporin c
41	81	10.2	804	2 AAQ53896	Aaq53896 Saporin c
42	81	10.2	804	2 AAQ85385	Aaq85385 Saporin c
43	81	10.2	804	2 AAQ85384	Aaq85384 Saporin c
44	81	10.2	804	2 AAQ99041	Aaq99041 M13mp18-G
45	81	10.2	804	2 AAQ99042	Aaq99042 M13mp18-G

ALIGNMENTS

RESULT 1	
AAAD42716	
ID	AAAD42716 standard; DNA; 792 BP.
AC	AAAD42716;
XX	
DT	15-NOV-2002 (first entry)
XX	
DE	Pokeweed mature PAP-S protein encoding DNA.
KM	Neurotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KW	gene; ds.
XX	
OS	Phytolacca americana.
XX	
PH	Location/Qualifiers
FT	1..792
FT	/*tag= a
FT	/product= "Mature PAP-S protein"
FT	1..29
FT	/*tag= b
FT	/bound_moiety= "Primer PS1BP"
FT	complement(436..462)
FT	/*tag= c
FT	/bound_moiety= "Primer PS1SR"
FT	463..492
FT	/*tag= d
FT	/bound_moiety= "Primer PS2BP"
FT	681..686
FT	/*tag= e
FT	/note= "Sequence replacing removed XbaI site"
FT	complement(765..792)
FT	/*tag= f
FT	/bound_moiety= "Primer PS2SR"
XX	
XX	
PN	WO200233107-A2.
XX	
XX	
PD	25-APR-2002.
XX	
PF	15-OCT-2001; 2001WO-GB004593.
XX	
PR	14-OCT-2000; 2000GB-00025217.

PAP', PAPi and PAP-S, where the gene(s) comprises a promoter which acts in response to the application of a specific stimulus to the plant so as to facilitate expression of the pokeweed antiviral protein in specific cells of the plant. The method is useful for inducing a necrotic effect in specific cells of a plant. The present sequence is pokeweed pro-PAP-S protein encoding DNA

Sequence 945 BP; 307 A; 187 C; 180 G; 271 T; 0 U; 0 Other;

Query Match 99.3%; Score 786.4; DB 6; Length 945;

Best Local Similarity 99.9%; Pred. No. 2e-215;

Matches 787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 4 ATAAATACATCACTTGTGATGCTGGAATGCCACATTAACAATATGCACTTATG 63
DB 73 ATAAATACATCACTTGTGATGCTGGAATGCCACATTAACAATATGCACTTATG 132
QY 64 GAATCTCTTGTATCAAGCGAAAGATCCAAAATAATGCTATGCGATACCAATGCTA 123
DB 133 GAATCTCTTGTATCAAGCGAAAGATCCAAAATAATGCTATGCGATACCAATGCTA 192
QY 124 CCGATATCTAATTCGACCCCTTAAGTACTTATGTTAAGTCCAAAGTGCAGAACTTAAA 183
DB 193 CCGATATCTAATTCGACCCCTTAAGTACTTATGTTAAGTCCAAAGTGCAGAACTTAAA 252
QY 184 ACCATTACACTAATGCTGAGACGAAATTAATTAAGTATGAGGCTATTCGATCCCTTC 243
DB 253 ACCATTACACTAATGCTGAGACGAAATTAATTAAGTATGAGGCTATTCGATCCCTTC 312
QY 244 AATGCGAATTAAGTGTGCTTACATATTAATTAATTAATTAATTAATTAATTAATTA 303
DB 313 AATGCGAATTAAGTGTGCTTACATATTAATTAATTAATTAATTAATTAATTAATTA 372
QY 304 GTGGAATTAAGTGTGCTTACATATTAATTAATTAATTAATTAATTAATTAATTA 363
DB 373 GTGGAATTAAGTGTGCTTACATATTAATTAATTAATTAATTAATTAATTAATTA 432
QY 364 AGCTTATATCCGACCATGAGAAAAGAAAGAAAGTAAATCAAGAAATCAAGTCCATG 423
DB 433 AGCTTATATCCGACCATGAGAAAAGAAAGAAAGTAAATCAAGAAATCAAGTCCATG 492
QY 424 GGAATTCAAATTAATCTGACAGTGAATTTGAAATATCTTGAAGTTGATTCCTCTGA 483
DB 493 GGAATTCAAATTAATCTGACAGTGAATTTGAAATATCTTGAAGTTGATTCCTCTGA 552
QY 484 AAAAAGAGGCTTTTCTTCTGATGCTGATCCATCCAAATGTTTCAAGGCGAGCCGATTC 543
DB 553 AAAAAGAGGCTTTTCTTCTGATGCTGATCCATCCAAATGTTTCAAGGCGAGCCGATTC 612
QY 544 AAGTACATAGAGAACCAAGTCAAGACTAATTTTAAATGAGCATTTCCGATCCCAA 603
DB 613 AAGTACATAGAGAACCAAGTCAAGACTAATTTTAAATGAGCATTTCCGATCCCAA 672
QY 604 GTAATTAATTTGAGAGGAAAGTGGGGCAAAATCTCTGAGCAATTCACAAATGCCAAGAT 663
DB 673 GTAATTAATTTGAGAGGAAAGTGGGGCAAAATCTCTGAGCAATTCACAAATGCCAAGAT 732
QY 664 GGGGCTTTTACCCAAACCACTTGAGCTATGATGTCCAAAGTACCAAGTATGTTCTT 723
DB 733 GGGGCTTTTACCCAAACCACTTGAGCTATGATGTCCAAAGTACCAAGTATGTTCTT 792
QY 724 AAGTGTGATGAATTCATGCTGATGTTGGGCACTGCTTAAGTACGTTAATGAGACCTGTCAG 783
DB 793 AAGTGTGATGAATTCATGCTGATGTTGGGCACTGCTTAAGTACGTTAATGAGACCTGTCAG 852
QY 784 ACAACTTA 791
DB 853 ACAACTTA 860

```

RESULT 3
AAD42729
ID AAD42729 standard; DNA; 1092 BP.

```

XX AAD42729;
AC 29-AUG-2003 (revised)
DT 15-NOV-2002 (first entry)
XX
DB Pokeweed PAP-S/TEV PCS/rice cysstatin delta D86 fusion DNA.
KW Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
XX chimeric; rice; cysstatin delta D86; N1A protease cleavage site; PCS; ds.
OS Phytotheca americana.
OS Oryza sativa.
OS Tobacco; Etch virus.
OS Chimeric.
XX
FH Key
FT primer_bind
FT 1..29
FT /*tag= a
FT /bound_moiety= "Primer PS1BP"
FT
FT misc_feature
FT 681..686
FT /*tag= b
FT /note= "Modified XbaI site"
FT complement (742..786)
FT /*tag= c
FT /bound_moiety= "Primer PCS-PAPSR"
FT 766..806
FT /*tag= d
FT /bound_moiety= "Primer PCS-Delta86F"
FT 766..786
FT /*tag= e
FT /note= "TEV N1A protease cleavage site"
FT complement (1066..1092)
FT /*tag= f
FT /bound_moiety= "Primer SYNPODELta86R"
XX
XX WO200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-GB004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADT8-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX Thomas CUR, Mcpherson WJ, Atkinson HJ, Neelam A;
XX WPI; 2002-489891/52.
XX
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX which acts in response to application of specific stimulus to plant.
XX
XX Disclosure; Page 83; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
XX specific cells of a plant. The method involves transforming the plant
XX with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX PAP', PAPi and PAP-S, where the gene(s) comprises a promoter which acts
XX in response to the application of a specific stimulus to the plant so as
XX to facilitate expression of the pokeweed antiviral protein in specific
XX cells of the plant. The method is useful for inducing a necrotic effect
XX in specific cells of a plant. The present sequence is a fusion DNA. This
XX sequence comprises pokeweed pro-PAP-S DNA, rice cysstatin delta D86 DNA
XX and Tobacco Etch virus (TEV) N1A protease cleavage site (PCS). (Updated
XX on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 1092 BP; 369 A; 195 C; 222 G; 306 T; 0 U; 0 Other;

```

Query Match 96.7%; Score 766; DB 6; Length 1092;
Best Local Similarity 100.0%; Pred. No. 1.5e-209;
Matches 766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGATTAATACGATCACCCTTTGATGCTGGAATGCGCACCTTAACAAATATGCCACTTT 60
DB 1 ATGATTAATACGATCACCCTTTGATGCTGGAATGCGCACCTTAACAAATATGCCACTTT 60
QY 61 ATGGAATCTCTTGATACGAAGGGAAGATCCAAATCTAAATGCTATGCGCATACCAATG 120
DB 61 ATGGAATCTCTTGATACGAAGGGAAGATCCAAATCTAAATGCTATGCGCATACCAATG 120
QY 121 CTACCTGATACCTAATTCGACCCCTTAAGTACTTATGCTTAAGCTCCAAAGGTGCAACCTA 180
DB 121 CTACCTGATACCTAATTCGACCCCTTAAGTACTTATGCTTAAGCTCCAAAGGTGCAACCTA 180
QY 181 AAAACCATTAACCTAATGCTGAGACGGAATTAATCTTAATGCTATGCTATGCTATGCTCC 240
DB 181 AAAACCATTAACCTAATGCTGAGACGGAATTAATCTTAATGCTATGCTATGCTATGCTCC 240
QY 241 TTCAATGGCAATAGTGTGCTTCAATATTTAAAGATATTAACAGCAACCGCACT 300
DB 241 TTCAATGGCAATAGTGTGCTTCAATATTTAAAGATATTAACAGCAACCGCACT 300
QY 301 GATGTGAGAAATACCTTTGCTCAAGTCTAGTTCGTGCTGCTCAATGTCATTAATAC 360
DB 301 GATGTGAGAAATACCTTTGCTCAAGTCTAGTTCGTGCTGCTCAATGTCATTAATAC 360
QY 361 AATAGCTTATATCCGACCATGGAAGAAAGCAAGTAATCTCAAGAAATCAAGTCCAA 420
DB 361 AATAGCTTATATCCGACCATGGAAGAAAGCAAGTAATCTCAAGAAATCAAGTCCAA 420
QY 421 TTGGGAATTCAAATATCTCAGCAGTGAATGGAAGAAATCTGGAAGTGAATTCATTCCTC 480
DB 421 TTGGGAATTCAAATATCTCAGCAGTGAATGGAAGAAATCTGGAAGTGAATTCATTCCTC 480
QY 481 GTAAAAAGTGAAGGCTTTTCTTACTGTAGTGAAGTCAATGCTTCAAGAGCGAGCGCA 540
DB 481 GTAAAAAGTGAAGGCTTTTCTTACTGTAGTGAAGTCAATGCTTCAAGAGCGAGCGCA 540
QY 541 TTCAAGTACATAGAGAACCAAGTCAAGTCAATTTTAAATGAGCATTTCAAGTATGCC 600
DB 541 TTCAAGTACATAGAGAACCAAGTCAAGTCAATTTTAAATGAGCATTTCAAGTATGCC 600
QY 601 AAAGTAAATTAATCTGAGAGGAGAGAGTGGGCAAAATCTGAGGCAATTCACAAATGCGCAG 660
DB 601 AAAGTAAATTAATCTGAGAGGAGAGAGTGGGCAAAATCTGAGGCAATTCACAAATGCGCAG 660
QY 661 AATGGGGCTTTTACCCCAACCACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 720
DB 661 AATGGGGCTTTTACCCCAACCACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 720
QY 721 CTTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 766
DB 721 CTTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 766

RESULT 4
AAT99556
ID AAT99556 standard; DNA; 882 BP.
AC AAT99556;
XX 17-OCT-2003 (revised)
DT 08-JUN-1998 (first entry)
XX
DB Phytolacca insularis antiviral protein gp12 gene.
XX Antiviral protein; gp12 gene; virucide; transgenic plant;
KM virus resistance; immunconjugate; AIDS; cancer; therapy; ss.
OS Phytolacca insularis; Nakai.
XX
FH Key Location/Qualifiers
FT CDS 1..882
FT /*tag= a
```

```
FT XX /transl_except= (pos:715..717, aa:11e)
PN XX EP808902-A2.
XX XX
PD 26-NOV-1997.
XX XX
PF 30-SEP-1996; 96EP-00307159.
XX XX
PR 22-MAY-1996; 96KR-00017404.
XX XX
PA (JINR-) JIN RO LTD.
XX XX
PI Moon Y, Choi J, Yun Y, Jin J, Hong E, Lee J, Choi K, Lee J;
PI Song S, Choi Y, Kim C, Kim M;
XX XX
DR WPI; 1998-001788/01.
XX XX
PT Antiviral proteins of Phytolacca insularis Nakai and their genes - useful
PT in plant antiviral agents and immunconjugates for the treatment of AIDS
PT and cancer.
XX XX
PS Claim 2; Page 10-12; 26pp; English.
XX XX
CC This polynucleotide comprises the coding region of the Phytolacca
CC insularis Nakai gene coding for a 32.8 kDa novel antiviral protein
CC designated gp12 (see AAM26773). The gp12 gene was isolated from leaf
CC genomic DNA by PCR amplification (see AAT99558-59). Another gene (see
CC AAT99557), encoding a 35.7 kDa protein (see AAM26774) designated gp150,
CC has also been isolated from P. insularis Nakai. Also claimed are vectors
CC encoding these antiviral proteins and host cells transformed or
CC transfected with these vectors. E. coli XL1-Blue MRF' (KCM-10080)
CC host cells are claimed, as is a process for preparing antiviral protein
CC by culturing these cells and purifying the protein from inclusion
CC bodies. The antiviral proteins and recombinant proteins inhibit protein
CC synthesis. They can be used as active ingredients of antiviral agents of
CC plant viruses, and employed in the manufacture of immunconjugates for
CC the treatment of AIDS and cancer. The isolated genes can be used in the
CC breeding of transgenic plants having viral resistance. (Updated on 17-OCT
CC -2003 to standardise OS field)
XX XX
SQ Sequence 882 BP; 301 A; 164 C; 174 G; 243 T; 0 U; 0 Other;

Query Match 67.6%; Score 535; DB 2; Length 882;
Best Local Similarity 79.8%; Pred. No. 3.5e-143;
Matches 631; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 1 ATGATTAATACGATCACCCTTTGATGCTGGAATGCGCACCTTAACAAATATGCCACTTT 60
DB 1 ATGATTAATACGATCACCCTTTGATGCTGGAATGCGCACCTTAACAAATATGCCACTTT 60
QY 61 ATGGAATCTCTTGATACGAAGGGAAGATCCAAATCTAAATGCTATGCGCATACCAATG 120
DB 61 ATGGAATCTCTTGATACGAAGGGAAGATCCAAATCTAAATGCTATGCGCATACCAATG 120
QY 121 CTACCTGATACCTAATTCGACCCCTTAAGTACTTATGCTTAAGCTCCAAAGGTGCAACCTA 180
DB 121 CTACCTGATACCTAATTCGACCCCTTAAGTACTTATGCTTAAGCTCCAAAGGTGCAACCTA 180
QY 181 AAAACCATTAACCTAATGCTGAGACGGAATTAATCTTAATGCTATGCTATGCTATGCTCC 240
DB 181 AAAACCATTAACCTAATGCTGAGACGGAATTAATCTTAATGCTATGCTATGCTATGCTCC 240
QY 241 TTCAATGGCAATAGTGTGCTTCAATATTTAAAGATATTAACAGCAACCGCACT 300
DB 241 TTCAATGGCAATAGTGTGCTTCAATATTTAAAGATATTAACAGCAACCGCACT 300
QY 301 GATGTGAGAAATACCTTTGCTCAAGTCTAGTTCGTGCTGCTCAATGTCATTAATAC 360
DB 301 GATGTGAGAAATACCTTTGCTCAAGTCTAGTTCGTGCTGCTCAATGTCATTAATAC 360
QY 361 AATAGCTTATATCCGACCATGGAAGAAAGCAAGTAATCTCAAGAAATCAAGTCCAA 420
DB 361 AATAGCTTATATCCGACCATGGAAGAAAGCAAGTAATCTCAAGAAATCAAGTCCAA 420
```


ADM74765
XX ID ADM74765 standard; cDNA; 1164 BP.
XX
XX ADM74765;
XX
XX
XX 03-JUN-2004 (first entry)
XX
XX HIV-1 inhibition activity related Tat cDNA.
XX
XX human immunodeficiency virus; HIV-1; tumour; plant;
XX Chinese phytoleuca leaf; trans-acting activation factor; Tat; mutant;
XX gene; ss.
XX
XX Human immunodeficiency virus 1.
XX
XX
XX Key Location/Qualifiers
XX FT CDS 2..943
XX FT /tag= a
XX FT /product= "Tat HIV-1 protein"
XX
XX CN1400220-A.
XX
XX 05-MAR-2003.
XX
XX 02-AUG-2001; 2001CN-00123911.
XX
XX 02-AUG-2001; 2001CN-00123911.
XX
XX (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
XX
XX Peng X, Bai L, Yin B;
XX WPI; 2003-469263/45.
XX P-PSDB; ADM74766.
XX
XX Two kinds of cDNA with activity capable of extensively inhibiting HIV and
XX its expression, separation and purification method in protokaryon.
XX
XX Example 9; Page 11-12; 17p; Chinese.
XX
XX The present invention relates to two kinds of cDNA which can inhibit
XX human immunodeficiency virus (HIV-1) activity, including separation clone
XX of two kinds of cDNA, external mutation, fusion expression in prokaryons
XX and application of the cDNA in preparation of preparation for curing the
XX virus and tumours. One of the described cDNAs is obtained by separation
XX and cloned from a plant Chinese phytoleuca leaf, and one from the trans-
XX acting activation factor (Tat) mutant coded by human immunodeficiency
XX virus HIV-1 gene. This polynucleotide sequence represents the Tat cDNA
XX used in the HIV-1 inhibition activity of the invention.
XX
XX Sequence 1164 BP; 403 A; 203 C; 218 G; 340 T; 0 U; 0 Other;
XX
XX
XX Query Match 67.2%; Score 532.6; DB 11; Length 1164;
XX Best Local Similarity 79.8%; Pred. No. 1.9e-142;
XX Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;
XX
XX 5 TAAATGAGTACACCTTGTGATGCTGAAATGSCACATTAACAATATGCACTTTATG 64
XX |||||
XX 69 TGAATACATCACTACATGTTGGAAGTACACATTCGCAATATGCACTTTCTG 128
XX |||||
XX 65 AATCTCTTGATATCAAGCGAAAGATCCAAACTAAATGCTATGCGATACCATGCTAC 124
XX |||||
XX 129 ATATATCTTGATATGAAGCGAAAGATCCAAAGTTTAAATGCTATGGAATCCATATGTGC 188
XX |||||
XX 125 CTGATCTAATGAGACCCCTTAATCTATGTTAGTTAGCTCCAGGTGCAAACTTAAAA 184
XX |||||
XX 189 CCAATACCAATCCAAATCCAAAGTACGTGTGTGAGCTCCAAAGTTCAAAATAAAAA 248
XX |||||
XX 185 CCATTACCTAATGCTGAGAGCAAAATTAATTAACGATGAGGCTATTCGATCCCTTCA 244
XX |||||
XX 249 CCATCACTAATGCTGAGAGCAAAATTAATTAATGATGAGGCTATTCGATCCCTTGG 308
XX |||||
XX 245 ATGGCAATAGTCTGATCCATATATTTAATATATTAACAGACCGAAAGCACTGATG 304
XX |||||

Db 309 ATACCAATAGTGTGCTTACCATATCTTTGTGATATCTCAGGATACGAAAGCCAAATG 368
|||
Qy 305 TGGAGAACTACTCTTTGCTCAAGTTCTAGTTCTGTGTGCAATGTCATTAATCAATA 364
|||
Db 369 TAGAGACTACTCTTTGCTCAAGTTCTAGTTCTGTGTGCAATGTCATTAATCAATA 428
|||
Qy 365 GCTTAATCCGACATGAGAAAGAAAGCAGAAAGTAACTCAAGAAATCAAGTCAATTTGG 424
|||
Db 429 GTGATATTCACATTTGGAATTCAAAGCGAGATTAATCAAGAAATCAAGTCAATTTGG 488
|||
Qy 425 GAAATCAATATCTCAGAGTGAATGAAATTTCTGAGTTGATTCATTCCTGTAA 484
|||
Db 489 GAAATCAATATCTCAGAGTGAATGAAATTTCTGAGTTGATTCATTCCTGTAA 548
|||
Qy 485 AATCTGAGGCTTTTCTATCTGTGATCCATTCCAATGTTTCAAGAGCGCCGATTC 544
|||
Db 549 AAACCGAAGCCGAATTTCTATCTGTGATCCATTCCAATGTTTCAAGAGCGCCGATTC 608
|||
Qy 545 AGTACATGAGAGCAAGTCAAGACTAATTTAATGAGCAATTCACCTGATCCCAAG 604
|||
Db 609 AGTACATGAGAGTCAAGTCAAGACTAATTTAATGAGCAATTCACCTGATCCCAAG 668
|||
Qy 605 TAAATTAATTTGAGAGAAAGTGGGCAAAATCTGAGGCAATTCACATGCAAGATG 664
|||
Db 669 TACTTAATTTGAGAGAAAGTGGGCAAAATCTGAGGCAATTCACATGCAAGATG 728
|||
Qy 665 GGGCTTTACCAACCACTGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 724
|||
Db 729 GAGTTTAACTCAACCACTGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 788
|||
Qy 725 GAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 784
|||
Db 789 GAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 848
|||
Qy 785 CAATCTTA 791
|||
Db 849 CAATCTTA 855
|||
RESULT 7
ADG76061
ID ADG76061 standard; DNA; 1378 BP.
XX
XX
XX ADG76061;
XX
XX
XX 11-MAR-2004 (first entry)
XX
XX
XX American pokeweed antiviral protein (PAP) DNA SeqID 1.
XX
XX
XX gene; ds; pokeweed antiviral protein; PAP; HIV-1; anti-HIV; antiviral;
XX nucleoside analogue inhibitor; viral protease inhibitor; viral infection;
XX american pokeweed; retroviral.
XX
XX
XX Phytoleuca americana.
XX
XX
XX WO2003106479-A2.
XX
XX
XX 24-DEC-2003.
XX
XX
XX 17-JUN-2003; 2003WO-US019141.
XX
XX
XX 17-JUN-2002; 2002US-0389649P.
XX
XX
XX (PARK-) PARKER HUGHES INST.
XX
XX
XX Uckun FM;
XX
XX
XX WPI; 2004-082156/08.
XX
XX P-PSDB; ADG76064.
XX
XX
XX Novel modified pokeweed antiviral protein useful for inhibiting viral
XX replication, for inducing depurination of viral RNA, or for treating
XX
XX
XX

PT viral infection in subject.

XX Example 2: SEQ ID NO 1; 62bp; English.

CC This invention relates to novel modified pokeweed antiviral proteins
CC (PAPs). Specifically, it refers to modifications relative to wild-type
CC PAP that confer increased activity towards viral RNA, particularly
CC retroviral RNA such as HIV-1 and drug resistant HIV-1. Furthermore,
CC modified PAP also exhibits decreased activity towards ribosomal RNA
CC relative to wild-type PAP. The present invention describes a molecular
CC model of PAP-HIV RNA interactions that have been used for the rational
CC redesign of PAP mutants with potent anti-HIV activity, where
CC modifications have been introduced in regions other than the active site.
CC Accordingly, these mutants represent antiviral agents that can work as
CC nucleoside analogue inhibitors of reverse transcriptase, as well as viral
CC protease inhibitors that can be used for treating viral infections. As
CC such, they are useful for inhibiting viral replication and for
CC deactivating viral RNA. This polynucleotide sequence is the DNA encoding
CC the wild type american pokeweed antiviral protein (PAP) of the invention.
XX

SQ Sequence 1378 BP; 487 A; 234 C; 268 G; 389 T; 0 U; 0 Other;

Query Match 67.2%; Score 532.6; DB 12; Length 1378;

Best Local Similarity 79.8%; Pred. No. 2e-142;

Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

QY 5 TAAATACGATCACCTTGATGCTGGAATGACACATTAAACAAATATGCGACTTTATG 64
DB 291 TGAATCAATATCTTCAATGATTTGGAATACCAATTTAGCAAAATACCGCACTTTCTGA 350
QY 65 AATCTCTCGTAATCAAGCGAAGATCCAAACTAAATGCTATGCTATACCAATGCTAC 124
DB 351 ATGATCTTCGTATGAGCGAAGATCCAAAGTTTAAATGCTATGAGTAATCAATGCTGC 410
QY 125 CTGATCTAATTCGACCCCTTAAGTACTTATGCTTAACTCCAGGTCGAACCTAA 184
DB 411 CCAATACAAATATCAATTCAAAGTACGTTGTGAGCTCAAGGTTCAATTA 470
QY 185 CCATTACCTAATGCTGAGCAAAATTAATTAATGAGTGGGCTATTCGATCCCTCA 244
DB 471 CCAATCACTAATGCTGAGCAAAATTAATTAATGAGTGGGCTATTCGATCCCTCA 244
QY 245 ATGCAATTAATGCTGAGCAAAATTAATTAATGAGTGGGCTATTCGATCCCTCA 304
DB 531 AAACCAATTAATGCTGAGCAAAATTAATTAATGAGTGGGCTATTCGATCCCTCA 590
QY 305 TGAAGATATCTTCTGCTCAAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 364
DB 591 TAGAGACTACTCTTCTGCTCAAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 650
QY 365 GCTTATATCCGACCATGGAAGAAAGAGAGTAATCTCAAGAAATCAATGCAATTGG 424
DB 651 GTGATATTCGACCATGGAAGAAAGAGAGTAATCTCAAGAAATCAATGCAATTGG 710
QY 425 GAATTCAAATAGCTGAGCAATGGAATAATCTCTGAGTGTATTCATTCCTGTA 484
DB 711 GAATTCAAATAGCTGAGCAATGGAATAATCTCTGAGTGTATTCATTCCTGTA 770
QY 485 AAATGAGGCTTTTCTTCTGCTGAGTGTATTCATTCCTGTA 544
DB 771 AAATGAGGCTTTTCTTCTGCTGAGTGTATTCATTCCTGTA 830
QY 545 AGTACATAGAGCAACAGTCAAGTAAATTTAATAGAGCTTCAATCCGATCCCAAG 604
DB 831 AGTACATAGAGCAACAGTCAAGTAAATTTAATAGAGCTTCAATCCGATCCCAAG 890
QY 605 TAAATTAATGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACATGCAAGATG 664
DB 891 TAAATTAATGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACATGCAAGATG 950
QY 665 GGGCTTAAACCAACCTTGAAGTATGATGCAAGGTAATGCAAGTATGTTCTTA 724
DB 951 GAGTTTAAACCAACCTTGAAGTATGATGCAAGGTAATGCAAGTATGTTCTTA 1010

QY 725 GAGTGAATGAATGATGCTGAGTCTTAACTAATGAACTGTCAGA 784
DB 1011 GAGTGAATGAATGATGCTGAGTCTTAACTAATGAACTGTCAGA 1070
QY 785 CAACTTA 791
DB 1071 CAACTTA 1077

RESULT 8
AAZ45197 standard; DNA; 1379 BP.
ID AAZ45197 standard; DNA; 1379 BP.
XX
XX AAZ45197;
AC
XX 29-FEB-2000 (first entry)
DT
XX
XX
DE Wild-type pokeweed antiviral protein (PAP) nucleotide sequence.
XX
KW Pokeweed antiviral protein; PAP; PAP II; antifungal; transgenic plant;
KW ribosome inhibiting protein; RIP; cereal crop; viral resistance; PVX;
KW potato virus X; cucumber mosaic virus; CMV; ss;
KW tomato yellow leaf curl virus.
OS
XX Phytolacca americana.
FH
FH Key Location/Qualifiers
FT CDS 225..1166
FT /*tag= a
FT /product= "PAP"
FT /note= "Pokeweed antiviral protein"

W09960843-A1.
02-DEC-1999.
21-MAY-1999; 99WO-US011301.
22-MAY-1998; 98US-0086374P.
XX
XX (RUTP) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Turner NE, Wang P;
XX WPI, 2000-062555/05.
XX P-PSDB; AAY58025.
XX
XX New antiviral DNA useful for generating transgenic plants resistant to
XX viruses and/or fungi.
XX
XX Example; Page 4-5; 43bp; English.

This is the Pokeweed antiviral protein (PAP) nucleotide sequence. PAP is
a type I ribosome-inhibiting protein (RIP) found in the cell walls of
Phytolacca americana (pokeweed). It is a single polypeptide chain that
catalytically removes a specific adenine residue from a highly conserved
stem-loop structure in the 28S rRNA of eukaryotic ribosomes. The pokeweed
antiviral protein II (PAP II) protein confers antiviral and or antifungal
activities to plants. A DNA molecule encoding a PAP II protein with an
inact catalytic active site amino acid residue (E172) is useful for
generating transgenic plants. PAP II DNA is useful for generating
transgenic plants (especially cereal crops) through transforming a
protoplast or introducing the DNA directly into a plant part prior to
regeneration. Cells and seeds which exhibit anti-viral and/or anti-fungal
activity thus have increased resistance to viruses and/or fungi. Viruses
include potato virus X (PVX), cucumber mosaic virus (CMV), and tomato
yellow leaf curl virus, and fungi include Pythium, Phytophthora,
Sclerotinia and Aspergillus. PAP II proteins also confer resistance to
other plants pests including insects, bacteria and nematodes. PAP II DNA
is also useful for identifying a PAP II protein having reduced
cytotoxicity. PAP II has a reduced cytotoxicity compared to PAP, so
unlike PAP transgenic plants which are stunted and sterile, PAP II

CC transgenic plants have a normal and fertile phenotype

XX Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Query Match 67.2%; Score 532.6; DB 3; Length 1379;

Best Local Similarity 79.8%; Pred. No. 2e-142;

Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

```
QY 5 TAAATACGATCACCTTGTGATGCGAAATGCGACCATTAACAATATATGCGACCTTATGG 64
   |||||
DB 292 TGAATACATCATCTACATATGTTGGAAGTACACCATTAAGCAATATAGCCACTTTTCTGA 351
   |||||

QY 65 AATCTCTTGGTAATCAAGCAAGATCCAAAATAAATGCTATGCAATCAATGCTTAC 124
   |||||
DB 352 ATGATCTTGGTAATGAAAGCAAGATCCAAATTAATGCTATGCAATCAATGCTTAC 411
   |||||

QY 125 CTGATCTAATGTAAGCCCTTAAGTACTTATGTTAGTTCGCAAGGTCGCAAACTATAAA 184
   |||||
DB 412 CCAATACAAATACAAATACCAAGTACGTTGGTGGTTCGCAAGGTCGCAAAATATAAA 471
   |||||

QY 185 CCATTAACATTAATGCTGAGACGAATTAATTAATGCTGATGGCTATTCGATCCCTTCA 244
   |||||
DB 472 CCATTAACATTAATGCTGAGACGAATTAATTAATGCTGATGGCTATTCGATCCCTTCA 531
   |||||

QY 245 ATGCAATTAATGCTGATCCATTAATTAATGATTAATTAATTAATTAATTAATTAATTA 304
   |||||
DB 532 AAACCAATTAATGCTGATCCATTAATTAATGATTAATTAATTAATTAATTAATTAATTA 591
   |||||

QY 305 TGGAGATATCTTGTGCTGAAGTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 364
   |||||
DB 592 TAGAGATATCTTGTGCTGAAGTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 651
   |||||

QY 365 GCTTATATCCGACCATGAGAAAGCAAGATTAATTAATTAATTAATTAATTAATTAATTA 424
   |||||
DB 652 GTGATATATCCGACCATGAGAAAGCAAGATTAATTAATTAATTAATTAATTAATTAATTA 711
   |||||

QY 425 GAATTCAAATATCTGAGATGACATTTGGAATTAATTTCTGAGATTGATTCATTCCTGTA 484
   |||||
DB 712 GAATTCAAATATCTGAGATGACATTTGGAATTAATTTCTGAGATTGATTCATTCCTGTA 771
   |||||

QY 485 AAATGAGGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 544
   |||||
DB 772 AAATGAGGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 831
   |||||

QY 545 AGTACATAGAGAACCAAGTCAAGTCAATTAATTAATGAGATTCATTCCTGATCCCAAG 604
   |||||
DB 832 AGTACATAGAGAACCAAGTCAAGTCAATTAATTAATGAGATTCATTCCTGATCCCAAG 891
   |||||

QY 605 TAATTAATCTTGAAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACATGCGAAGATG 664
   |||||
DB 892 TACTTAATTTGCAAGAGACATGGGGTAAAGATTTCAACAGCAATTCATGATGCCAAGATG 951
   |||||

QY 665 GGGCTTAAACCAACCACTGAGCTAGTGTGATGCGCAAGGTACCAAGTGTGATGTTCTTA 724
   |||||
DB 952 GAGTTTAAACCAACCACTGAGCTAGTGTGATGCGCAAGGTACCAAGTGTGATGTTCTTA 1011
   |||||

QY 725 GAGTGTAGTAATCAATCTGATGTGCACTCTTAAAGTACGTTAATGAAAGCTGTGAGA 784
   |||||
DB 1012 GAGTGTAGTAATCAATCTGATGTGCACTCTTAAAGTACGTTAATGAAAGCTGTGAGA 1071
   |||||

QY 785 CAACTTA 791
   |||||
DB 1072 CAACTTA 1078
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RESULT 9

AA259220

ID AA259220 standard; cDNA; 1379 BP.

AC AA259220;

XX

DT 20-APR-2000 (first entry)

XX

DE Pokeweed antiviral protein coding sequence spring leaf form.

XX Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;

KW resistance; potato virus X; potato virus Y; potato leaf roll virus;

KM tuber; ss.

XX Phytojalca americana.

OS US6015940-A.

XX 18-JAN-2000.

XX 07-APR-1992; 92US-00865169.

XX 07-APR-1992; 92US-00865169.

XX (MONS) MONSANTO CO.

XX Kanlewski WK, Turner NE, Lodge JK;

XX WPI; 2000-126326/11.

XX Production of transgenic potato plants or tubers expressing pokeweed

PT antiviral protein which are resistant to potato virus X or Y.

XX Claim 6; Fig 4; 30pp; English.

CC This is the coding sequence for the spring leaf form of the pokeweed

CC antiviral protein (PAP) which is used to generate transgenic potato

CC plants. PAP is able to confer resistance to infection by potato virus X

CC (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in the

CC potato plant or tuber expressing PAP

XX Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Query Match 67.2%; Score 532.6; DB 3; Length 1379;

Best Local Similarity 79.8%; Pred. No. 2e-142;

Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

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QY 5 TAAATACGATCACCTTGTGATGCGAAATGCGACCATTAACAATATGCGACCTTATAG 64
   |||||
DB 292 TGAATACATCATCTACATATGTTGGAAGTACACCATTAAGCAATATAGCCACTTTTCTGA 351
   |||||

QY 65 AATCTCTTGGTAATCAAGCAAGATCCAAAATAAATGCTATGCAATCAATGCTTAC 124
   |||||
DB 352 ATGATCTTGGTAATGAAAGCAAGATCCAAATTAATGCTATGCAATCAATGCTTAC 411
   |||||

QY 125 CTGATCTAATTTGACCCCTTAAGTACTTATTTGTTAAAGTCCAGGTGCAAACTATAAA 184
   |||||
DB 412 CCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 471
   |||||

QY 185 CCATTAACATTAATGCTGAGACGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 244
   |||||
DB 472 CCATTAACATTAATGCTGAGACGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 531
   |||||

QY 245 ATGCAATTAATGCTGCTTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 304
   |||||
DB 532 AAACCAATTAATGCTGCTTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 591
   |||||

QY 305 TGGAGATATCTTGTGCTGAAGTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 364
   |||||
DB 592 TAGAGATATCTTGTGCTGAAGTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 651
   |||||

QY 365 GCTTATATCCGACCATGAGAAAGCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 424
   |||||
DB 652 GTGATATATCCGACCATGAGAAAGCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 711
   |||||

QY 425 GAATTCAAATATCTGAGATGACATTTGGAATTAATTTCTGAGATTGATTCATTCCTGTA 484
   |||||
DB 712 GAATTCAAATATCTGAGATGACATTTGGAATTAATTTCTGAGATTGATTCATTCCTGTA 771
   |||||

QY 485 AAATGAGGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 544
   |||||
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Db 772 AACCGAAGCCGAATTCCTATTGGTAGCCATACAAATGTATCAGAGGCGAGCAAGATTCA 831
Qy 545 AGTACATAGAGAACCAAGTCAAGACTAATTTTAAATAGAGCAATTCACCTGATCCCAAG 604
Db 832 AGTACATAGAGAACCAAGTCAAGACTAATTTTAAATAGAGCAATTCACCTGATCCCAAG 891
Qy 605 TAAATTAATTGAGAGAGAGTGGGCAAAATCTGTAGGCAATTGACAAATGCCAAGATG 664
Db 892 TACTTAATTTGCAAGAGACATGGGGTAGATTTCAGACGCAATTCATGATGCCAAGATG 951
Qy 665 GGGCTTACCCCAACCACTTGAAGCTAGTGCATGCCAAGGTAACCAAGTGAATGTTCTTA 724
Db 952 GAGTTTACCCCAACCTCTCGAGTGAATGCCAGTGGCCAAAGTGAATGTTGTTGA 1011
Qy 725 GAGTGAATGAATCAATCGTGAATGGCACTCTTAAGTAACTTAATGAAACCTGTGCA 784
Db 1012 GAGTGAATGAATCAAGCTCATATGTAGCACTTTAACTAAGTGGTGGAGCTGTGCA 1071
Qy 785 CAACCTTA 791
Db 1072 CAACCTTA 1078

RESULT 10

AAD42738
ID AAD42738 standard; DNA; 1379 BP.

XX AAD42738;

DT 15-NOV-2002 (first entry)

DE Pokeweed PAP' DNA #1.

XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds.

OS Phytolacca americana.

XX Key Location/Qualifiers
FH misc_feature 290..1076

FT /note= "Mature PAP' sequence"

XX WO200233107-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-GB004593.

XX 14-OCT-2000; 2000GB-00025217.

XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.

XX Thomas CJR, McPherson MJ, Atkinson HJ, Neelam A;

XX WPI; 2002-489891/52.

PT Inducing necrotic effect in specific cells of plant by transforming plant
PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT which acts in response to application of specific stimulus to plant.
XX Claim 5; Page 86; 87pp; English.

XX The invention relates to a method of inducing a necrotic effect in
CC specific cells of a plant. The method involves transforming the plant
CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC PAP', PAVI and PAP-S, where the gene(s) comprises a promoter which acts
CC in response to the application of a specific stimulus to the plant so as
CC to facilitate expression of the pokeweed antiviral protein in specific
CC cells of the plant. The method is useful for inducing a necrotic effect
CC in specific cells of a plant. The present sequence is pokeweed PAP' DNA
SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Query Match 67.2%; Score 532.6; DB 6; Length 1379;
Best Local Similarity 79.8%; Pred. No. 2e-142;
Matches 628; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

Qy 5 TAAATAGAGTACCTTGTGATGCTGAAATGCGACCATTAACAAATATGCACTTTATG 64
Db 292 TGAATACATCATCTACAAATGTTGAAAGTACCAATTAAGCAAAATAGCCACTTTTCTGA 351
Qy 65 AATCTCTCGTAATCAAGCCGAAATCCAAACTTAAATGTATGCAATACATATGCTAC 124
Db 352 ATGATCTTGTGAATGAAGCCGAAATCCAAAGTTTAAATGTCTAATGAATACCAATGCTGC 411
Qy 125 CTGATCTAATTTGACCCCTTAATGATTAATGTTAGTCAAGTCCAGGTCGAAACCTTAAAA 184
Db 412 CCAATTAATTAATCAAAATCCAAAGTACGTTGGTGGAGCTCCAAAGTTCAAAATTAATAAAA 471
Qy 185 CCATTACACTAATGCTGAGAGAAATTAATTAATGATGAGGCTAATTCGATCCCTTCA 244
Db 472 CCATCACACTAATGCTGAGAGAAATTAATGATGATGATGATGATGATGATGATGATGATGATG 531
Qy 245 ATGCGATTAATGCTGCTTACATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 304
Db 532 AATCAATTAATTAATGCTGCTTACATATTAATTAATTAATTAATTAATTAATTAATTAAT 591
Qy 305 TGAGAAATTAATGCTGCTTACATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 364
Db 592 TAGAGACTACTCTTGTGCTCAAGTTCTAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 651
Qy 365 GCTTAATTAATGCTGCTTACATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 424
Db 652 GTGATATCCAAATGCTGCTTACATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 711
Qy 425 GAATTCAAATTAATGCTGCTTACATATTAATTAATTAATTAATTAATTAATTAATTAAT 484
Db 712 GAATTCAAATTAATGCTGCTTACATATTAATTAATTAATTAATTAATTAATTAATTAAT 771
Qy 485 AATCTGAGGCTTTTCTAATGCTGCTTACATATTAATTAATTAATTAATTAATTAATTAAT 544
Db 772 AATCTGAGGCTTTTCTAATGCTGCTTACATATTAATTAATTAATTAATTAATTAATTAAT 831
Qy 545 AGTACATAGAGAACCAAGTCAAGACTAATTTTAAATAGAGCAATTCACCTGATCCCAAG 604
Db 832 AGTACATAGAGAACCAAGTCAAGACTAATTTTAAATAGAGCAATTCACCTGATCCCAAG 891
Qy 605 TAAATTAATTGAGAGAGAGTGGGCAAAATCTGTAGGCAATTGACAAATGCCAAGATG 664
Db 892 TACTTAATTTGCAAGAGACATGGGGTAGATTTCAGACGCAATTCATGATGCCAAGATG 951
Qy 665 GGGCTTACCCCAACCACTTGAAGCTAGTGCATGCCAAGGTAACCAAGTGAATGTTCTTA 724
Db 952 GAGTTTACCCCAACCTCTCGAGTGAATGCCAGTGGCCAAAGTGAATGTTGTTGA 1011
Qy 725 GAGTGAATGAATCAATCGTGAATGGCACTCTTAAGTAACTTAATGAAACCTGTGCA 784
Db 1012 GAGTGAATGAATCAAGCTCATATGTAGCACTTTAACTAAGTGGTGGAGCTGTGCA 1071
Qy 785 CAACCTTA 791
Db 1072 CAACCTTA 1078

RESULT 11

AD105787
ID AD105787 standard; DNA; 1379 BP.

XX AD105787;

DT 15-APR-2004 (first entry)

DE DNA encoding the wild-type pokeweed antiviral protein.

XX ribosome depurination; antifungal; antiviral; viroinide; anti-HIV;
KM cytosolic; immunosuppressive; agricultural biotechnology; pharmaceuticals;

KM medicine; cancer; AIDS; viral infection; autoimmune disease; T-cell;
 KW B-cell; transgenic; plant; wild-type; pokeweed antiviral protein; gene;
 XX de.
 OS Phytolacca americana.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 225..1166
 FT /*tag= a
 FT /product= "wild-type pokeweed antiviral protein"
 PN W0200262952-A2.
 XX
 PD 15-AUG-2002.
 XX
 PF 01-FEB-2002; 2002MO-US002792.
 XX
 PR 02-FEB-2001; 2001US-0266396P.
 XX
 PA (RUTP) UNIV RUTGERS STATE NEW JERSEY.
 XX
 PI Tumer NB, Hudak KA, Parikh B;
 XX WPI; 2003-156656/15.
 DR P-PSDB; ADI05788.
 XX
 DR
 XX
 PT New Pokeweed Antiviral Protein (PAP) mutant that is less toxic than wild-
 PT type PAP, useful in agricultural biotechnology or in the fields of
 PT pharmaceuticals and medicine, e.g. treating cancer, AIDS, viral infection
 PT or autoimmune disease.
 XX
 PS Disclosure; SEQ ID NO 1; 51bp; English.
 XX
 CC The invention relates to a novel Pokeweed Antiviral Protein (PAP) mutant
 CC that is less toxic than wild-type PAP and exhibits ribosome depurination
 CC activity, where the mutant is a central domain mutant or N-terminal
 CC domain mutant. The PAP mutants have the following activities: antifungal,
 CC antiviral, virucide, anti-HIV, cytostatic and immunosuppressive. The PAP
 CC mutants are useful in agricultural biotechnology as well as in the fields
 CC of pharmaceuticals and medicine. The PAP mutants and methods are useful in
 CC treating mammals with cancer. AIDS, viral infection or autoimmune
 CC diseases associated with proliferations of unwanted T-cells or B-cells.
 CC The transgenic plants are useful in exhibiting resistance to a broad
 CC spectrum of plant pests e.g. viruses and fungi. This polynucleotide
 CC sequence represents the DNA encoding the wild-type pokeweed antiviral
 CC protein of the invention.
 XX
 XX
 SO Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
 Query Match 67.2%; Score 532.6; DB 10; Length 1379;
 Best Local Similarity 79.8%; Pred. No. 2e-142;
 Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

QY 305 TGGAGATACCTCTTGGCTCAAGTTCAGTTCGCTGTTGGCAATGCCATTAACATACATA 364
 |||||
 DB 592 TAGAGACTACTCTTTGGCCAAATGCCAATTCGTGTGTAGTAAACATAAATTGATA 651
 |||||
 QY 365 GCTTATATCCGACCATGGAAGAAAGCAGAGTAACTCAAGAAATCAAGTCCATTGG 424
 |||||
 DB 652 GTGATATCCAAATTCGAAATCAAAAGCGGAGATTAANAAGTCAAGTCCAGTCCACTGG 711
 |||||
 QY 425 GAAATCAATACCTCAGCAGTGCATTTGGAAGAAATCTCTGGAGTTGATTCCTCTGTA 484
 |||||
 DB 712 GAATTCAAATACCTCAGCAGTGCATTTGGAAGAAATCTCTGGAGTTGATTCCTCTGTA 771
 |||||
 QY 485 AAACCTGAGCTTTTCTTCTAGTGCATTCGCAATGATTTGAGAGCAGCGGATTTCA 544
 |||||
 DB 772 AAACCGAAGCCGAATTCCTATTGTGTAGCCATTAACAAATGTATCAGAGGCAAGATTTCA 831
 |||||
 QY 545 AGTACATAGGAACCAAGTCAAGCTAATTTTAATAGAGATTCCTGATCCCAAG 604
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 DB 832 AGTACATAGGAATCAAGTCAAGCTAATTTTAACAGAGATTCACCTTAATCCCAAG 891
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 QY 605 TAAATTACTTGGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACATGCCAAGATG 664
 |||||
 DB 892 TACTTAATTTTGCAGAGAGACATGGGGTAAATTTCAACAGCAATTCATGATGCCAAGATG 951
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 QY 665 GGGCTTTACCCCAACCACTTGAAGCTAGTGATGCCAAGGTACCAAGTGGATGTTCTTA 724
 |||||
 DB 952 GAGTTTACCCCAACCTCTGAGCTAGTGATGCCAAGGTGGTCAAGTGGATGTTCTTA 1011
 |||||
 QY 725 GAGTGGATGAATCAATCGTATGTGGCACTCTTAAATGCTTAATGAACTGTGCA 784
 |||||
 DB 1012 GAGTGGATGAATCAATCGTATGTGGCACTCTTAAATGCTTAACTGTTGGAGGCTGTGCA 1071
 |||||
 QY 785 CAACCTTA 791
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 DB 1072 CAACCTTA 1078
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RESULT 12
 AA056672
 ID AA056672 standard; cDNA; 1195 BP.
 XX
 AC AA056672;
 XX
 XX
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 04-SEP-1994 (first entry)
 XX
 DE Sequence of Phytolacca antiviral protein (PAP) cDNA.
 XX
 XX
 KW Antiviral protein; PAP; virus-resistance; transgenic plant; ss.
 XX
 OS Phytolacca americana; L.
 XX
 FH Key Location/Qualifiers
 FT CDS 33..974
 FT /*tag= a
 PN BP585554-A1.
 XX
 PD 09-MAR-1994.
 XX
 PF 30-JUN-1993; 93BP-00110445.
 XX
 PR 16-AUG-1992; 92KR-00014895.
 XX
 XX (JINR-) JIN RO LTD.
 XX
 PA Kim M, Lee K, Na B, Jeong H, Choi K, Moon Y, Jeon H;
 XX WPI; 1994-076002/10.
 DR P-PSDB; AAR48548.
 XX
 PT Expression vector for phytolacca antiviral protein - used for producing

PT transgenic virus-resistant plants and for producing the antiviral agent.
XX
PS Disclosure; Fig 1; 15pp; English.
v

CC To isolate PAP gene, total cellular mRNA was purified from leaves of
CC *Phytolacca americana* L. obtd. in Korea. A cDNA library was constructed.
CC The PAP gene was selected by immunoscreening employing anti-PAP antibody
CC A deletion mutant was prepd. from the isolated PAP gene, and the DNA
CC sequence of the PAP genome was determined. (Updated on 25-MAR-2003 to
CC correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)

Sequence 1195 BP; 420 A; 201 C; 230 G; 344 T; 0 U; 0 Other;

Query Match	Score	DB 2;	Length
Best Local Similarity	67.08;	531;	1195;
Best Local	70.78;	531;	1195;

Matches 627; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY	5	TAAATACAGTACACTTATGCTGGAAATGCGACCACTTAACAAAATATGCACTTTATGG	64
Db	100	TGAATACAAATCATCTCAATATGTTGGAAATGACCAACATTCGAATTAACGCACTTTTCGA	159
QY	65	AATCTCTTGTAATCAAGCGAAAGATCCAAACTTAAATGCTATGGAATACCAATGCTAC	124
Db	160	ATGATCTCTGTAATGAAAGCAAAAGATCCAAAGTTTAAATGCTATGGAATACCAATGCTGC	219
QY	125	CTGATCTAAATTTCCACCCCTTAAGTCTTATTTGGTTAAAGTCCAAAGTGAACCTTAAAAA	184
Db	220	CCAAATACAAATACAAATCCAAAGTACGGTTGGTTGAAGTCTCCAAAGTTCAATTAATAAAA	279
QY	185	CCATTTACACTATGCTGGAGCAAAATTACTTATACGTATGGGCTATTTCTGATCCCTTCA	244
Db	280	CCATTCACACTATGCTGGAGCAAAATTTGTAATGTAATGGGTTATTTCTGATCCCTTGG	339
QY	245	ATGGCAATAGTGTGTTACCATATATTTAATGATATTAACAAGCCGAAGCACTGATG	304
Db	340	AAACCACTAAATGCTGTACCAATATCTTTAAATGATATCTCAGGTACTGAACGCAAGATG	399
QY	305	TGGGAATATCTTTGCTCAAGTTCTAATTTCTCGTGTGGCAATGTCCTTAATCTACATA	364
Db	400	TAGAGACTACTCTTTGGCCCAATGCAATTTCTCGTGAATGAATAAACAATTGATTA	459
QY	365	GCTTATATCCGACCATGGAAGAAAGCAAGATTAATCTCAAGAAATCAAGTCCAAATTGG	424
Db	460	GTGATATCCAACTGGAATCAAAAGGGGAGTAAATCAAGAAATCAAGTCCAACTGG	519
QY	425	GAATTCAAATATCTCAGCAGTACATTTGAAAAATCTCTGAGTTGATTCATTTCCCTGTA	484
Db	520	GAATTCAAATATCTCAGCAGTAAATTTGAAAAATTTCTGAGTGAATTCATTTCACTGAGA	579
QY	485	AAACTGAGGGCTTTTCTACTGATGAGCAATCCAAATGTTTCCAGGGCAACGGATTTCA	544
Db	580	AAACCGAAGCCGAATTTCTATTTGGAGCAATCAAAATGTAATCAAGGCAAGCAAGATTTCA	639
QY	545	AGTACATAGAGAACCAAGTCAAGACTAATTTTAAATAGACATTTCAACCTGATCCCAAG	604
Db	640	AGTACATAGAGAAATCAAGTGAATTTTAAACAAGCAATTTCAACCTGATTTCCCAAG	699
QY	605	TAAATTACTTGGAGAGAAATGTTGGCAAAATCTCTGAGGCAATTCACATGCCAAGATG	664
Db	700	TACTTAATTTGCAAGAGACATGTTGGTAAAGATTTCAACAGCAATTCATATCCAAAGATG	759
QY	665	GGGCTTTATCCCAACCTTGAGGCTAGTGAATGCAAGATTCACCAAGGATAGTTCTTA	724
Db	760	GAGTTTATCCCAACCTTCTGAGCTAGTGAATGCCAGTGGGCAAGGGAATAGTTTGA	819
QY	725	GAGTGAATGAATCAATCTGATGATGTCGACTCTTAATGATCGTTAATGAACTGTGAGA	784
Db	820	GAGTGAATGAATCAAGCTGATGATGACACTTAAATTAAGTGTGGAGCTGTGAGA	879
QY	785	CAACTTA 791	
Db	880	CAACTTA 886	

RESULT 13

ID AAC87929 standard; DNA; 1379 BP.

AC AAC87929

DT 06-MAR-2001 (first entry)
XX

DE F. americana pokeweed antiviral protein encoding DNA SEQ ID NO:1.

NM
NM
Nylolaacca americana; pokeweed; pokeweed antiviral protein; PAP; cancer,
biotherapeutic; fusion protein; immunocytinate; mutant; cytostatic;
KW

KW brain tumour: neuroblastoma: soft tissue sarcoma: osteosarcoma: aa.

Phytolacca americana.

	Key	Location/Qualifiers
FH		

FT / *tag= a

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PA (LYNE-) UNIV STATE NEW JERSEY.
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060001 FM, 100101 NS;

DR ME 1, 2001-070722/03
DR P-PSDB: AAB36500.

PT	Immunconjugates used
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moiety that binds a

PS Disclosure; Col 47-1

CC The present invention describes a fu

CC acid substitution at residue 75, 97 or 176 of native PAP and a targeting

anti-HIV activities, and is an inhibitor of cellular RNA or protein

CC Leukaemia, lymphoma, neuroblastoma, osteosarcoma, soft tissue sarcoma, brain tumour.

improved throughout containing either wild

CC type PAP or variant PAP. The present sequence encodes the wild-type PAP, which is given in the exemplification of the present invention

Sequence 1379 BP: 488 A: 234 C: 268 G: 389 T: 0 II: 0 Other: 0

Query Match 67.0%: Score 531: DB 4: Length 1379:

```

Matches 627; Conservative 0; Mismatches 160; Indels 0; Gaps

```

5 TAAATACGATCACCTTGTATGCTGGAATGCCACCATTAACAATATGCCACCTTATGG 64

Db 292 TGAATACAATCATCTACAATGTTGGAAGTACCACCATTAGCAATACGCCACTTTCTGA 35

65 AATCTTGTGTAATCAAGCGAAGATCCAAACTAAATGCTATGGCATACCAATGCTAC 12

Db 352 ATGATCTTGGTAATGAAGCAGATCCAAGTTTAAATGCTATGGAATACCAATGCTGC 41

125 CTGATACTAATTGACCCCTAAGTACTTATTGGTTAAGCTCCAAGGTGCAAACTAATAA 18

125 CTGATACTAATTGACCCCTAAGTACTTATTGGTTAAGCTCCAAGGTGCAAACTAATAA 18

QY 541 TTCAAGTACATAGAGAACCAAGTCAAGCTAATTTAATAGACATTCACCTGATCCC 600
 DB 1620 TTCAAGTACATAGAGAACCAAGTCAAGCTAATTTAATAGACATTCACCTGATCCC 1679
 QY 601 AAAGTATTAATCTTGAGAGAGAGTGGGCAAAATCTCTGAGCAATTCACATGCGAG 660
 DB 1680 AAAGTATTAATCTTGAGAGAGAGTGGGCAAAATCTCTGAGCAATTCACATGCGAG 1739
 QY 661 AATGGGCTTTACCCAAACCACTTGAAGTGAATGCGAAAGGATACCAAGTGAATGTT 720
 DB 1740 AATGGGCTTTACCCAAACCACTTGAAGTGAATGCGAAAGGATACCAAGTGAATGTT 1799
 QY 721 CTGAGAGTGAATGAATCAATCGTGAATGCGACCTCTTAAGTACGTTAATGAACTGT 780
 DB 1800 CTGAGAGTGAATGAATCAATCGTGAATGCGACCTCTTAAGTACGTTAATGAACTGT 1859
 QY 781 CAGGCAACTTA 791
 DB 1860 CAGGCAACTTA 1870

RESULT 15

AA081457
 ID AA081457 standard; cDNA; 1195 BP.

AC AA081457;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-AUG-1995 (first entry)
 DE Phytolecta antiviral protein (PAP) cDNA.
 XX
 KM Antiviral protein; vector pMJ12; KCCM 10037; PAP; SB.
 XX
 OS Phytolecta americana; L.
 XX
 PN AU9350642-A.
 XX
 PD 19-JAN-1995.
 XX
 PP 11-NOV-1993; 93AU-00050642.
 XX
 PR 02-JUL-1993; 93KR-00012360.
 XX
 PA (JINR-) JIN RO LTD.
 XX
 PI Lee K, Choi K, Jeon H, Kim M, Moon Y;
 DR WPI; 1995-067518/10.
 XX
 PT Recombinant vector for producing Phytolecta anti-viral protein - and
 PT transformed B. coli useful for making immunconjugates for treatment of
 PT AIDS.
 PS
 XX
 PS Claim 1; Fig 1; 27pp; English.
 XX
 CC Total cellular mRNA from leaves of P. americana was used to produce a
 CC cDNA library and this screened with anti-PAP antibody raised in rabbits
 CC against purified PAP. Inserts were isolated from 2 clones and sequenced
 CC to identify a 1195 ORF (AA081457) that encodes a 313 AA PAP including a
 CC 22 AA signal peptide. The mature PAP gene was subjected to PCR
 CC amplification using primers AA081458 and AA081459. The amplification
 CC product was cut with Hind III and inserted into the commercial pLAC (RM)
 CC vector cut with the same enzyme to form pMJ12. pMJ12 is deposited with
 CC the Korean Collection of Culture and Microorganism (KCCM), an
 CC International Depository Authority, on June 30 1993, ad deposition No.
 CC KCCM 10037, and claimed. (Updated on 16-OCT-2003 to standardise OS field)
 XX
 SO Sequence 1195 BP; 420 A; 203 C; 229 G; 343 T; 0 U; 0 Other;

Query Match 66.8%; Score 529.4; DB 2; Length 1195;
 Best Local Similarity 79.5%; Pred. No. 1.6e-141;
 Matches 626; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

QY 5 TAAATGATACCTTTGATGCTGGAATGCGAACCAATTAATAATATGCACTTATNG 64
 DB 100 TAAATGATACCTTTGATGCTGGAATGCGAACCAATTAATAATATGCACTTATNG 159
 QY 65 AATCTCTTCTTAATCAAGCAAGATCAAAATCTTAATATGCAATCAATGCTAC 124
 DB 160 AATCTCTTCTTAATCAAGCAAGATCAAAATCTTAATATGCAATCAATGCTAC 219
 QY 125 CTGATCTAATTTGACCCCTTAAGTCTTATTTGTTAAGTCTCAAGTGCAAACTTAAA 184
 DB 220 CCAATTCAAATTAACAAATCCAAAGTCTGTTGAGTCTCAAGGTTCAAAATPAAAAA 279
 QY 185 CCAATTCAAATGCTGAGAGCAAAATTAATCTTAATAGGATGAGGCTATTTGATCCCTCA 244
 DB 280 CCAATTCAAATGCTGAGAGCAAAATTAATGATGATGATGATGATGATGATGATGATG 339
 QY 245 ATGGCAATTAATGCTGTTACCATATATTAATGATATTAACAGCAAGCACTGATG 304
 DB 340 AATCACTAATATGCTGTTACCATATCTTAATGATATCTCAGGATCAAGCAAGCAATG 399
 QY 305 TGAAGATTAATCTTTGCTCAAGTTCTAAGTCTGCTGTTGCAATGTCATTAACAATA 364
 DB 400 TAGAGACTACTCTTGGCCAAATGCGAATCTGCTGATGATGATGATGATGATGATGATG 459
 QY 365 GCTTAATTCGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 424
 DB 460 GTCGATTCGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 519
 QY 425 GAATTCAAATTAATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 484
 DB 520 GAATTCAAATTAATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 579
 QY 485 AAATGAGCTTTTCTTCTAATGATGATGATGATGATGATGATGATGATGATGATGAT 544
 DB 580 AAATGAGCTTTTCTTCTAATGATGATGATGATGATGATGATGATGATGATGATGAT 639
 QY 545 AGTACATTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 604
 DB 640 AGTACATTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 699
 QY 605 TAATTAATCTTGAGAGAGAGTGGGCAAAATCTCTGAGCAATTCACATGCGAGATG 664
 DB 700 TAATTAATCTTGAGAGAGAGTGGGCAAAATCTCTGAGCAATTCACATGCGAGATG 759
 QY 665 GGGCTTTACCCAAACCACTTGAAGTGAATGCGAAAGGATACCAAGTGAATGTTCTTA 724
 DB 760 GAGTTTACCCAAACCTCTGAGCTAGTGAATGCGAGTGGTCCAAAGTGAATGTTCTTA 819
 QY 725 GAGTGAATGAATCAATCGATGATGCGACTCTTAAGTACGTTAATGAACTGTCAGA 784
 DB 820 GAGTGAATGAATCAATCGATGATGCGACTCTTAAGTACGTTAATGAACTGTCAGA 879
 QY 785 CAACTTA 791
 DB 880 CAACTTA 886

Search completed: April 9, 2006, 00:50:31
 Job time : 479.387 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:25:18 ; Search time 3751.92 Seconds
(without alignments)
9876.364 Million cell updates/sec

Title: US-09-978-274A-3

Perfect score: 792
Sequence: 1 atgataataatcgatcacctt.....gaacctgtcgacacactaa 792

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: gb_ests1.*
2: gb_ests2.*
3: gb_ests3.*
4: gb_hnc.*
5: gb_ests4.*
6: gb_ests5.*
7: gb_ests6.*
8: gb_ests7.*
9: gb_gss81.*
10: gb_gss82.*
11: gb_gss83.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	88.6	11.2	993	2	BR035039 MM02A03 M
C 2	82.2	10.4	816	2	BR035038 MM02A01 M
C 3	64	8.1	1033	2	BR036541 MP01B07 M
4	62.2	7.9	498	5	BQ588134
5	61.6	7.8	829	7	CN7882289 EST00385
6	57.4	7.2	649	6	CA838757 MCT020B02
7	57.4	7.2	649	6	CA839330 MCT026C11
8	57.4	7.2	661	6	CA835532 MCS038A11
9	57.4	7.2	671	6	CA839511 MCT028D04
10	57.4	7.2	689	6	CA833333 MCS021A09
11	57.4	7.2	689	6	CA833383 MCS021F04
12	53.8	7.0	639	6	CA835855 MCS004G12
13	53.8	6.8	1038	2	BR035546
14	52.4	6.6	405	8	T24255
15	51.6	6.5	639	2	BR037217 MP18B02 M
16	46.6	5.9	487	2	BE130330 L48-484T3
17	45.6	5.8	839	1	AM053634 L30-1401T
18	45.4	5.7	267	1	AA856221 L30-242T3
19	45.2	5.7	919	10	CNS0296A
C 20	44	5.6	701	9	BE2031330 oej24109.
21	43	5.4	1021	2	BR036639 MP03B03 M
22	42.6	5.4	414	10	CG637661 OST365110

C 23	42.4	5.4	561	9	AQ156306
C 24	41.8	5.3	658	10	CZ857242
C 25	41.1	5.2	788	10	CG690741
26	40.8	5.2	1001	10	CNS0078E
27	40.4	5.1	228	10	CG503780
28	40.4	5.1	307	4	AK190946
29	40.4	5.1	431	10	CG517501
30	40.4	5.1	525	6	CA548609
31	40.4	5.1	526	10	CL256443
32	40.4	5.1	557	1	AM230870
33	40.4	5.1	563	9	AQ670952
34	40.4	5.1	575	5	BUT43805
35	40.4	5.1	579	3	BJ365833
36	40.4	5.1	616	5	BY729128
C 37	40.4	5.1	630	7	CO102355
38	40.4	5.1	635	1	AM323815
39	40.4	5.1	685	2	BG920190
40	40.4	5.1	717	9	BH974953
41	40.4	5.1	810	6	CA751457
42	40.4	5.1	812	7	CV557169
43	40.4	5.1	813	5	BU961361
44	40.4	5.1	831	5	BU961701
45	40.4	5.1	918	6	CB183067

ALIGNMENTS

RESULT 1
BR035039 993 bp mRNA linear EST 07-JUN-2000
DEFINITION MM02A03 MM Mesembryanthemum crystallinum cDNA 5' similar to
LOCUS
ACCESSION BR035039
VERSION BR035039.1 GI:8330048
KEYWORDS
SOURCE
ORGANISM
EST.
Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Aizoaceae; Mesembryanthemum.
1 (bases 1 to 993)

REFERENCE
Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Baton, M.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu
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TITLE
JOURNAL
COMMENT

FEATURES
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XhoI; Plants stressed 6 weeks in 500mM NaCl"

ORIGIN

Query Match 11.2%; Score 88.6; DB 2; Length 993;
Best Local Similarity 60.5%; Pred. No. 4.6e-13;

Matches 164; Conservative 0; Mismatches 104; Indels 3; Gaps 1;

QY 386 AGAAGACGAGATTAACCAAGAAATCAAGTCAATGGGAATTAATCAAGACAGT 445
DB 681 AGAAGCTGCCGCTCAAGACGAAACAGTATGATTTGGGGCTTCAACTAGAGTTTG 622

QY 446 ACAATGGAAAAATCTCTGAGTTGATTCATTCCTCTGTAATAAAAGTAGAGCTTTTCTTAC 505
 DB 621 CCATCGATGATTTATGTGTAATAAAAGATCGATGGAAATCTGAGGCCAAATCTTAC 562
 QY 506 TGTGATCCATCCAAATGGTTTCAGAGGACGGCATTCATCACTAGAGAACCAAGT-- 563
 DB 561 TGATTCGATCCATCGATGGTTTCAGAGGACGGCATTCATCACTAGAGAACCAAGT 502
 QY 564 -CAAGACTAATTTTAAATAGACATTCCTGATTCCTCAAAATGTAATTAATCTGAGAGAGA 622
 DB 501 CCGAAATGGGTGTCATGTTCTGTTCAAAACCGGATCCGAAAGTATTAATCTGAGAGACA 442
 QY 623 AGTGGGCAAAATCTCTGAGGCAATTCACA 653
 DB 441 ACTGGGAAAGATTTCCGATGAGATTCATTA 411

RESULT 2
 BE035038/c 816 bp mRNA linear EST 07-JUN-2000
 LOCUS NM02A01 MM Mesembryanthemum crystallinum cDNA 5' similar to
 DEFINITION
 ACCESSION BE035038
 VERSION BE035038.1 GI:8330047
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)
 ORGANISM Mesembryanthemum crystallinum
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
 1 (bases 1 to 816)
 Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M., Ferreira,H., Kawasaki,S., McCollough,A., Michalowski,C.B., Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
 Functional Genomics of Plant Stress Tolerance
 Unpublished (2000)
 Contact: Michalowski,C.B.
 University of Arizona
 Bio Sciences West room 513, Tucson, AZ 85721, USA
 Tel: 520-621-7982
 Fax: 520-621-1697
 Email: cbm@u.arizona.edu.
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 /note="Vector: Bluescript SK+; Site 1: EcoRI; Site 2: XhoI; Plants stressed 6 weeks in 500mM NaCl"

ORIGIN
 Query Match 10.4%; Score 82.2; DB 2; Length 816;
 Best Local Similarity 59.0%; Pred. No. 2.5e-11;
 Matches 160; Conservative 0; Mismatches 108; Indels 3; Gaps 1;

QY 386 AGAAGACGAAGTAATCTCAAGAAATCAAGTCCATTTGGGAATTCAAATCTCAGCAGTG 445
 DB 680 AGAACTGCGGTGCAAGCAGAAACGATATGCGTGGGCGTCTGTAATAGAGTTG 621
 QY 446 ACAATGGAAAAATCTCTGAGTTGATTCATTCCTCTGTAATAAAAGTAGAGCTTTTCTTAC 505
 DB 620 CCATCGATGATTTATGTGTAATAAAAGATCGATGGAAATCTGAGGCCAAATCTTAC 561
 QY 506 TGTGATCCATCCAAATGGTTTCAGAGGACGGCATTCATCACTAGAGAACCAAGT-- 563
 DB 560 TGATTCGATCCATCGATGGTTTCAGAGGACGGCATTCATCACTAGAGAACCAAGT 501
 QY 564 -CAAGACTAATTTTAAATAGACATTCCTGATTCCTCAAAATGTAATTAATCTGAGAGAGA 622

DB 500 CCGAAATGGGTGTCATGTTCTGTTCAAAACCGATCCGAAAGTATTAATCTGAGAGACA 441
 QY 623 AGTGGGCAAAATCTCTGAGGCAATTCACA 653
 DB 440 ACTGGGAAAGATTTCCGATGAGATTCATTA 410

RESULT 3
 BE036541 1033 bp mRNA linear EST 07-JUN-2000
 LOCUS MF01B07 MP Mesembryanthemum crystallinum cDNA 5' similar to
 DEFINITION
 ACCESSION BE036541
 VERSION BE036541
 KEYWORDS BE036541.1 GI:8331550
 SOURCE EST.
 ORGANISM Mesembryanthemum crystallinum (common iceplant)
 Mesembryanthemum crystallinum
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
 1 (bases 1 to 1033)
 Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M., Ferreira,H., Kawasaki,S., McCollough,A., Michalowski,C.B., Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
 Functional Genomics of Plant Stress Tolerance
 Unpublished (2000)
 Contact: Michalowski,C.B.
 University of Arizona
 Bio Sciences West room 513, Tucson, AZ 85721, USA
 Tel: 520-621-7982
 Fax: 520-621-1697
 Email: cbm@u.arizona.edu
 An open reading frame exists.
 Location/Qualifiers
 source 1..1033
 /organism="Mesembryanthemum crystallinum"
 /mol_type="mRNA"
 /db_xref="taxon:3544"
 /cigar_type="apical meristem and leaf primordia"
 /dev_stage="6 weeks"
 /clone_lib="MP"
 /note="3 d 500mM NaCl"

ORIGIN
 Query Match 8.1%; Score 64; DB 2; Length 1033;
 Best Local Similarity 54.8%; Pred. No. 2.8e-06;
 Matches 149; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

QY 384 AAGAAAGCAGAAGTAATCTCAAGAAATCAAGTCCATTTGGGAATTCAAATCTCAGCAG 443
 DB 193 AGAAGAGGTGCAAGCAGGCGGAATGCAATAGATTAGGGGTGAATTAATAGAGTT 252
 QY 444 TGACATTTGAAAAATCTCTGAGATTGATTCATTCCTCTGTAATAAAAGTAGAGCTTTTCT 503
 DB 253 TGGATTCGAGTCTGTTTGGTAAGAACCGATTAATGGGACGTTGAGGCCAAATCTT 312
 QY 504 ACTGTAGCCATCCAAATGGTTTCAGAGGACGGCATTCATCACTAGAGAACCAAGT 563
 DB 313 GCTGATTCGATCACTAGTGGTTTCAGAGGACGGCATTCATCACTAGAGAACCAAGT 372
 QY 564 CA---AGACTAATTTTAAATAGACATTCCTGATTCCTCAAAATGTAATTAATCTGAGAGA 620
 DB 373 GACCCAAAGTGGTTTATGATGCTCGTTCAATACCCGACCCGAAAGTCTGATTTGAGAGA 432
 QY 621 GAAGTGGGCAAAATCTCTGAGGCAATTCACA 652
 DB 433 CAATGGGGGAAAGATTTCCAGAGATTCATA 464

RESULT 4
 BQ588134 498 bp mRNA linear EST 06-DEC-2002
 LOCUS BQ588134
 DEFINITION B012337-024-009-G14-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone

024-009-G14 5-PRIME, mRNA sequence.
 ACCESSION BO588134
 VERSION BO588134.1 GI:26117717
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 498)
 REFERENCE Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,W., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radejof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 12472698
 COMMENT Contact: Weisshaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
 Insert Length: 498 Std Error: 0.00
 Plate: 9 row: G column: 14
 Seq primer: SP6; CATGCACTTGGTGACACTATAG.
 Location/Qualifiers
 1..498
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultiVar="KWS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:184726"
 /db_xref="taxon:161934"
 /clone="024-009-G14"
 /issue_type="leaf"
 /lab_host="EMDH10B"
 /clone_1lb="MP12-ADIS-024-leaf"
 /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinfeldleber Saatzucht AG Bindeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
 SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
 Query Match 7.9%; Score 62.2; DB 5; Length 498;
 Best Local Similarity 56.7%; Pred. No. 7.3e-06;
 Matches 140; Conservative 0; Mismatches 98; Indels 9; Gaps 1;
 14 TCACCTTGAATGCTGAATGCGCACCATTAACAATATGCCACTTATGGAATCTCTC 73
 169 TAACCTTTGACCTTGAACAGCTTCAAGCAAAATATGACATTTTCTAAGCATATAC 228
 74 GTATCAAGCAAGATCCAAACTAAATAGTATGCGATACCAATGCTACTGATCTA 133
 229 GCAACATATGTAAGATTCAAAGCTAGTATACGAAGAAATCCATGCTCCCTGACCAT 288
 134 ATTGACCCCTAAGTACTTATGTTAGTTCGACCAAGTGCAGAA-----CCTAAAA 184
 289 CAAAACAGCAAAATACCTTTAGCCGAGCTAAAGCTAAAGACCGGTACTGACATTA 348
 185 CCATTACATTAATGCTGAGCAAGAAATAGTATAGTATGCTATGATCCCTTCA 244
 349 CCATCAACACTTGTCTTAGCAAAATAGCTTATATGATAGTCTTTTACGATCAAGTAG 408
 245 ATGGCAA 251
 409 CAGGTAA 415

RESULT 5
 CN782289
 LOCUS
 DEFINITION CN782289 829 bp mRNA linear EST 21-MAY-2004
 EST00385 cgsed Chenopodium quinoa cDNA clone S02J22 5' similar to antiviral ribosome-inactivating protein CAP308 [Chenopodium album], mRNA sequence.
 ACCESSION CN782289
 VERSION CN782289.1 GI:47561753
 KEYWORDS EST.
 SOURCE Chenopodium quinoa (quinoa)
 ORGANISM Chenopodium quinoa
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Chenopodium.
 1 (bases 1 to 829)
 REFERENCE Coles,N.D., Coleman,C.E., Christensen,S.A., Jellen,B.N., Stevens,M.R., Bonifacio,A., Rojas-Beltran,J.A., Fairbanks,D.J. and Maughan,P.J.
 Development and use of an expressed sequenced tag library in quinoa (Chenopodium quinoa Willd.) for the discovery of single nucleotide polymorphisms
 Plant Sci. 168 (2), 439-447 (2005)
 CONTACT: Coleman, Craig B.
 Department of Plant and Animal Sciences
 Brigham Young University
 275 WIDB, Brigham Young University, Provo, UT 84602, USA
 Tel: (801) 422-5145
 Fax: (801) 422-0008
 Email: craig.coleman@byu.edu
 Plate: 02 row: J column: 22
 Seq primer: M13 Forward
 High quality sequence stop: 829.
 Location/Qualifiers
 1..829
 /organism="Chenopodium quinoa"
 /mol_type="mRNA"
 /cultiVar="Real"
 /db_xref="taxon:63459"
 /clone="S02J22"
 /issue_type="Developing Seed"
 /lab_host="XL-1 Blue"
 /clone_1lb="cgsed"
 /note="Vector: pRip1B2; Site 1: SfiI; Site 2: SfiI; Developing Seed cDNA library from Chenopodium quinoa"

ORIGIN
 Query Match 7.8%; Score 61.6; DB 7; Length 829;
 Best Local Similarity 51.2%; Pred. No. 1.2e-05;
 Matches 291; Conservative 0; Mismatches 244; Indels 33; Gaps 5;
 30 AAATGCCACCATTAACAATATGCGACCTTATGATCTCTTGTATCAAGCAAGA 89
 115 AAAACCTACAGAGATCTTATTAACCTTTTCGAAAGATAGCGCAAACTAAGA 174
 90 TCCAAACTTAATATGCTATGCGCATACCAATGCTAGTACTTAATTCGACCCCTAAGTA 149
 175 TCCAAAGTTAGTATGTAAGAAATCCCAATGATCCGACCAACCAACCAAGTATATA 234
 150 CTTATTTGTTAGTTCGAAGTGAACCTTAATAC-----CATTACACTAATGCT 200
 235 TCTTTTGTGACCTTGAACTTAAAGATTAAGATAGATATTCATTAACCTTGCTTT 294
 201 GAGACGAATTAATTAATGCTATGATGCGCTATTCCTTCAATGCGATTAAGTCTG 260
 295 AAGTAAAGACACTGTATGATGATGCGCTTGTGTAATTTGAGGCAAGTGGCGG 354
 261 TTACATATATTTAATGATATTTCAAGCACCGCAAGCACTGATGTAATATCTTTG 320
 355 CCAATTCCTTTTCAACTTAACTTGAACACCATTTGATAGGCAAGAA---AGTTTTTC 410
 321 CTCAGTTTCTAGTTCTGTGTCGAATGTCATTAATTAATAGCTTATATCCGACCAT 380

Db 411 CAGAGTTCAGGTTTC-----ATTAATATACCTAAGGGGAAAGTTACAGTCAAT 462
Qy 381 GGAAGAAAGACAGAGTAACCAAGAAATCAAGATCCAAATGGGAATTCAAAATACAG 440
Db 463 CGAAGACAGATGCTGATCAAAACGATTAAGT---TTTCGGTTGGGTTTGATACCTTAA 519
Qy 441 CAGTGAATTGGAAGAAATCTCTGAGATTGATTCATTCCTGTGTA-----AAACTGA 491
Db 520 AACTACATGAGAAAGGCTATGGATGATGATACTAAGGCCAAAGATTATAGCAAAATCGA 579
Qy 492 GGGTTTTTCTACTGTAGTACCATCCAAATGTTTCAGAGCCAGCCGATTCAGATCAT 551
Db 580 AGCTCGGTTCTCTACTCGCGATTCAAATGGTTGCAGAGCCGCGAGTTTCAAGTACAT 639
Qy 552 AGAGAACCAAGTCAAGACTAATTTAAT 579
Db 640 CCAAGGAAGAGCTATCTTACTACAAAT 667

RESULT 6
CA838757 649 bp mRNA linear EST 12-DEC-2002
LOCUS MCT020B02.167445 Ice plant Lambda Uni-Zap XR expression library, 5
DEFINITION days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
(5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT020B02.5,
mRNA sequence.

ACCESSION
VERSION CA838757
KEYWORDS CA838757.1 GI:26566522
SOURCE EST.

ORGANISM Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 649)

AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum

JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer

Plate: 020 row: B column: 02
Seq primer: T3 20mer
High quality sequence stop: 649.
Location/Qualifiers

FEATURES
source 1..649
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT020B02"
/issue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR. Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; library construction was performed
according to Stratagene's recommended protocol for the
Lambda UnizapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 7.2%; Score 57.4; DB 6; Length 649;
Best Local Similarity 53.5%; Pred. No. 0.00016;
Matches 146; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

Qy 384 AAAGAAAGCAGAGTAACCAAGAAATCAAGTCCATTTGGGAATTCAAATACCTAGCAG 443
Db 87 AGAAGATGCTGCAAAACCAACGACGAGAGCATAGAGTTAGGGGTGATTAACATAGATT 146
Qy 444 TGAATTTGGAAGAAATCTCTGAGATTGATTCATTCCTGTAAATACTGAGGCTTTTTCCT 503
Db 147 TGGATTCAGAGTCGGTTTATGTGAATGACATGACAACTGAGAAATGAGGCCAAATTCCT 206
Qy 504 ACTGTAGCCATCAATAGGTTTCAGAGGAGCGCATTCATCACTAGATGAGAACCAAGT 563
Db 207 GCTGATTCATCAATAGGTTTCTAAGCAGCAAGTTCAAGTATATGAGATAGT 266
Qy 564 CAAGACTAATTT-----TAATAGCAATTCACCTGATCCCAAGTAATTAATCTTGA 617
Db 267 GAACCAAGTCGCTTATGATTAATGATCGTTCTTACCGACGACCAAAATGCTGTTTGA 326
Qy 618 GGAAGATGGGGCAAAATCTCTGAGCAATTCA 650
Db 327 GACCAATTTGGGGGAGATTTCCGACGAGATTCA 359

RESULT 7
CA839330 649 bp mRNA linear EST 12-DEC-2002
LOCUS MCT026C11.171755 Ice plant Lambda Uni-Zap XR expression library, 5
DEFINITION days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
(5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT026C11.5,
mRNA sequence.

ACCESSION
VERSION CA839330
KEYWORDS CA839330.1 GI:26567095
SOURCE EST.

ORGANISM Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 649)

AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum

JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer

Plate: 026 row: C column: 11
Seq primer: T3 20mer
High quality sequence stop: 649.
Location/Qualifiers

FEATURES
source 1..649
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT026C11"
/issue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR. Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; library construction was performed
according to Stratagene's recommended protocol for the
Lambda UnizapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 7.2%; Score 57.4; DB 6; Length 649;

	Beet	Local	Similarity	53.5%	Pred.	No.	0.00016	
	Matches	146	Conservative	0	Mismatches	121	Indels	6
								Gaps
								1.
QY	384	AAAGAAACGAGAGTAACTCAAGAAATCAAGTCCAAATTGGAAATTCAAATATCTCAGACG	443					
Db	87	AGAGAAATCTGCAAAACCAACGACGAAAGCCATAGATTAGGGGTGGATTAACCTAGAGTT	146					
QY	444	TGACATTGGAAAAATCTCGAGAGTTGATTCATTCCTCTGTAATAACTGAGGCTTTTTTCT	503					
Db	147	TGCGATCGAGTCGGTTTATATGGTAGACATCGAACAAGTCAGAAAAATGAGGCCAAATTCCT	206					
QY	504	ACTGTTAGCCATCCAAATGTTTTCAGAGGACGCGCATTCAGTACATAGAAACCAAGT	563					
Db	207	GCTGATTCGCATACGAGATGGTTTTCTGAAAGCAGCAAGTTCCAAGTATATGGAGAGTAAAGT	266					
QY	564	CAAGACTTAATT-----TAATAGAGCAATTCACCTGATCCCAAGTAATTAATTGACTTGA	617					
Db	267	GAACCAAAAGTGTGATGATTAATGATTCGTTCTTAACCCGACCGAAAAATGCTGCTTTTGA	326					
QY	618	GGAGAGTGGGGCAAAATCTCGAGGCAATTC	650					
Db	327	GACCAATTTGGGGAGAGATTTTGGCAGAGAGATTCA	359					

LOCUS				
CA835532	661 bp	mRNA	linear	EST 12-DEC-2002
MCS038A11_160572				
DEFINITION	Ice plant Lambda Uni-Zap XR expression library, 5			

ACCESSION	CA835532
VERSION	CA835532.1
	GI:26563297

SOURCE ORGANISM	crystallinum (common iceplant)
Mesembryanthemum	crystallinum
Mesembryanthemum	crystallinum

REFERENCE 1 (bases 1 to 661)

JOURNAL
COMMENT
Unpublished (1997)
Contact: Cushman JC

FEATURES	Location/Qualifiers
source	1. .661

according to Stratagene's recommended protocol for the Lambda UnizapXR vector and cDNA synthesis kit."

	Query Match	5.2%;	Score 57.4;	DB 6;	Length 661;
	Best Local Similarity	53.5%;	Pred. No. 0.0016;		
	Matches 146;	Conservative 0;	Mismatches 121;	Indels 6;	Gaps 1
QY	384	AAAGAAACGACAGATGAACTCAAGAAATTCAGTCCATTGGGAAATTCAAATATCTCGACGAC	443		
DB	98	AGAGATATCTGCAAACCAACGACGAGAAAGCCATAGAGTTAAGGGTGAATAACTAGAGTT	157		
QY	444	TGACATTGGAAAAATCTCTGAGATTGATTCCCTGTAAGAAATGAGAGCTTTTTCCT	503		
DB	158	TGCGATCGAGTCGGTTTATGGTAAGACATCGACAAATGAGGCCAAATTCCT	217		
QY	504	ACTGTAGACCATCCAAATGCTTTCGAGAGCAGCGGATTCAGTACATAGAACCAAGT	563		
DB	218	GCTATATGCCATACAGATGCTTTTCGAAAGCAGCAAGTTCAAGTATATTTGAAGATAGGT	277		
QY	564	CAAGCTAATTT-----TAATAGAGCATTCACCTGATCCCAAGTAAATTAATCTTGA	617		
DB	278	GATCAAAAGTCGGTTATGATTAATGATTCGTTCTTACCCGACCCGAAAAATCTGCTTTTGA	337		
QY	618	GGAAAGTGGGGCAAAATCTCTGAGGCAATTC	650		
DB	338	GACCAATTTGGGGGAAGATTTGGCAGAGATTTCA	370		

RESULT 9	LOCUS	DEFINITION
CA839511	671 bp	mRNA
CA839511	127117	linear EST 12-DEC-2002
MCT02SD04_172117		Ice plant Lambda Uni-Zap XR expression library, 5

(5:30 PM). *Mesembryanthemum crystallinum* cDNA clone MCT028D04 5' mRNA sequence.

SOURCE ORGANISM	crystallinum (common iceplant)
Mesembryanthemum	crystallinum
Mesembryanthemum	crystallinum

REFERENCE 1 (bases 1 to 671)

JOURNAL COMMENT
Unpublished (1997)
Contact: Cushman JC

FEATURES	Location/Qualifiers
source	1. .671

/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1
EcoRI; Site_2: XhoI; Library construction was performed
according to Stratagene's recommended protocol for the

ORIGIN Lambda UnizapXR vector and cDNA synthesis kit."

Query Match 7.2%; Score 57.4; DB 6; Length 671;
Best Local Similarity 53.5%; Pred. No. 0.00017;
Matches 146; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

QY 384 AAGAAAGCAGAACTAATCAAGAAATCAAGTCCAAATGGAAATTCATACTACAG 443
DB 87 AGGAATGCTGCACAAACGACGACGAGCAATGATAGGGGTGATTAACAGAGT 146
QY 444 TGACATTTGAAAAATCTCTGGAAGTGAATTCATCCCTGTAATACTAGAGCTTTTCT 503
DB 147 TGGATGAGTCCGTTTATGTTAAGACATGACAAATGAGAAATGAGCCAAATCTT 206
QY 504 ACTGTAGCCATCCAAATGTTTCAGAGGAGCGCATTCAGATACATAGAACCAAGT 563
DB 207 GCTGATGGCATACAGATGTTTCTGAGCAGCAAGTTCAAGTATTTAGAGTAAGT 266
QY 564 CAAAGCTAATTT-----TAATAGAGCATTCTACCCGTGATCCCAAGTAAATTAATTGA 617
DB 267 GAACCAAGTGCCTTGAATTAATGATGCTTCTTACCGACCCGAAATGCTGCTTTGGA 326
QY 618 GGAAAGTGGGGCAAAATCTCTGAGGCAATTC 650
DB 327 GACCAATGGGGGAAGATTTCGAGAGATTCA 359

RESULT 10 689 bp mRNA linear EST 12-DEC-2002
LOCUS CA833333
DEFINITION MCS021A09_151944 Ice plant Lambda Uni-Zap XR expression library, 5

days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS021A09 5, mRNA

sequence.

ACCESSION CA833333
VERSION CA833333.1 GI:26561098
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)

ORGANISM Mesembryanthemum crystallinum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzooceae; Mesembryanthemum.

REFERENCE 1 (bases 1 to 689)
AUTHORS Cushman, J.C.

TITLE An expressed sequence tag database for the common ice plant,

JOURNAL Mesembryanthemum crystallinum
COMMENT Unpublished (1997)

CONTACT: Cushman JC
DEPARTMENT OF Biochemistry
UNIVERSITY OF Nevada
MS200, Reno, NV 89557-0014, USA
TEL: 775-784-1918
FAX: 775-784-1650
EMAIL: jcushman@unr.edu

PCR PRIMERS
FORWARD: T3 20mer
BACKWARD: T7 21mer
PLATE: 021 row: A column: 09
SEQ PRIMER: T3 20mer
HIGH QUALITY SEQUENCE STOP: 689.

FEATURES
source Location/Qualifiers

1..689
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCS021A09"
/cistype="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase I (2 AM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-, Site_1:"

ORIGIN EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UnizapXR vector and cDNA synthesis kit."

Query Match 7.2%; Score 57.4; DB 6; Length 689;
Best Local Similarity 53.5%; Pred. No. 0.00017;
Matches 146; Conservative 0; Mismatches 121; Indels 6; Gaps 1;

QY 384 AAGAAAGCAGAACTAATCAAGAAATCAAGTCCAAATGGGAATTCATACTACAG 443
DB 98 AGGAATGCTGCACAAACGACGACGAGCAATGATAGGGGTGATTAACAGAGT 157
QY 444 TGACATTTGAAAAATCTCTGGAAGTGAATTCATCCCTGTAATACTAGAGCTTTTCT 503
DB 158 TGGATGAGTCCGTTTATGTTAAGACATGACAAATGAGAAATGAGCCAAATCTT 217
QY 504 ACTGTAGCCATCCAAATGTTTCAGAGGAGCGCATTCAGATACATAGAACCAAGT 563
DB 218 GCTGATGGCATACAGATGTTTCTGAGCAGCAAGTTCAAGTATTTAGAGTAAGT 277
QY 564 CAAAGCTAATTT-----TAATAGAGCATTCTACCCGTGATCCCAAGTAAATTAATTGA 617
DB 278 GAACCAAGTGCCTTGAATTAATGATGCTTCTTACCGACCCGAAATGCTGCTTTGGA 337
QY 618 GGAAAGTGGGGCAAAATCTCTGAGGCAATTC 650
DB 338 GACCAATGGGGGAAGATTTCGAGAGATTCA 370

RESULT 11 689 bp mRNA linear EST 12-DEC-2002
LOCUS CA833383
DEFINITION MCS021F04_152044 Ice plant Lambda Uni-Zap XR expression library, 5

days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS021F04 5, mRNA

sequence.

ACCESSION CA833383
VERSION CA833383.1 GI:26561148
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)

ORGANISM Mesembryanthemum crystallinum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzooceae; Mesembryanthemum.

REFERENCE 1 (bases 1 to 689)
AUTHORS Cushman, J.C.

TITLE An expressed sequence tag database for the common ice plant,

JOURNAL Mesembryanthemum crystallinum
COMMENT Unpublished (1997)

CONTACT: Cushman JC
DEPARTMENT OF Biochemistry
UNIVERSITY OF Nevada
MS200, Reno, NV 89557-0014, USA
TEL: 775-784-1918
FAX: 775-784-1650
EMAIL: jcushman@unr.edu

PCR PRIMERS
FORWARD: T3 20mer
BACKWARD: T7 21mer
PLATE: 021 row: F column: 04
SEQ PRIMER: T3 20mer
HIGH QUALITY SEQUENCE STOP: 689.

FEATURES
source Location/Qualifiers

1..689
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCS021F04"
/cistype="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid

Best Local Similarity 52.4%; Pred. No. 0.0018;
Matches 143; Conservative 0; Mismatches 127; Indels 3; Gaps 1;

QY 384 AAGAGAGAGAGATTAACCAAGATCAAGTCCATTGGGAATTCAATTAATACACAG 443
DB 286 AG 345
QY 444 TGACATTGAAAAATCTCTGAGATTGATTCCTCTGTAATAAATGAGGCTTTTCT 503
DB 346 CGGATGAGAGTCCGTTTGTGTAAGAACCCGATTAATGGGAGAGTTGAGCCAAATCTT 405
QY 504 ACTGTGATGATCCCAATATGTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563
DB 406 GCTGATGATGATCAAGATGTTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
QY 564 CA---AGACTAATTTTAAATGAGCATTCACCTGATCCCAAGATTAATTAATCTGAGGA 620
DB 466 GAGCCAAAGTGTGTACATGCTTTGTTCAAAACCCGAGAGAGAGAGAGAGAGAG 525
QY 621 GAAGTGGGCAAAATCTCTGAGGCAATTCACAA 653
DB 526 CAATGGGTGAACATTTTCATGAGACTCATTA 558

RESULT 14
T24255 405 bp mRNA linear EST 28-JUL-1995
LOCUS crr1345 lambdaZAPST Ricinus communis cDNA clone pcr1345, mRNA
DEFINITION sequence.

ACCESSION T24255
VERSION T24255.1 GI:689074
KEYWORDS EST.
SOURCE Ricinus communis (castor bean)
ORGANISM Ricinus communis

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosids; eustosida I; Malpighiales; Euphorbiaceae; Acalyphoideae; Acalyphaeae; Ricinus.
1 (bases 1 to 405)
Vandeloo, F.J., Turner, S. and Somerville, C.
Expressed sequence tags from developing castor seeds
Plant Physiol. 108, 1141-1150 (1995)
COMMENT Contact: Somerville CR
Carnegie Institution
290 Panama St., Stanford, CA 94305
Tel: 4153251521
Email: crosendrew.stanford.edu
Seq primer: T3

FEATURES
source
Location/Qualifiers
1..405
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/mol_type="mRNA"
/strain="Baker 296"
/db_xref="taxon:3988"
/clone="pcr1345"
/clone_lib="lambdaZAPST"
/note="Vector: lambdaZAPII; Site 1: EcoRI; Site 2: XhoI; Poly(A) + RNA was purified from developing stage III to stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760, 1982) endosperm plus embryo of immature castor fruits. cDNA was synthesized and cloned into lambdaZAPII according to the instructions of the manufacturer (Stratagene); synthesis was primed from the poly(A) tail, and cloned directionally into XhoI (3') and EcoRI (5') sites. In few cases, sequence data indicated that this directionality was reversed. Partial cDNA clones predominate."

ORIGIN

Query Match 6.6%; Score 52.4; DB 8; Length 405;
Best Local Similarity 59.2%; Pred. No. 0.0035;
Matches 125; Conservative 0; Mismatches 79; Indels 7; Gaps 2;

QY 486 AACTGAGGCTTTTCTACTGTGATCCCAATGTTTTCAGAGGAGCGGCAATTCAA 545

DB 82 AACTGGGCTGTTCTCTTAATGTTTGATCCAAATGATTTCAGAGGAGAGATTCCA 141

QY 546 GTTACTAGAGAACCAAGTCAAGCTAATTTT-----AATAGCAATTCACCTGATCC 599

DB 142 GTTCAATGAGGAGAAATGCGAGAAATTAAGTACACCGAGAGATCTGACACAGATCC 201

QY 600 CAAGTAATTAATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 658

DB 202 TAGCGTATTAACACTTNAAGATAGTTGGGGAGACTTTCACCTGCAATTCAGAGCTTA 261

QY 659 AGAATGGGCTTTTACCAACCACTTGAGCT 689

DB 262 ACCAAGAGGCTTTGCTATGCAATTCAACT 292

RESULT 15
BE037217 639 bp mRNA linear EST 07-JUN-2000
LOCUS MP18B02 MP Mesembryanthemum crystallinum cDNA 5' similar to ribosome-inactivating protein/antiviral protein, mRNA sequence.
DEFINITION BE037217
ACCESSION BE037217
VERSION BE037217.1 GI:8332233
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 639)
Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferreira, H., Kawasaki, S., McColough, A., Michaelowski, C.B., Palacios, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michaelowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: chm@u.arizona.edu

FEATURES
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Location/Qualifiers
1..639
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/ribseq_type="apical meristem and leaf primordia"
/dev_stage="6 weeks"
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/clone="3 d 500mM NaCl"
/note="3 d 500mM NaCl"

ORIGIN

Query Match 6.5%; Score 51.6; DB 2; Length 639;
Best Local Similarity 57.0%; Pred. No. 0.0065;
Matches 139; Conservative 0; Mismatches 94; Indels 11; Gaps 2;

QY 394 GAAGTAATCAAGAAATCAATGATTCATTTGGGAATCAATTAATCTGAGGATTCGGA 453

DB 308 GAGCTCAG 367

QY 454 AAAATCTGAGATTGATTCATTCCTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAG 513

DB 368 AACAGC-----GATTAATGATGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 418

QY 514 ATCCAAATGTTTCAG 573

DB 419 ATTCAATGTTTGTGAGGCTGACGTTCTCTTACATACAGAGAGAGAGAGAGAG 476

QY 574 TTTAATAGAGCATTTACCTGATCCCAAGTAATTAATCTGAGAGAGAGAGAGAGAG 633

DB 477 TTGAGCAAAATTTCAAGAGGCTATGACTTCAGATTTGCTTAGAGAGAGAGAGAG 536

QY 634 ATCT 637

Db 537 GCCT 540

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Job time : 3754.92 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 8, 2006, 09:19:56 ; Search time 274.935 Seconds
(without alignments)
5120.590 Million cell updates/sec

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Perfect score: 792
Sequence: 1 atgataatcagatcacctt.....gaacctgcagacaactta 792

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	534.2	67.4	1195	2 US-08-373-858-1	Sequence 1, Appl
2	534.2	67.4	1195	2 US-08-342-7868-1	Sequence 1, Appl
3	532.6	67.2	1379	2 US-08-500-611-1	Sequence 1, Appl
4	532.6	67.2	1379	2 US-08-500-694-1	Sequence 1, Appl
5	532.6	67.2	1379	3 US-07-865-169-1	Sequence 1, Appl
6	532.6	67.2	1379	3 US-09-005-273-1	Sequence 1, Appl
7	532.6	67.2	1379	6 PCT-US95-11546-1	Sequence 1, Appl
8	531	67.0	1379	3 US-08-501-253A-1	Sequence 1, Appl
9	529.4	66.8	1379	3 US-07-865-169-2	Sequence 2, Appl
10	529.4	66.8	1379	3 US-09-005-273-3	Sequence 3, Appl
11	460.6	58.2	918	2 US-08-138-636-1	Sequence 1, Appl
12	460.6	58.2	918	2 US-08-319-622A-1	Sequence 1, Appl
13	460.6	58.2	918	2 US-08-471-564-1	Sequence 1, Appl
14	88.2	11.1	774	6 PCT-US91-05766-1	Sequence 1, Appl
15	82	10.4	1233	3 US-08-718-904-80	Sequence 80, Appl
16	82	10.4	1233	3 US-09-449-249-80	Sequence 80, Appl
17	81	10.2	804	2 US-08-356-161-6	Sequence 80, Appl
18	81	10.2	804	2 US-08-356-161-7	Sequence 7, Appl
19	81	10.2	804	3 US-08-718-904-22	Sequence 23, Appl
20	81	10.2	804	3 US-08-718-904-23	Sequence 23, Appl
21	81	10.2	804	3 US-09-449-249-22	Sequence 22, Appl
22	81	10.2	804	3 US-09-449-249-23	Sequence 22, Appl
23	81	10.2	804	6 PCT-US93-05702-6	Sequence 6, Appl
24	81	10.2	804	6 PCT-US93-05702-7	Sequence 7, Appl

25	81	10.2	804	6 PCT-US95-10973A-6	Sequence 6, Appl
26	81	10.2	804	6 PCT-US95-10973A-7	Sequence 7, Appl
27	75	9.5	1167	6 PCT-US95-10973A-57	Sequence 57, Appl
28	75	9.5	1230	2 US-08-356-161-12	Sequence 12, Appl
29	75	9.5	1230	2 US-08-356-161-13	Sequence 12, Appl
30	75	9.5	1230	3 US-08-718-904-53	Sequence 53, Appl
31	75	9.5	1230	3 US-09-449-249-53	Sequence 53, Appl
32	75	9.5	1230	6 PCT-US93-05702-12	Sequence 12, Appl
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34	75	9.5	1230	6 PCT-US95-10973A-12	Sequence 12, Appl
35	75	9.5	1230	6 PCT-US95-10973A-13	Sequence 12, Appl
36	75	9.5	1251	3 US-08-718-904-74	Sequence 74, Appl
37	75	9.5	1251	3 US-09-449-249-74	Sequence 74, Appl
38	75	9.5	1260	3 US-08-718-904-72	Sequence 72, Appl
39	75	9.5	1260	3 US-09-449-249-72	Sequence 72, Appl
40	75	9.5	1266	3 US-08-718-904-75	Sequence 75, Appl
41	75	9.5	1266	3 US-09-449-249-75	Sequence 75, Appl
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43	75	9.5	1269	3 US-09-449-249-78	Sequence 78, Appl
44	75	9.5	1275	3 US-08-718-904-73	Sequence 73, Appl
45	75	9.5	1275	3 US-09-449-249-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1
US-08-373-858-1
; Sequence 1, Application US/08373858
; Patent No. 5633155
; GENERAL INFORMATION:
; APPLICANT: Kim, Man-Keun
; APPLICANT: Lee, Kwan-Ho
; APPLICANT: Na, Byoung-Kook
; APPLICANT: Jeong, Han-Seung
; APPLICANT: Choi, Kyu-Whan
; APPLICANT: Moon, Young-Ho
; APPLICANT: Jeon, Hong-Seob
; TITLE OF INVENTION: Expression Vector for Phytolecta
; TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
; TITLE OF INVENTION: Plant Transformed Thereof.
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,858
; FILING DATE: 18-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0136/17986-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7770
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: cDNA to mRNA

HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Phytolacca americana*
TISSUE TYPE: Leaf
US-08-373-858-1

Query Match 67.4%; Score 534.2; DB 2; Length 1195;
Best Local Similarity 79.9%; Pred. No. 1.9e-150;
Matches 629; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 5 TAAATACGATCACTTTGATGCTGGAATGCGCATTAACTAAATATGCACTTTATG 64
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QY 185 CCATTACATTAATGCTGAGGCAATTAATTAATGCTGAGGCTATTCGATCCCTTCA 244
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DB 820 GAGTGAATGAATCAATGCTGAGTCCAAAGTCAATGAGTATGCTTCA 879
QY 785 CAACCTTA 791
DB 880 CAACCTTA 886

RESULT 2
US-08-342-786B-1
Sequence 1, Application US/08342786B
Patent No. 5648234
GENERAL INFORMATION:

APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
APPLICANT: Choi, Kyu-Whan
APPLICANT: Lee, Kwan-Ho
APPLICANT: Kim, Man-Keun
TITLE OF INVENTION: A No. 5648234e1 Expression Vector for *Phytolacca*
TITLE OF INVENTION: Antiviral Protein
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Darby & Darby
STREET: 805 Third Ave.
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,786B
FILING DATE: 21-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,024
FILING DATE: 01-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/08862-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
TELEFAX: (212)753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Phytolacca americana* L.
IMMEDIATE SOURCE:
CLONE: PAP
US-08-342-786B-1

Query Match 67.4%; Score 534.2; DB 2; Length 1195;
Best Local Similarity 79.9%; Pred. No. 1.9e-150;
Matches 629; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 5 TAAATACGATCACTTTGATGCTGGAATGCGCATTAACTAAATATGCACTTTATG 64
DB 100 TGAATACATCACTCAATGTTGGAATGACCATATGCAATATGCGCATCTTTCTGA 159
QY 65 AATCTCTGTAATCAAGGAAAGATCCAAACTAAATGTAATGCAATCAATGCTAC 124
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DB 340 AAACCAATTAATGCTGATCAATATTAATTAATTAATTAATTAATTAATTAATTAATTA 399

QY 305 TGAGAACTACTTCTGCTCAAGTCTAGTCTCGGTGCAATGTCATTACATACATA 364
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 QY 365 GCTTATATCCGACATGAAAAAGACAGAACTCAAGAACTCAAGTCCAAATGG 424
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 QY 545 AGTACATAGAGAACCAAGTCAAGCTAATTTTAAATAGAGCAATTCACCTGATCCAAAG 604
 DB 640 AGTACATAGAGAACCAAGTCAAGCTAATTTTAAATAGAGCAATTCACCTGATCCAAAG 699
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 QY 785 CAACCTTA 791
 DB 880 CAACCTTA 886

RESULT 3

US-08-500-611-1

Sequence 1, Application US/08500611
 Patent No. 5756322
 GENERAL INFORMATION:
 APPLICANT: Tumer, Nilgun B.
 TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ierner, David, Littenberg, Krumholz & Mentlik
 STREET: 600 South Avenue West
 CITY: Westfield
 STATE: NJ
 COUNTRY: USA
 ZIP: 07090-1497
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/500,611
 FILING DATE: 11-JUL-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Foley, Shawn P.
 REFERENCE/DOCKET NUMBER: OCIRS 3.0-034
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-654-5000
 TELEFAX: 908-654-7866
 TELEX: 139-125
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1379 base pairs
 TYPE: nucleic acid

STRANDEDNESS: double
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 225..1163
 FEATURE:
 NAME/KEY: mutation
 LOCATION: replacement(233, "a")
 FEATURE:
 NAME/KEY: mutation
 LOCATION: replacement(349, "g")
 FEATURE:
 NAME/KEY: mutation
 LOCATION: replacement(435, "c")
 US-08-500-611-1

Query Match 67.2%; Score 532.6; DB 2; Length 1379;
 Best Local Similarity 79.8%; Pred. No. 6e-150;
 Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

QY 5 TAATTAAGATCACCTTGTGATGCGAAATGCCACATTAATAAATATGCCACTTATNG 64
 DB 292 TGAATACATCATCTTCAATATGTTGAAGTACCAATTCAGAAATAGCCACTTTCTGA 351
 QY 65 AATCTTCTGTAATCAAGCAAGATCCAAATCTAAATGCTATGCGATACCAATGCTAC 124
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 QY 125 CTGATTAATTTGACCCCTTAAGTCTTATGTTAAGTCCAAAGTGAACCTTAAAA 184
 DB 412 CCAATACAAATATCAATTCAAAGTACGTTGTTGAGCTCCAAAGTTCAAAATAAAAA 471
 QY 185 CCAATTAATTAATGCTGAGAGCAAAATTAATTAATGAGAGGCTATTCATCCCTTCA 244
 DB 472 CCAATCACTTAATGCTGAGAGCAAAATTAATTAATGAGAGGCTATTCATCCCTTCA 531
 QY 245 ATGCAATTAATGCTGAGAGCAAAATTAATTAATGAGAGGCTATTCATCCCTTCA 304
 DB 532 AAACCAATTAATGCTGAGAGCAAAATTAATTAATGAGAGGCTATTCATCCCTTCA 591
 QY 305 TGAGAACTACTCTTGGCCAAATGCCAATCTCTGTTAGTAAAACTAACTTTGATA 364
 DB 592 TAGAGACTACTCTTGGCCAAATGCCAATCTCTGTTAGTAAAACTAACTTTGATA 651
 QY 365 GCTTATATCCGACATGAAAAAGACAGAACTCAAGAACTCAAGTCCAAATGG 424
 DB 652 GTGATATCCAACTTGGATTCAAAGCGGAGTAAATCAAGAACTCAAGTCCAACTGG 711
 QY 425 GAATTCAAATCTCAGAGTCACTTGGAAAAATCTCGAGTGTATTCATTCCTGTA 484
 DB 712 GAATTCAAATCTCAGAGTCACTTGGAAAAATCTCGAGTGTATTCATTCCTGTA 771
 QY 485 AAATCGAGCTTTTCTTCTACTGTAGCCATCCAAATGTTCCAGGACGCGAATTCA 544
 DB 772 AAATCGAGCTTTTCTTCTACTGTAGCCATCCAAATGTTCCAGGACGCGAATTCA 831
 QY 545 AGTACATAGAGAACCAAGTCAAGCTAATTTTAAATAGAGCAATTCACCTGATCCAAAG 604
 DB 832 AGTACATAGAGAACCAAGTCAAGCTAATTTTAAATAGAGCAATTCACCTGATCCAAAG 891
 QY 605 TAATTAATCTGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCCAATGCCAAGATG 664
 DB 892 TACTTAATTTGCAAGAGACATGGGTAAGTTTCAACAGCAATTCATGATCCAAAGATG 951
 QY 665 GGGCTTACCCAAACCACTTGAGCTAGTGAATCCAAAGTACCAAGTGAATGTTCTTA 724
 DB 952 GAGTTTACCCAAACCTCTGAGCTAGTGAATCCAAAGTGAATGTTCTTA 1011
 QY 725 GAGTGAATGAATCAATCGTATGTGCACTCTTAAGTACGTTAATGAACTGTGCA 784
 DB 1012 GAGTGAATGAATCAAGCTGATGTGCACTTAACTAAGTGTGGAGGCTGTGCA 1071
 QY 785 CAACCTTA 791

Db 1072 CAACTTA 1078

RESULT 4

US-08-500-694-1
Sequence 1, Application US/08500694
Patent No. 5880329
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein
TITLE OF INVENTION: Mutants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,694
FILING DATE: 11-JUL-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-694-1

Query Match 67.2%; Score 532.6; DB 2; Length 1379;
Best Local Similarity 79.8%; Pred. No. 6e-150;
Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

QY 5 TAAATCGATCACCCTTGTGCTGGAAGTCCACCAATTAACAATAATGCACTTTATG 64
DB 292 TGAATCAATCACTCAATGTTGGAAGTACCACTTAACAATAATGCACTTTATG 351
QY 65 AATCTGTGATCAAGGGAAGATCCAAATCAAAATGCTATGCGATCAATGCTAC 124
DB 352 ATGATCTTGATGAGGCAAGATCCAAATGTTAAATGCTATGGAATCAATGCTGC 411
QY 125 CTGATCTAATTCGACCCCTAAGTACTTATGTTAAGTCCAAAGTGCAAACTAAAA 184
DB 412 CCAATCAAAATCAAAATCCAAATGCTGTTGTTGAGTCCAAAGTCCAAATAAAAA 471
QY 185 CCAATCACTAATGCTGAGAGCAAAATTAATTAATGCTATGCTATGATCCCTCA 244

Db 472 CCATCACTAATGCTGAGCAAAATTTGATGATGGGTTATTTGATCCCTTG 531

QY 245 ATGCAATAAGTCTCGTACCAATATTAATATATATACAGACCGAAGCATGATG 304

DB 532 AAACAAATAAATCGTATGCAATATCTTAATATATATCTCAGGATCTGAACGCAAGT 591

QY 305 TGAAGATACTCTTGTCTCAAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 364

DB 592 TAGAGTACTCTTGTCCCAATGCGCAATTTCTGTTAGTAAAAATTAACCTTTGATA 651

QY 365 GCTTATATCCGACATGAAAGAAAGCAAGATTAATCTCAAGAAATCAAGTCAATGG 424

DB 652 GTCGATATCCAACTTGAATCAAAAGCGGAGTAAATCAAGAGTCAAGTCAACTGG 711

QY 425 GAATTCAAATACACAGATGACATTTGAAAAATCTCTGAGTTGATTCCTCTGTAA 484

DB 712 GAATTCAAATACCTGACAGTAAATATGGAAGATTTCTGAGTATGATCATCACTGAG 771

QY 485 AAATGAGGCTTTTCTACTGTAGCCATCCAAATGTTTCAAGGCGAGCATTC 544

DB 772 AAACGAGCGCAATTCCTATTTGATGCAATATGATGAGGCGAGCAAGATTC 831

QY 545 AGTACATGAGAAACCAAGTCAAGACTAATTTTAATAGACATTCACCTGATCCCAAG 604

DB 832 AGTACATGAGATCAGTGAAATTAATTTTAAAGACATTCACCTGATCCCAAG 891

QY 605 TAATTAATCTGAGGAGAGTGGGCAAAATCTCTAGCAATTCACATCCAAATG 664

DB 892 TACTTAATTTGCAAGGACATGGGGTAAAGATTTCAACCAATTCATGATCCCAAGT 951

QY 665 GAGCTTACCAACCACTGAGTATGATGAGTCCAAAGTACCAAGTATGATCTTA 724

DB 952 GAGTTTACCAACCACTCTGAGTATGATGAGTCCAAAGTATGATCTTA 1011

QY 725 GAGTGAATGAATCAATCTGATGAGTCACTCTTAAGTATGAACTGTGCA 784

DB 1012 GAGTGAATGAATCAAGCTGATGATGATCTTAAGTATGAACTGTGCA 1071

QY 785 CAACTTA 791

DB 1072 CAACTTA 1078

RESULT 5

US-07-865-169-1
Sequence 1, Application US/07865169
Patent No. 6015940
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
APPLICANT: Lodge, Jennifer K.
APPLICANT: Kaniewski, Wojciech K.
TITLE OF INVENTION: Virus Resistant Potato Plants
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Dennis R. Hoerner, Jr., Monsanto Co. B84F
STREET: 700 Chesterfield Parkway No. 6015940ch
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865,169
FILING DATE: 19920407
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914

QY 5 TAAATCGATCACCCTTGTGCTGGAAGTCCACCAATTAACAATAATGCACTTTATG 64
DB 292 TGAATCAATCACTCAATGTTGGAAGTACCACTTAACAATAATGCACTTTATG 351
QY 65 AATCTGTGATCAAGGGAAGATCCAAATCAAAATGCTATGCGATCAATGCTAC 124
DB 352 ATGATCTTGATGAGGCAAGATCCAAATGTTAAATGCTATGGAATCAATGCTGC 411
QY 125 CTGATCTAATTCGACCCCTAAGTACTTATGTTAAGTCCAAAGTGCAAACTAAAA 184
DB 412 CCAATCAAAATCAAAATCCAAATGCTGTTGTTGAGTCCAAAGTCCAAATAAAAA 471
QY 185 CCAATCACTAATGCTGAGAGCAAAATTAATTAATGCTATGCTATGATCCCTCA 244

REFERENCE/DOCKET NUMBER: 38-21 (10547) A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6099
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-865-169-1

Query Match 67.2%; Score 532.6; DB 3; Length 1379;
Best Local Similarity 79.8%; Pred. No. 6e-150;
Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

5 TAAATGATGACCTTTGATGCTGGAATGCGACCATTAACAATATGCGACCTTTATGG 64
292 TGAATCAATCATCTCAATGTTGGAAGTACACCATTAAGCAATAGCGCATTTTCTGA 351
65 AATCTCTGATCAAGCGAAAGATCCAAACTAAATGCTATGCGATACCATCTAC 124
352 ATGATCTTGTAAGAGCGAAGATCAAGTTAAATGCTATGGAATACCAATGCTGC 411
125 CTGATTAATTTGACCCCTAAGTCTTATTTGTTAGTCCAAAGTGCAACCTAATA 184
412 CCAATCAATATCAAAATCCAAAGTCTGTTGTTAGTCCAAAGTCCAAATTAATA 471
185 CCAATTAATGCTGAGAGCAAAATTAATGATGAGGCTATTTGATCTCTCA 244
472 CCAATCAATGCTGAGAGCAAAATTAATGATGAGGCTATTTGATCTCTCA 244
245 ATGCAATATGCTGAGAGCAAAATTAATGATGAGGCTATTTGATCTCTCA 304
532 AAACCAATATGCTGAGAGCAAAATTAATGATGAGGCTATTTGATCTCTCA 591
305 TGAATGATGCTGAGAGCAAAATTAATGATGAGGCTATTTGATCTCTCA 364
592 TGAATGATGCTGAGAGCAAAATTAATGATGAGGCTATTTGATCTCTCA 651
365 GCTTATATCCGACGAGAAAGAAAGCAAGTAACTCAAGAAATCAAGTCAATGG 424
652 GTGATATCCGACGAGAAAGAAAGCAAGTAACTCAAGAAATCAAGTCAATGG 711
425 GAATGATATCCGACGAGAAAGAAAGCAAGTAACTCAAGAAATCAAGTCAATGG 484
712 GAATGATATCCGACGAGAAAGAAAGCAAGTAACTCAAGAAATCAAGTCAATGG 771
485 AAATGATGCTGAGAGCAAAATTAATGATGAGGCTATTTGATCTCTCA 544
772 AAACCAATATGCTGAGAGCAAAATTAATGATGAGGCTATTTGATCTCTCA 831
545 AGTACATAGAGAAAGCAAGTAACTCAATTTAATGAGCAATTTCACTGATCCCAAG 604
832 AGTACATAGAGAAAGCAAGTAACTCAATTTAATGAGCAATTTCACTGATCCCAAG 891
605 TAATTAATGAGAGCAAGTAACTCAATTTAATGAGCAATTTCACTGATCCCAAG 664
892 TAATTAATGAGAGCAAGTAACTCAATTTAATGAGCAATTTCACTGATCCCAAG 951
665 GGGCTTTACCAACCACTGAGTATGAGTCAAGGTTCAAGGTTCAAGTATGTTCTTA 724
952 GAGTTTACCAACCACTGAGTATGAGTCAAGGTTCAAGGTTCAAGTATGTTCTTA 1011
725 GAGTATGATCAATCAATGATGATGAGTCACTCTTAAGTCAAGTATGTTCTTA 784
1012 GAGTATGATCAATCAATGATGATGAGTCACTCTTAAGTCAAGTATGTTCTTA 1071
785 CAACCTTA 791
1072 CAACCTTA 1078

RESULT 6
US-09-005-273-1
Sequence 1, Application US/09005273
Patent No. 6137030
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLTZ &
ADDRESS: MENTILIK
STREET: 600 South, Avenue West
CITY: Westfield
STATE: New Jersey
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,273
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,611
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE: 11-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: 33,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS ..1163
LOCATION: 225..290
NAME/KEY: sig_peptide
LOCATION: 225..290
US-09-005-273-1
Query Match 67.2%; Score 532.6; DB 3; Length 1379;
Best Local Similarity 79.8%; Pred. No. 6e-150;
Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

5 TAAATGATGACCTTTGATGCTGGAATGCGACCATTAACAATATGCGACCTTTATGG 64
292 TGAATCAATCATCTCAATGTTGGAAGTACACCATTAAGCAATAGCGCATTTTCTGA 351
65 AATCTCTGATCAAGCGAAAGATCCAAACTAAATGCTATGCGATACCATCTAC 124
352 ATGATCTTGTAAGAGCGAAGATCAAGTTAAATGCTATGGAATACCAATGCTGC 411
125 CTGATTAATTTGACCCCTAAGTCTTATTTGTTAGTCCAAAGTGCAACCTAATA 184
412 CCAATCAATATCAAAATCCAAAGTCTGTTGTTAGTCCAAAGTCCAAATTAATA 471

Db 892 TACTTAATTTGCAAGAGATGGGGTAAGATTTCACAGCAATTCATGATGCCAAGATG 951
QY 665 GGGCTTACCCAAACCTTGAGCTAGTGAATGCGAAAGTACCAAGGATTAATTTCTTA 724
Db 952 GAGTTTACCCAAACCTCTGAGCTAGTGAATGCGCAAGGATTAATTTCTTA 1011
QY 725 GAGTGATGAATCAATCGTATGTGGCACTCTTAAGTAAATGGAACCTGTGCA 784
Db 1012 GAGTGATGAATCAAGCTGATGTAGCACTTAACCTAGTTGGTGGAGCTGTGCA 1071
QY 785 CAACCTTA 791
Db 1072 CAACCTTA 1078

RESULT 8
US-08-501-253A-1
Sequence 1, Application US/08501253A
Patent No. 6146628
GENERAL INFORMATION:
APPLICANT: Tumey, Fatih
APPLICANT: Tumey, Nilgun
TITLE OF INVENTION: Biotherapeutic Agents Comprising
TITLE OF INVENTION: Recombinant PAP and PAP Mutants
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 6146628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: US
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501.253A
FILING DATE: 11-JUL-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kettlerberger, Denise M.
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 600.323US01
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
US-08-501-253A-1

Query Match 67.0%; Score 531; DB 3; Length 1379;
Best Local Similarity 79.7%; Pred. No. 1.8e-149;
Matches 627; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 5 TAAATACGATCACCCTTGTGATGCTGAAATGCGACCATTAACAATATGCCACTTATG 64
Db 292 TGAATACATCATATACATGTTGAAATGACACCATTAAGCAATAGCCACTTTCTGA 351
QY 65 AATCTCTGTAATCAAGCGAAAGATCCAAACCTAAATGCTATGATGCAATGCTAC 124
Db 352 ATGATCTTCTGTAAGGCGAAATCCAGTTTAAATGCTATGAAATGCCAATGCTGC 411
QY 125 CTGATACATTAATCGACCCCTAAGTATTAATGTTAAGTCCAGTGCAAACTTAATA 184

Db 412 CCAATGAATATACAAATCCAAAGTACTGTTGGTGAAGCTTCAAGTTCAATTAATAAAAA 471
QY 185 CCATTACATTAATGCTGAGACGAATTAATTAATGCTGATGGGCTATTTGATCCCTTCA 244
Db 472 CCATCACTAATGCTGAGACGAATTAATTAATGCTGATGGGCTATTTGATCCCTTCA 531
QY 245 ATGCAATTAATGCTGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 304
Db 532 AAACCAATTAATGCTGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 591
QY 305 TGAATATCTCTTGTGCTCAAGTTCTGATGCTGATGCTGATGCTGATGCTGATGCTG 364
Db 592 TAGAGTACTCTTGTGCTCAAGTTCTGATGCTGATGCTGATGCTGATGCTGATGCTG 651
QY 365 GCTTATATCCAGCAGTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 424
Db 652 GTCATATCCAACTGGAATCAAAAGCGAGATTAATCAAGAGAGAGAGAGAGAGAGAG 711
QY 425 GAATTCATATCTGAG 484
Db 712 GAATTCATATCTGAG 771
QY 485 AAATGAGGCTTTTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 544
Db 772 AAACCAAGCGAATCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 831
QY 545 AGTACATGAG 604
Db 832 AGTACATGAG 891
QY 605 TAAATTAATCTGAG 664
Db 892 TACTTAATTTGCAAG 951
QY 665 GGGCTTACCCAAACCTTGAGCTAGTGAATGCGAAAGTACCAAGGATTAATTTCTTA 724
Db 952 GAGTTTACCCAAACCTCTGAGCTAGTGAATGCGAAAGTACCAAGGATTAATTTCTTA 1011
QY 725 GAGTGATGAATCAATCGTATGTGGCACTCTTAAGTAAATGGAACCTGTGCA 784
Db 1012 GAGTGATGAATCAAGCTGATGTAGCACTTAACCTAGTTGGTGGAGCTGTGCA 1071
QY 785 CAACCTTA 791
Db 1072 CAACCTTA 1078

RESULT 9
US-07-865-169-2
Sequence 2, Application US/07865169
Patent No. 6015940
GENERAL INFORMATION:
APPLICANT: Tumey, Nilgun E.
APPLICANT: Lodge, Jennifer K.
APPLICANT: Kaniewski, Wojciech K.
TITLE OF INVENTION: Virus Resistant Potato Plants
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Parkway No. 6015940th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865,169
FILING DATE: 19920407

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21 (10547)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-865-169-2

Query Match 66.8%; Score 529.4; DB 3; Length 1379;
Best Local Similarity 79.5%; Pred. No. 5.5e-149;

Matches 626; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

5 TAAATACGATCACCCTTGTGATGCTGGAATGCGACCATTAACAATATGCCACCTTTATGG 64
292 TGAATCAATCACTACATCAATGTTGGAAGTACCACTTACCAATATGCCACCTTTTGG 351
65 AATCTCTTGTGAATCAAGCGAAAGATCCAAACTAAATGCTATGGCATACCAATGCTAC 124
352 ATGATCTTGTGAATCAAGCGAAAGATCCAAAGTTTAAATGCTATGGAATCAATGCTGC 411
125 CTGATCTATTTGAGACCCCTTAAGTACTTATTTGTTAGCTCCAAAGTGCACCACTTAAA 184
412 CCAATCAATTAATCAATTCACCAACACGTTGTTGAGCTCCAAAGTTTCAATTAATTA 471
185 CCATTAACATTAATGCTGAGACGAATTAATACGTATGAGGCTATTTGATCCCTTCA 244
472 CCATCACTAATGCTGAGACGAATTAATGATGAGGCTATTTGATCCCTTCA 531
245 ATGGCAATTAATGCTGAGACGAATTAATGATGAGGCTATTTGATCCCTTCA 304
532 AAACCAATTAATGCTGAGACGAATTAATGATGAGGCTATTTGATCCCTTCA 591
305 TGGAGAAATCTCTTGTGCTGAAGTTTGAATGCTGCTGTTGCAATGCTTCACTAATCA 364
592 TAAAGACTACTCTTGTGCTGAAGTTTGAATGCTGCTGTTGCAATGCTTCACTAATCA 651
365 GCTTATATCCGACCATGAAAGAAAGACAGAACTTAATCAAGAAATCAATGCTTCACT 424
652 GTGATATCAATCAATGAAATCAAGAAAGACAGAACTTAATCAAGAAATCAATGCTTCA 711
425 GAATTAATCAATCAATGAAATCAAGAAAGACAGAACTTAATCAAGAAATCAATGCTTCA 484
712 GAATTAATCAATCAATGAAATCAAGAAAGACAGAACTTAATCAAGAAATCAATGCTTCA 771
485 AAACGAGGCTTTTCTATCTGCTGAGCAATCAATGCTTCAAGGCGAGCGCGATCA 544
772 AAACGAGGCTTTTCTATCTGCTGAGCAATCAATGCTTCAAGGCGAGCGCGATCA 831
545 AGTACATAGAGAACCAAGTCAAGTCAATTAATTAATGAGCAATTAATGAGCAATTAATGAG 604
832 AGTACATAGAGAACCAAGTCAAGTCAATTAATTAATGAGCAATTAATGAGCAATTAATGAG 891
605 TAAATTAATTAATGAGCAATTAATGAGCAATTAATGAGCAATTAATGAGCAATTAATGAG 664
892 TAAATTAATTAATGAGCAATTAATGAGCAATTAATGAGCAATTAATGAGCAATTAATGAG 951
665 GGGCTTACCCCAACCACTTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 724
952 GAGTTTACCCCAACCACTTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1011
725 GAGTGAATTAATCAATGCTGATGAGCAATTAATGAGCAATTAATGAGCAATTAATGAGCA 784
1012 GAGTGAATTAATCAATGCTGATGAGCAATTAATGAGCAATTAATGAGCAATTAATGAGCA 1071

QY 785 CAACTTA 791
Db 1072 CAACTTA 1078

RESULT 10
US-09-005-273-3
Sequence 3, Application US/0905273
Patent No. 6137030
GENERAL INFORMATION:
APPLICANT: Turner, Nigun E.
TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
ADDRESS: MENTLIK
STREET: 600 South, Avenue West
CITY: Westfield
STATE: New Jersey
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,273
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,611
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE: 11-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 225..290
US-09-005-273-3

Query Match 66.8%; Score 529.4; DB 3; Length 1379;
Best Local Similarity 79.5%; Pred. No. 5.5e-149;

Matches 626; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

5 TAAATACGATCACCCTTGTGATGCTGGAATGCGACCATTAACAATATGCCACCTTTATGG 64
292 TGAATCAATCACTACATCAATGTTGGAAGTACCACTTACCAATATGCCACCTTTTGG 351
65 AATCTCTTGTGAATCAAGCGAAAGATCCAAACTAAATGCTATGGCATACCAATGCTAC 124
352 ATGATCTTGTGAATCAAGCGAAAGATCCAAAGTTTAAATGCTATGGAATCAATGCTGC 411

QY 125 CTGATCTAATTCGACCCCTAAGTACTTATTGGTTAGCTCCAGGTGCAAACTTAAAA 184
DB 412 CCAATAGCAAAATACAAATCCAAAGACGCTTGGTGGAGCTCCAGGTTCAAAATAAAAA 471
QY 185 CCAATTACCTAATGCTGAGACGAATTAATTATACGTATGCGCTATTCTGATCCCTTCA 244
DB 472 CCATCAGCACTAATGCTGAGACGAATTAATTATGATGAGGCTATTCTGATCCCTTCA 531
QY 245 ATGCAATTAAGTCTGATCACTAATTATTAATTAATTAATTAATTAATTAATTAATTA 304
DB 532 AAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 591
QY 305 TGGAGATTAATCTTGGTCTCAAGTTAGTCTCGTGTGCAATGTCATTAATTAATTAATTA 364
DB 592 TAGAGACTACTCTTTGGCCCAATGCAATCTCGTGTGCAATGTCATTAATTAATTAATTA 651
QY 365 GCTTATATCCGACCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 424
DB 652 GTCATATCCCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 711
QY 425 GAATTCATTAATCTGAGCTGATGATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 484
DB 712 GAATTCATTAATCTGAGCTGATGATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 771
QY 485 AAATGAGGCTTTTCTTCTAGCTGATGATGCAATGCAATGCAATGCAATGCAATGCAATG 544
DB 772 AAACCGAAGCGCAATCTTATTTGATGATGCAATGCAATGCAATGCAATGCAATGCAATG 831
QY 545 AGTACATAGAGAACCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 604
DB 832 AGTACATAGAGAACCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 891
QY 605 TAATTAATCTGAG 664
DB 892 TACTTAATTTGCAAG 951
QY 665 GGGCTTATACCAACCACTGAGCTGATGATGCAATGCAATGCAATGCAATGCAATGCAATG 724
DB 952 GAGTTTATCCCAATCTTCAAGCTGATGATGCAATGCAATGCAATGCAATGCAATGCAATG 1011
QY 725 GAGTGAATGAATCAATGATGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 784
DB 1012 GAGTGAATGAATCAATGATGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 1071
QY 785 CAACCTTA 791
DB 1072 CAACCTTA 1078

RESULT 11
US-08-138-636-1
Sequence 1, Application US/08138636
Patent No. 5348865
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seoh
APPLICANT: Choi, Kyeon-Ho
APPLICANT: Lee, Kwan-Ho
APPLICANT: Kim, Man-Kaun
TITLE OF INVENTION: No. 5348865el Genome Coding Phytoleuca Antiviral
TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 THIRD AVE.
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,636
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/08818
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytoleuca insularis
IMMEDIATE SOURCE:
CLONE: antiviral protein (PIP)
US-08-138-636-1

Query Match 58.2%; Score 460.6; DB 2; Length 918;
Best Local Similarity 76.7%; Pred. No. 2.3e-118;
Matches 604; Conservative 0; Mismatches 174; Indels 9; Gaps 3;

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QY 65 AATCTTCTGGAATCAAG 124
DB 128 A---CTTCTGAG 181
QY 125 CTGATCTAATTCGACCCCTAAGTACTTATTGGTTAGCTCCAGGTGCAAACTTAAAA 184
DB 182 CCAATATGATCAAAATCCAAATGATGATGATGATGATGATGATGATGATGATGATGATG 241
QY 185 CCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 244
DB 242 GCATCACTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 301
QY 245 ATGCAATTAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 304
DB 302 A---CAATTAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 358
QY 305 TGGAGATTAATCTTGGTCTCAAGTTCTAGTTCTCGTGTGCAATGTCATTAATTAATTAATTA 364
DB 359 TAGAGACTACTCTTTGGCCCAATGCAATCTCGTGTGCAATGTCATTAATTAATTAATTAAT 418
QY 365 GCTTATATCCGACCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 424
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QY 425 GAATTCATTAATCTGAGCTGATGATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 484
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QY 485 AAATGAGGCTTTTCTTCTAGCTGATGATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 544
DB 539 GAACCGAAGCTGAATCTTCTAGCTGATGATGCAATGCAATGCAATGCAATGCAATGCAATG 598
QY 545 AGTACATAGAGAACCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 604
DB 599 AGTACATAGAGAACCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 658

Qy 715 ATAGTCTTAGAGTGAT 732
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Db 1186 AAAGATTGCGAGATGGT 1203

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Job time : 276.935 secs

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GenCore version 5.1.7
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OM protein - nucleic search using frame p2n model

Run on: April 9, 2006, 01:20:32 ; Search time 6004.59 Seconds
(without alignments)
2489.732 Million cell updates/sec

Title: US-09-978-274A-4

Perfect score: 1357
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 segs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-Q=/abs/ASSWB.spool/US0978274/runat_07042006_173032_28388/arp_query.fasta.1
-DB=GenMdb1 -QPM=faalap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blousum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pico -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs04
-USRR=US0978274.@CGN.1.1.5548.@runat.07042006_173032_28388 -NCPU=6 -ICPU=3
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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3: gb_env.*
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15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1357	100.0	792	6	AX427704 Sequence
2	1352	99.6	945	6	AX427702 Sequence
3	1352	99.6	1249	15	PAPAPSRIP X98079 P.americana

4	1332	98.2	786	15	AB071855
5	1312	96.7	1092	6	AX427720
6	1099.5	81.0	783	15	AB071854
7	1052	77.5	882	6	A67183
8	1050	77.4	942	15	AY547315
9	1050	77.4	942	15	AY572976
10	1050	77.4	1164	15	PAPAP
11	1050	77.4	1195	6	A42103
12	1050	77.4	1195	6	I43835
13	1050	77.4	1195	6	I55866
14	1050	77.4	1379	6	AR009535
15	1050	77.4	1379	6	AR136704
16	1050	77.4	1379	6	AX427731
17	1047	77.2	1379	6	AR141172
18	1045.5	77.0	939	15	AY327475
19	1044	76.9	1164	15	AY049785
20	1044	76.9	1195	6	A36639
21	1043	76.9	1114	15	AF533515
22	1042	76.8	1378	6	AX427732
23	1042	76.8	1379	6	AR136705
24	1014.5	74.8	2472	6	E05033
25	1014.5	74.8	2472	15	PTCAPAP
26	995.5	73.4	1052	15	AY137202
27	977.5	72.0	951	6	A67185
28	977.5	72.0	2369	15	AF141331
29	965	70.7	1113	15	AY071928
30	960	70.7	714	15	AY603354
31	953	70.2	711	15	AF338910
32	952	70.2	714	15	AY603352
33	947	69.8	714	15	AY603353
34	862.5	63.6	918	6	A43003
35	862.5	63.6	918	6	A48150
36	862.5	63.6	918	6	I60482
37	862.5	63.6	918	6	I89987
38	793	58.4	465	6	AX427706
39	701	51.7	1226	15	CAANTIPR
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43	453	33.4	1187	15	PAPAP11
44	452	33.3	902	15	AF533516
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ALIGNMENTS

RESULT 1
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DEFINITION Sequence 3 from Patent WO0233107.
ACCESSION AX427704
VERSION AX427704.1 GI:21537816
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
1 Neelam, A., Atkinson, H.J., Mcpherson, M.J. and Thomas, C.J.R.
AUTHORS
TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A.3 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
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/db_xref="taxon:3527"
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/note="Binding site for primer PS1BP"
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/note="Initiation codon added via PCR primer"
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misc_feature /note="Binding site for primer PS1SR"
 463..492 /note="Binding site for primer PS2BP"
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 /note="Sequence replacing removed XbaI site"
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 790..792
 /note="Stop codon added via PCR primer"

ORIGIN

Alignment Scores:

Pred. No.: 1,03e-110 Length: 792
 Score: 1357.00 Matches: 263
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 6 Gaps: 0

US-09-978-274A-4 (1-263) x AK427704 (1-792)

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 DB 1 ATGATTAATACGATACACCTTGATGCTGGAATGCCACATTAACAATATGCCACCTTT 60
 QY 21 MetGlySerLeuArgAaSnAlaLysAaSPProLyLeuLySeyTyTgLyileProMet 40
 DB 61 ATGGAATCTTCTGTATACAGCGAAGATCCAAACCTAAATGCTATGGCATGCCAATG 120
 QY 41 LeuProAaPThraAaSerThrProLyTyTleuLeuValLyLeuGlnGlyAlaAaSnLeu 60
 DB 121 CTACCTGATAGTACTAATTCGACCCCTTAAGTACTTATGTGTTAGCTCCAAAGTGCAACTA 180
 QY 61 LyvThrLleThrLeuMetLeuArgAaAaSnLeuTyTAlaMetGlyTyTserAaSPPro 80
 DB 181 AAAACCAATTAACCTAAATGCTGAGACGAATTAACCTTAACCTGATGCTATTCGATCCC 240
 QY 81 PheAaSnGlyAaSnLySeyTyTgLyilePheAaAaSPilleThraAaPThrGlnArgThr 100
 DB 241 TTCAATGGCAATAGTTCCTTACCAATATTTATATATATACAGCACGAAAGCACT 300
 QY 101 AaPValGlyAaSnThrLeuCySeySerSerSerSerArgValAlaMetSerilleAaSnTy 120
 DB 301 GATGTGGAGAAATCTCTTCTGCTCAAGTTCTGTTCTGTCGAATGTCATTAATAC 360
 QY 121 AaAaSerLeuTyThraAaMetGlyLyLeuValGlyValAaAaSerArgAaSnGlnValGln 140
 DB 361 AATAGCTTATATCCGACCATGAAAGAAAGCAAGAACTCAAGAAATCAAGTCCAA 420
 QY 141 LeuGlyTilleGlnLleAaSerSerAaPilleGlyLySeySerGlyValAaSPSerPhePro 160
 DB 421 TTGGGAATTCAAATATCTCAGCAGTACGACATTGGAAATATCTCTGAGATGTGATTCCT 480
 QY 161 ValLySerThrGlnAaPhePheLeuLeuValAlaLleGlnMetValSerGlnAlaAaArg 180
 DB 481 GTAAAAAATGAGGCTTTTCTTACTGCTGAGCCATCAATGGTTTCAGAGGCGCGCA 540
 QY 181 PheLyTyTilleGlnAaSnGlnValLySeyThraAaPheAaAaArgAlaPheTyTProAaSPPro 200
 DB 541 TTCAAGTACATAGAACCAAGTCAGAACTAATTTTAATAGACATTCCTGATGCC 600
 QY 201 LyvValilleAaSnLeuGlnGlyTyTgLyileSeyGlnAlaLleHSAaSnAlaLyS 220
 DB 601 AAAGTAATTAATCTTGGAGAGAAAGTGGGCAAAATCTCTAGGCAATTCACATGCCAAG 660
 QY 221 AaSnGlyAlaLeuProLySeySerSerSerSerArgValAaPAlaLySeyTyTThrLyTilleVal 240
 DB 661 AATGGGAGCTTACCCAAACCACTTAGCTAGTGAATGCCAAAGTACCAAGTGAATGTT 720
 QY 241 LeuArgValAaSnGlnLleAaAaArgAaPValAlaLeuLeuLyTyTValAaSnGlyThra 260

DB 721 CTAGAGTGTAGTAATCAATCGTATGTGCACTCCTTAAGTACGTTAATGAACCTGT 780
 QY 261 GlnThrThr 263
 DB 781 CAGACAACT 789

RESULT 2
 AX427702
 LOCUS Sequence 1 from Patent WO023107.
 DEFINITION AX427702
 ACCESSION AX427702.1 GI:21537815
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

PhytoIaccia americana (American pokeweed)
 PhytoIaccia americana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; PhytoIaccaceae; PhytoIaccia.

REFERENCE
 1
 Neelam, A., Atkinson, H.J., Mcpherson, M.J. and Thomas, C.J.R.
 Plant cell death system
 Patent: WO 023107-A.1 25-APR-2002;
 JOURNAL CAMBRIDGE ADVANCED TECH (GB)

FEATURES
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 /db_xref="taxon:3527"

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misc_feature complement (735..776)

misc_feature /note="Binding site for primer PSXDR"

variation 736..777

750..759

/note="Sequence replacing removed XbaI site"

complement (922..945)

/note="Binding site for primer PPS2SR"

ORIGIN

Alignment Scores:
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 Score: 1352.00 Matches: 262
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 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 99.6% Indels: 0
 DB: 6 Gaps: 0

US-09-978-274A-4 (1-263) x AK427702 (1-945)

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 DB 73 ATTAATACATCACTTGTATGCTGAAATGCCACATTAACAATATGCCACCTTTATG 132
 QY 22 GlySerLeuArgAaSnAlaLysAaSPProLyLeuLySeyTyTgLyileProMetLeu 41
 DB 133 GAATCTCTGTAATCAAGAAAGATCCAAACCTAAATGCTATGCAATACCAATGCTA 192
 QY 42 ProAaPThraAaSerThrProLyTyTleuLeuValLyLeuGlnGlyAlaAaSnLeu 61
 DB 193 CTGATATCAATTCGACCCCTTAAGTACTTAATGGTTAACTCCAAAGTGGCAACCTA 252
 QY 62 ThrLleThrLeuMetLeuArgAaAaSnLeuTyTAlaMetGlyTyTserAaSPProPhe 81
 DB 253 ACCATTAACATATGCTGAGCAAACTTAATCTTACGTATGGCTATTTCTGATCCCTTC 312
 QY 82 AaSnGlyAaSnLySeyTyTgLyilePheAaAaSPilleThraAaPThrGlnArgThra 101
 DB 313 AATGGCAATAGAGTGTGTTACCATATATTTAATGATATTAACAAGCACCGAAGCACTGAT 372
 QY 102 ValGlyAaSnThrLeuCySeySerSerSerSerArgValAlaMetSerilleAaSnTy 121
 DB 373 GTGGAAATATCTCTTGTCTCAAGTTCAGTTCTGTTGCAATGTCATTAATCAAT 432

Qy 122 SerLeuTYrProThrMetGluLysValaGluValaansSerArgAsnGluValaGlnLeu 141
Db 433 AGCTTATTCGACCATGGAAGAAAGAAAGAAAGTCAAGAAATCAAGTCCAAATTG 492
Qy 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValaAspSerPheProVal 161
Db 493 GGAATTCAAATATCTACGACGATGACATTCGAAAAATCTCTGGAGTTGATTCAATCCCTGTA 552
Qy 162 LysThrGluAlaPhePheLeuLeuValaIleGlnMetValaSerGluAlaAlaArgPhe 181
Db 553 AAAACGTAGGCTTTTCTTCTACTGTACCATCCAAATGTTTCAGAGCGACGCGGATTC 612
Qy 182 LysTrillegluAsnGlnValaLysThrAsnPheAsnArgAlaPheTYrProAspProLys 201
Db 613 AAGTACATAGAGAACCAAGTCAAGCTAATTTTATAGCATTTTACCTGATCCCAAA 672
Qy 202 ValIleAsnLeuGluGluLysTrpGlyLysIleSerGluAlaIleHisAsnAlaLysAsn 221
Db 673 GTAATTAAATTTGGAGAGAGAGTGGGGCAAAATCTCTGAGGCAATTCAAATGCCAAGAT 732
Qy 222 GlyValaLeuProLysProLeuGluLeuValaAspAlaLysGlyThrLysTrpIleValLeu 241
Db 733 GGGGCTTTACCAACCACTGAGCTAGTGAGTGCAAAGGTACCAAGTGAATGTTCTT 792
Qy 242 ArgValaAspGluIleAsnArgAspValaAlaLeuLeuLysTYrValaAsnGlyThrCysGln 261
Db 793 AGACTGATGAAATCAATCGTGAATGGCACTCTTAAAGTACGTTAATGGAACCTGTGAC 852
Qy 262 ThrThr 263
Db 853 ACAACT 858

RESULT 3
PAPASRIP 1249 bp mRNA linear PLN 18-APR-2005
LOCUS P.americana mRNA for pokeweed antiviral protein. X98079
DEFINITION X98079.1 GI:1707648
ACCESSION PAP-S.gene; pokeweed antiviral protein (PAP); ribosome-inactivating
VERSION X98079.1 GI:1707648
KEYWORDS Protein.
SOURCE Phytolacca americana (American pokeweed)
ORGANISM Phytolacca americana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE 1 Poyet,J.L. and Hoeveler,A.
AUTHORS cDNA cloning and expression of pokeweed antiviral protein from
TITL seeds in Escherichia coli and its inhibition of protein synthesis
in vitro
JOURNAL FRBS Lett. 406 (1-2), 97-100 (1997)
PUBMED 9109394
REFERENCE 2 (bases 1 to 1249)
AUTHORS Poyet,J.L.
TITL Direct Submission
JOURNAL Submitted (22-MAY-1996) J.L. Poyet, Laboratoire de
Biochimie-Biologie Moléculaire, UFR Sciences et Techniques, 16
rue de Gray, 25030 Besancon Cedex, FRANCE
REMARK Revised by author 20-SEP-1996
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Score: 1352.00 Matches: 262
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.6% Indels: 0
DB: 15 Gaps: 0
US-09-978-274A-4 (1-263) x PAPASRIP (1-1249)
Qy 2 IleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTYrAlaThrPheMet 21
Db 178 ATAAATACGATCACCTTGTGATGCTGGAATAGCCACCAATTAAACAATATGCACTTATATG 237
Qy 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTYrGlyIleProMetLeu 41
Db 238 GAATCTCTTGATATCAAGAGAAAGATCCAAACTTAAATGCTATGAGCATRCCAAATGCTA 297
Qy 42 ProAspThrAsnSerThrProLysTYrLeuLeuValaLysLeuGlnGlyAlaAsnLys 61
Db 298 CCTGATATCTAATTCAGCCCTTAAGTACTTATGGTTAAGCTCCAAAGGTGCAAACTTAAA 357
Qy 62 ThrIleThrLeuMetLeuAlaGlyAsnAsnLeuTYrValMetGlyTYrSerAspProPhe 81
Db 358 ACCATTACACTTAATGCTGAGACGAATTAATTAATGATGAGGCTATTCGATCCCTTC 417
Qy 82 AsnGlyAsnLysCysArgTYrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db 418 AATGGCAATTAATGATGCTTACCATTAATTTATATGATATTAACAGCACCGAAGCATGAT 477
Qy 102 ValGluAsnThrLeuCysSerSerSerSerSerArgValaIleMetSerIleAsnTYrAsn 121
Db 478 GTGAGATATATCTTTCTCAAGTTTAAATGTTCTCGTTCGATCAATGTCATTAACTAACAT 537
Qy 122 SerLeuTYrProThrMetGluLysValaGluValaansSerArgAsnGlnValaGlnLeu 141
Db 538 AGCTTATATTCGACCAAGAAAGAAAGAAAGTAAATCAAGAAATCAAGTCCAAATTG 597
Qy 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValaAspSerPheProVal 161
Db 598 GGAATTCAAATATCTACGACGATGACATTCGAAAAATCTCTGAGTTGATTCAATCCCTGTA 657
Qy 162 LysThrGluAlaPhePheLeuLeuValaIleGlnMetValaSerGluAlaAlaArgPhe 181
Db 658 AAAACGTAGGCTTTTCTTCTACTGTAGTCCATCAATATGTTTCAGAGCGACGCGCATTC 717
Qy 182 LysTrillegluAsnGlnValaLysThrAsnPheAsnArgAlaPheTYrProAspProLys 201
Db 718 AAGTACATAGAGAACCAAGTCAAGATTAATTTAATGACATTCATCCCTGATCCCAAA 777
Qy 202 ValIleAsnLeuGluGluLysTrpGlyLysIleSerGluAlaIleHisAsnAlaLysAsn 221

Db	778	GPAATTAATTTCGAGAGACGTGGGGCAAAATCTTGAGGCATTTCAATGCCAAGAT	837
Oy	222	GIYAlALEuProlYeProLeugLUeUvAlJaPaLaLyBgLYThrLyeTrPlleValIeu	241
Db	838	GGGGCTTTCACCMAACTCTTAGAGCTAGTGGAATGCCAAGTACCAAGTGGATGATCTT	897
Oy	242	ATGVAlAPeGLuILASAsArhApVAlAlAleuLeuLYTYrVAlJAsnGLYThrCtyeGln	261
Db	898	AGAGCGATGAATCATCATCGATGATGCGACTCTTAAGTACGTTAAATGAACTCTGAG	957
Oy	262	ThrThr 263 	
Db	958	ACAACT 963	
RESULT 4	AB071855	786 bp DNA linear	PLN 19-MAR-2002D
LOCUS	AB071855	Phytolacca americana paps2 gene for PAP-S2, partial cds.	
DEFINITION	AB071855		
ACCESSION	AB071855.1	GI:19570839	
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS	Honjo,E. and Watanabe,K.		
TITLE	Cloning of genomic DNA encoding two types of pokeweed antiviral protein in seeds, PAP-S1 and PAP-S2, and functional comparison of their recombinant proteins with other PAP isoforms		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 786)		
AUTHORS	Watanabe,K. and Honjo,E.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-SEP-2001) Keiochi Watanabe, Saga University,		
	Department of Applied Biological Sciences; Honjo-machi, Saga city,		
	Saga 840-8502, Japan (E-mail:watake@cc.saga-u.ac.jp,		
	Tel:81-952-28-8774, Fax:81-952-28-8774)		
FEATURES	Location/Qualifiers		
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	KTEAFPLVLAVQMSSEARFKTIENQVTINRRFAIPDPKVITLSEKMGKISEAIHNA		
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ORIGIN			
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Query Match:	98.2%	Indels:	0
DB:	15	Gaps:	0
US-09-978-274A-4 (1-263) x AB071855 (1-786)			
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Db		61	GAATCTCTCGTAATCAAGCAGAAAGATCCAAAATCAAATGTCTTAGGCATCCAAATGCTA	120
Oy		42	ProaepThraansarThProLyvTyrleneuVallysleugInglYlaAsnLeuys	61
Db		121	CCTGATACATAATTGACCCCCCTAAGTACTTATTTGGTTAAGCTCAAGGGTGCAACCTTA	180
Oy		62	ThrileThreuleMeleuArGaAsnLeuTyValMetGlyTYrSeraspProbe	81
Db		181	AACATTACACATNAAGCTGAGACGAATTAATTAAACGTAAGGGGCTATTTCGATCCCCTTC	240
Oy		82	AanGlyAenLYsvCyAxyTYrHiallIephensnapriIethrsertAnGluayxThrasP	101
Db		241	AATGGCAATNAGTGTGCTTACCAATATTTATATATATATACAAACCCGAAACGACATGAT	300
Oy		102	ValGluAenthreLyuCyserSerSerSerSerXargValAlametserlleasnyTrasn	121
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Oy		122	SerleutyrrProthmetGluLyalyeAlagluValamserrAgaengInvalGlnleu	141
Db		361	AGCTTATNATCCGACCTTGAAAAAAGAACAGAAAGTAAATCAAGAAAGTCAAGTCCAATYG	420
Oy		142	GlylllegInlleuserserSeraPlleglylsrIlesergilyValaaSPserPhaProval	161
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Oy		162	LysThrgluAlaphelheLeuValalIegInMecValSergluAlaalaxyphe	181
Db		481	AAAACGTGAGGCTTTTTTCTACTGTGAGCCATCCAAAATGTTTCAAGAGCGACGCCGATTC	540
Oy		182	LysTYrIllegluAangInvalIyeThrasnPheasnrglaaPeTYrPrroaspProlys	201
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Db		721	AGAGTGAATGAATCAATCGTGAATGTGGCACTCTTAAGTACGTTAATGACACTGTCTCAG	780
Oy		262	ThrThr 263	
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RESULT 5				
AX427720				
LOCUS	AX427720	1092 bp	DNA	linear PAT 20-JUN-2002
DEFINITION	Sequence 19 from Patent WO023107.			
ACCESSION	AX427720			
VERSION	AX427720.1	GI:21537829		
KEYWORDS	.			
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS	1			
TITLE	Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.			
JOURNAL	Plant cell death system Patent: WO 023107-A 19 25-APR-2002;			
FEATURES	CAMBRIDGE ADVANCED TECH (GB)			
Source	Location/Qualifiers 1..1092 /organism="synthetic construct" /mol_type="unassigned DNA"			

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ORIGIN

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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 96.7% Indels: 0
DB: Gaps: 0

US-09-978-274a-4 (1-263) x AX42720 (1-1092)

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QY 21 MetGluSerLeuArgAsnGlnAlaIleAspProIleLeuIleValaIleProMet 40
DB 61 ATGGAATCTCTTGATATCAAGGAAAGATCCAAATCAATATGATGCAATCCATG 120
QY 41 LeuProAspThrAsnSerThrProIleValaIleLeuValaIleGlnIleVala 60
DB 121 CTACCGATGATCTAATTCAGCCCTTAAGTACTTATGTTAGTCAAGGTCGAAACCTA 180
QY 61 LysThrIleThrIleMetLeuArgAsnAsnLeuValaMetGlyTyrSerAspPro 80
DB 181 AAAACCTTACATTAATGCTGAGAGCAAAATTAATTAACGATGGCTATTCGATCCC 240
QY 81 PheAsnGlyAsnIleValaIleAspIleThrSerThrGluArgThr 100
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DB 301 GATGTGAGAAATCTCTTCTCAAGTTCTAGTTCTGTTGCAATGTCATTAACTAC 360
QY 121 AsnSerLeuIleProThrMetGluValaIleGluValaIleAsnSerArgAsnGlnIle 140
DB 361 AATAGCTTAATATCCGACCAATGAAAGAAAGCAAAATTAATCAAAATTCAGATCC 420
QY 141 LeuGlyIleGlnIleLeuSerSerSerAspIleGlyIleSerGlyValaIleAspSerPhePro 160
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QY 161 ValIleThrGluAlaPhePheLeuLeuValaIleGlnMetValaIleSerGluAlaIle 180
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QY 181 PheIleValIleGluAsnGlnIleValaIleThrAsnPheAsnArgAlaPheTyrProAspPro 200
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DB 601 AAAGTATTAATCTTGAAGGAGAGTGGGCAAAATCTCTGAGGCAATTCAGATCCAG 660
QY 221 AsnGlyValaIleAspProIleValaIleAspAlaIleValaIleValaIleVala 240
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RESULT 6
LOCUS AB071854 783 bp DNA linear PLN 19-MAR-2002
DEFINITION Phytolacca americana papal gene for PAP-S1, partial cds.
ACCESSION AB071854
VERSION AB071854.1 GI:19570837
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Phytolacca viridiflora; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS Honjo, E. and Watanabe, K.
TITLE Cloning of genomic DNA encoding two types of pokeweed antiviral
protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
their recombinant proteins with other PAP isoforms
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 783)
AUTHORS Watanabe, K. and Honjo, E.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2001) Keiichi Watanabe, Saga University,
Department of Applied Biological Sciences, Honjo-machi, Saga city,
Saga 840-8502, Japan (E-mail: watake@cc.saga-u.ac.jp,
Tel:81-952-28-8774, Fax:81-952-28-8774)

FEATURES
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ORIGIN

Alignment Scores:
Pred. No.: 5,71e-88 Length: 783
Score: 1099.50 Matches: 218
Percent Similarity: 88.2% Conservative: 13
Best Local Similarity: 83.2% Mismatches: 30
Query Match: 81.0% Indels: 1
DB: Gaps: 1

US-09-978-274a-4 (1-263) x AB071854 (1-783)

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DB 1 ATCAATACGATTAATCGTTCGAGCTGAAATGCAACATTAACAGATATGCTATCTTATG 60
QY 22 GluSerLeuArgAsnGlnAlaIleAspProIleLeuIleValaIleProMetLeu 41
DB 61 GAATCTCTTGATATGAAGGAAAGATCCAGTTTAAAGTATTAAGATTAACCAATGTTG 120
QY 42 ProAspThrAsnSerThrProIleValaIleLeuValaIleGlnIleValaIleAsnLeu 61
DB 121 CCCAATATCAATTCACATCAAGTACTGTTGATTAAGTCCAAAGTCCAAAGCTTAATA 180
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KEYWORDS	SOURCE ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	PUBLISHED	REFERENCE	AUTHORS	TITLE	JOURNAL		
Phytolacca americana (American pokeweed)	Phytolacca americana	Phytolacca americana (American pokeweed)	Bukarjota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.	1 (bases 1 to 942)	zhao, Y., Wang, X., Zhou, G. and Li, H.	A pokeweed antiviral protein gene in roots of Phytolacca americana	Acta Virol. 48 (2), 131-132 (2004)	15462289	2 (bases 1 to 942)	Zhao, Y., Wang, X. and Li, H.	Direct Submission	Submitted (11-FEB-2004) Plant Virology, Institute of Plant Protection, CAAS, No.2 Yuanmingyuan Road West, Beijing 100094, P.R. China

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Pred. No.:	1,666-83
Score:	1050.00
Percent Similarity:	87.0%
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US-09-978-274A-4 (1-263) x AY547315 (1-942)	
Length:	942
Matches:	200
Conservative:	28
Mismatches:	34
Indels:	0
Gaps:	0

[illegible]

Db	427	AGTGAATTC	CCAACTTGGAAATCAAAAGCGGAGTAAATCAAGAAATCAGGTC	CAACTG	486
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Db	487	GGAAATCAAA	TACTGCAGATTAATTCGAAAGATTTCTGGAGTATGTCATTC	ACTGAG	546
Qy	162	LYSTHRI	IVALAPHEPHELEULEVALAII	EGINECTVALISERGI	VALAIIAARPHe 181
Db	547	AAACCGAAG	CGCAATTCCTATGGTAGCCATTA	CAAAATGTAATCAGAGCGCAAGATTC	606
Qy	182	LYSTYRI	IEGIUASNGINVALLYSTHRA	SPHEASNAI	ALAPHeTyrProAspP
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Qy	222	GLYAL	ALAEUPROLYSPROLEUGIULEVALASPA	IALYSGIYTHRYST	TRIIIEVALLEU 241
Db	727	GGAGTTT	TACCCAAACCTCTGAGCTAGTGGATGCCAGTGGCCAAATGGAGTATGTTG		786
Qy	242	ARGVAL	ASPGIUIIEASNAI	ASPVAlAIALEULE	ULYSTYRVALASNGIYTHRCysGln 261
Db	787	AGAGTGA	TGAAATCAAGCCGTAGTACACTTTAA	CTACAGTGGTGGAGCTGTGAG	846
Qy	262	THYTR	263		
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LOCUS	942 bp	mRNA	linear	PLN 05-APR-2004
DEFINITION	Phytolacca americana antiviral protein (PAP) mRNA, complete cds.			
ACCESSION	AY572976			
VERSION	AY572976.1	GI:45826466		
KEYWORDS				
SOURCE				
ORGANISM	Phytolacca americana (American pokeweed)			
REFERENCE	Phytolacca americana			
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolacaceae; Phytolacca.			
REFERENCE	1 (bases 1 to 942)			
AUTHORS	Xiao, Z.A. and Jiang, Y.			
REFERENCE	A gene encoding the pokeweed antiviral protein in the leaf of Phytolacca americana			
REFERENCE	2 (bases 1 to 942)			
AUTHORS	Xiao, Z.A.			
REFERENCE	Direct Submission			
REFERENCE	Submitted (13-MAR-2004) College of Life Sciences, Beijing Normal University, No. 19 Xijiekouwai Street, Haidian District, Beijing 100875, China			
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Alignment Scores:

Pred. No.: 1,66e-83 Length: 942
 Score: 1050.00 Matches: 200
 Percent Similarity: 87.0% Conservative: 28
 Best Local Similarity: 76.3% Mismatches: 34
 Query Match: 77.4% Indels: 0
 DB: 15 Gaps: 0

US-09-978-274A-4 (1-263) x AY572976 (1-942)

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DB 67 gtaaatracaaatcattacaaatgttggaagaccacattgacaaatgacacattttctg 126
QY 22 gluserleuarganginalayaspProlyseuleuyscytyrtyrtyrtyrtyrtyrtyr 41
DB 127 aatgattcttctgtaataagacgaagacacattgtaataatgtaataatgtaataatgta 186
QY 42 proaspthrasensthrProlystyryleuleuValyleuenglyalaaasleuLys 61
DB 187 cccaatracaaatcattacaaatgttggaagaccacattgacacattttctg 246
QY 62 thrllethrlleuethleuargasnaaleuLysValmetcglytyrserapprophe 81
DB 247 accatcacactaatgctgagacgaacaaatgttgtaataatgctgtaataatgctgta 306
QY 82 aenglyasnytyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyr 101
DB 307 gaacacaaatracaaatcattacaaatgttggaagaccacattgacacattttctg 366
QY 102 valgluasnthrlleuyscyserseuSerseuSerseuSerseuSerseuSerseuSer 121
DB 367 gtagaagacttctgtaataatgctgtaataatgctgtaataatgctgtaataatgctgta 426
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DB 727 ggaatttctcattggaatcgaacgaatcgaacgaatcgaacgaatcgaacgaatcgaac 786
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RESULT 10

PAPAP 1164 bp mRNA linear PLN 18-NOV-1991
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 DEFINITION X55383
 ACCESSION X55383.1 GI:20421
 VERSION

KEYWORDS

antiviral protein; cell wall protein; PAP gene; ribosome inactivating protein.

SOURCE

Phytolacca americana (American pokeweed)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE

1 (bases 1 to 1164)
 Ian O., Chen, Z. C., Antoniw, J. F., and White, R. F.
 Isolation and characterization of a cDNA clone encoding the anti-viral protein from Phytolacca americana

TITLE

Plant Mol. Biol. 17 (4), 609-614 (1991)

JOURNAL

1912488

PUBMED

2 (bases 1 to 1164)
 Antoniw, J. F.
 Direct Submission
 Submitted (05-NOV-1990) Antoniw, J. F., AFRC Inst of Arable Crops Research, Dept. of Plant Pathology, Rothamsted Experimental Station, Harpenden, Herts, AL5 2JQ, UK

FEATURES

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CDS

2. 943
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ORIGIN

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US-09-978-274A-4 (1-263) x PAPAP (1-1164)

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QY 2 11aasnthrllethrpheapalaaglyasnaalethrlleasnytyrallathrphemec 21
DB 67 gtaaatracaaatcattacaaatgttggaagaccacattgacaaatgacacattttctg 127
QY 22 gluserleuarganginalayaspProlyseuleuyscytyrtyrtyrtyrtyrtyrtyr 41
DB 127 aatgattcttctgtaataatgacgaagacacattgtaataatgtaataatgtaataatgta 187
QY 42 proaspthrasensthrProlystyryleuleuValyleuenglyalaaasleuLys 61
DB 187 cccaatracaaatcattacaaatgttggaagaccacattgacacattttctg 247
QY 62 thrllethrlleuethleuargasnaaleuLysValmetcglytyrserapprophe 81
DB 248 accatcacactaatgctgagacgaacaaatgttgtaataatgctgtaataatgctgta 307
QY 82 aenglyasnytyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyr 101
DB 308 gaacacaaatracaaatcattacaaatgttggaagaccacattgacacattttctg 367

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JOURNAL Patent: US 5633155-A 1 27-MAY-1997;
FEATURES Location/Qualifiers
source 1..1195

ORIGIN

Alignment Scores:

Pred. No.:	2.16e-83	Length:	119
Score:	1050.00	Matches:	200
Percent Similarity:	87.0%	Conservative:	28
Best Local Similarity:	76.3%	Mismatches:	34
Query Match:	77.4%	Indels:	0
DB:	6	Gaps:	0

US-09-978-274A-4 (1-263) X I43835 (1-1195)

QY	2	11	leamThrIleThrPheAbaPalaGlyAsnAlaThrIleAsnIleGlyTyrAlaThrPheMet	21
Db	99	GTGAATCAATCATCTTCATCAATGTTGGAAAGTACACCAATTAAGCAATACGCCACTTTCTG	150	
QY	22	GlusIleuLeuArgAnginalAlaIysAspProIysLeuLysCysTyrGlyIleProMetLeu	41	
Db	159	AATGATCTTGTAATGTAAGAGGAAGATCCAAAGTTTAAATGCTAATGAAATACCAATGCTG	210	
QY	42	ProAspIhrzrAsnSerThrProIysTyrIleuLeuValLysLeuGlnGlyAlaAsnLeuLys	61	
Db	219	CCCAATCAAAATCAAAATCCAAAGTACGAGTGGTGGTGAACCTCCAAAGTTCAAAATAAAAA	270	
QY	62	ThrIleThrIleuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe	81	
Db	279	ACCATCACTAATATGCTGAGACCAAAACAATTTGTATGTATAGGTATTTCTGATCCCTTT	330	
QY	82	AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp	101	
Db	339	GAACAACAAATAAAGTCGTTACCATATCTTTAATGATATCTCAAGTACGAAGCCAAAGAT	390	
QY	102	ValGluAsnThrIleuCysSerSerSerSerSerArgValAlaMetSerIleAsnIhrzrAsn	122	
Db	399	GTGAAGCTACTCTCTTGCCCAAAATGCAAAATCTCGGTGATGTAAGAAACAATTAACCTTGAT	450	
QY	122	SerLeuTyrProThrMetGluIysValAlaGluValAsnSerArgAsnGlnValGlnLeu	142	
Db	459	AGTGAATATCCAACTTGGAAATCAAAAGGGGAGTAATCAAGAAGTCAATCCAACTG	510	
QY	142	GlyTyrIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPheProVal	162	
Db	519	GGAATTCAAATTAATCTCCACAGTAAATTTGGAAAGATTTCTGAGATGATGCATTCACCTGAG	570	
QY	162	LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaIaPhe	182	
Db	579	AAAACCGAACCCGAATTCCTATTGGTAGCCATACAAATGATATCAAGGGCAGCAAGATTC	630	
QY	182	LysTyrTyrIleGluAnginalIysTyrAsnPheAsnArgAlaPheTyrProAspProLys	202	
Db	639	AAGTACATAGAGATCAGGTGAAGAACTAATTTTAAACAGAGCATTCAAACCTTAATCCAAA	690	
QY	202	ValIleAsnLeuGlnGluIysTyrProGlyLysIleSerGluAlaIleHisAsnAlaLysAsn	222	
Db	699	GTACTTAATTTGGCAAGACATGGGGGTAAAGATTTCAACAGCAATTCATGAATGCCAAGAT	750	
QY	222	GlyAlaLeuProLysProLeuGlnGluLeuValAspAlaLysGlyThrLysThrIleValLeu	242	
Db	759	GGAAGTTTACCCAAACCTCTCGAGCTAGTGGATGCCAGTGGTGGCCAAAGTGAATGTGTG	810	
QY	242	ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsnGlyThrCysGln	262	
Db	819	AGAGTGAATGAATCAAGCCTGATGTAGACACTTAACTAAGCTTGGTGGAGGCTGTGAG	870	
QY	262	ThrThr	263	
Db	879	ACAAT	884	

RESULT 13

LOCUS	155866	1195 bp	DNA	linear	PAT 07-OCT-1997
DEFINITION	Sequence 1 from patent US 5648234.				
ACCESSION	155866				
VERSION	155866.1	GI:2476660			
KEYWORDS					
SOURCE	Unknown.				

REFERENCE	1 (bases 1 to 1195)
AUTHORS	Moorn,Y.-H., Jeon,H.-S., Choi,K.-W., Lee,K.-H. and Kim,M.-K.
TITLE	Expression vector for Phytolaccase anti-viral protein
JOURNAL	Patent: US 5648234-A 1 15-JUL-1997;
FEATURES	Location/Qualifiers
source	1..1195

ORIGIN

Alignment Scores:

Pred. No.:	2,16e+83	1199
Score:	1050.00	Matches:
Percent Similarity:	87.0%	Conservative:
Best local Similarity:	76.3%	Mismatches:
Query Match:	77.4%	Indels:
DB:	6	Gaps:

US-09-978-274A-4 (1-263) X I55866 (1-1195)

Oy		2	LleasnhrilrlerhpheapalaglVasnaIThrilleamnystrAlatrrhemec	21
Dd		99	GtGAAATCAATCATCTGAAGTGGAAAACCAACATTGGCAAATAGCCACTTTTCG	158
Oy		22	GlusertleuarqanginalalyAspProlyseuleysCystrgilylPromeLeu	41
Dd		159	AATGATCTCGTGATAGAAGGAAAGATCCAAGTTTAATAATGCATAGSAATACCAGTCTG	218
Oy		42	ProAsphTrhnserrThrProlystrYrleuleuValylseungngiyalaenleulyS	61
Dd		219	CCCMAATCAAAATCCAAATCCAAAGTAGTGTGGTGAAGCTCCAAAGGTTCAAAATAAAAA	278
Oy		62	ThrilethruemetleuarqArqAsnAsnLeutyryValmetglYrTSerAspProPh	81
Dd		279	ACCATCACAATAGCTGAGACCAACAAATTTGTATGTATGGGTTATTTCTGATCCCTTT	338
Oy		82	AsnqlVasnuLyCyArgrYrhalelpheAsnaplleThrserrThrguaigrThrasp	101
Dd		339	GAACCAATAAAGTGGTACCATATCTTTAATAGATATCTCAGGATCAAGCCCAAGAT	398
Oy		102	ValGlubsnhrleuCyserSerSerSerSerArgvalAmetserrlleantYrAsn	121
Dd		399	GTMAGACTACTCTTTCGCCAAAGCCAAATTCGCGTGAATAAAACATPAACTTGTAT	458
Oy		122	SerdenuyrProThrmecglulysylsalagluValasnserrArqaenglnValglneu	141
Dd		459	AGTGAATATCAACATTCGATGAAATCAAAAGCGGAGTAAATCAAGAAATCAAGTCCACTG	518
Oy		142	GlyllleglnlleuseSerAspilleglylysrilleserglyValaspSerpheProval	161
Dd		519	GGATTTCAAAATACTCGACAGTAATATTGGAAAGATTTCTCGAGAGATGATTCATTCACGTAG	578
Oy		162	LysThrcilualAphePheleuleuValAlilleglmerValserguialaIaaargPhe	181
Dd		579	AAAACCGAAGCCGAATTCCTATTGTGAGCCATCAAAATGGTATCAAGGCGACGACGATTC	638
Oy		182	LysEYrilleglubsnnglnValylsrThAsnpheAsnarghlaPheYrProAspProlys	201
Dd		639	AAGTACATAGAGATCAGTGAATAACTAATTTTAACAGACATTCAACCTAATCCAAA	698
Oy		202	ValilleasneugluguluystrPgilylysllesergluallelhbaenalalyAsn	221
Dd		699	GTCATTAATTCGACAGACATGGGGTGAATTTCAACGCAATTCATGATGCGCAAGAT	758

Qy 222 G1yAlaleuProlysProleuGluLeuValAspAlaLysGlyThrIleTyrPheValIleu 241
Db 759 GGAATTAAACCAACCTCTGAGCTATGATGCAATGCGCAATGATAGTGTG 818
Qy 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuIleTyrValAsnGlyThrCysGln 261
Db 819 AGAGTGAATGAATCAACCTGATGACCTTAACCTAGTGTGGAGCTGTGAG 878
Qy 262 ThrThr 263
Db 879 ACAACT 884

RESULT 14
AR009535 1379 bp DNA linear PAT 04-DEC-1998
LOCUS AR009535
DEFINITION Sequence 1 from patent US 5756322.
ACCESSION AR009535
VERSION AR009535.1 GI:3968340
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1379)
AUTHORS Tumer,N.B.
TITL Pokedeod antiviral protein mutants
JOURNAL Patent: US 5756322-A 1 26-MAY-1998;
FEATURES
source location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 2.54e-83 Length: 1379
Score: 1050.00 Matches: 200
Percent Similarity: 87.0% Conservative: 28
Best Local Similarity: 76.3% Mismatches: 34
Query Match: 77.4% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-4 (1-263) x AR009535 (1-1379)

Qy 2 11eAnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnIleTyrAlaThrPheMet 21
Db 291 GTGAATCAATCATCTACATGTTGGAAGTACCACTTACCAATACGCACTTTCTG 350
Qy 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeu 41
Db 351 AATGATCTTCGTATGAAGCAAGATCCAGTTTAAATGCTATGGAATACCAATGCTG 410
Qy 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
Db 411 CCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 470
Qy 62 ThrIleThrIleuLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
Db 471 ACCATCACTTAATGCTGAGACGAAACAAATTTGATGAGGGGATTTCTGATCCCTT 530
Qy 82 AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db 531 GAAACCAATTAATTCGTTACCATATCTTTAATGATATCTCAGGTACGAAACGCAAGAT 590
Qy 102 ValGluAsnThrIleuLysSerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
Db 591 GTAAAGCTACTCTTCCCAAAAGCCAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 650
Qy 122 SerLeuTyrProThrMetGluLysValGluValAsnSerArgAsnGlnValGlnLeu 141
Db 651 AGTGAATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 710
Qy 142 GlyIleGlnIleuLeuSerSerAspIleGlyLysIleSerGlyValAspSerPheProVal 161

Db 711 GGAATCAAAATCTCGACATTAATATGAAAGATTTCTGAGATGATGATCATCACTGAG 770
Qy 162 LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 181
Db 771 AAAACCAAGCCGAATTCCTAATGTTAGCCATCAAAATGATATCAAGGACGAAAGATTC 830
Qy 182 LysTyrIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyrProAspProLys 201
Db 831 AAGTACATAGAGATCAAGTGAATCAATTAATTTTAACAGACATTCACCTTAATCCCAA 890
Qy 202 ValIleAsnLeuGlnGluLysTyrGlyLysIleSerGluAlaIleHisAsnAlaLysAsn 221
Db 891 GTACTTAATTTGCAAGAGACATGGGTTAAGATTTCAACAGCAATTCATGATGCCAAGAT 950
Qy 222 G1yAlaleuProlysProleuGluLeuValAspAlaLysGlyThrIleTyrPheValIleu 241
Db 951 GGAATTAAACCAACCTCTGAGCTATGATGCAATGCGCAATGATAGTGTG 1010
Qy 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuIleTyrValAsnGlyThrCysGln 261
Db 1011 AGAGTGAATGAATCAACCTGATGACCTTTAAACTAGTGTGGAGCTGTGAG 1070
Qy 262 ThrThr 263
Db 1071 ACAACT 1076

RESULT 15
AR136704 1379 bp DNA linear PAT 16-JUN-2001
LOCUS AR136704
DEFINITION Sequence 1 from patent US 6137030.
ACCESSION AR136704
VERSION AR136704.1 GI:14477376
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1379)
AUTHORS Tumer,N.B.
TITL Pap mutants that exhibit anti-viral and/or anti-fungal activity in
JOURNAL plants
FEATURES Patent: US 6137030-A 1 24-OCT-2000;
source location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 2.54e-83 Length: 1379
Score: 1050.00 Matches: 200
Percent Similarity: 87.0% Conservative: 28
Best Local Similarity: 76.3% Mismatches: 34
Query Match: 77.4% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-4 (1-263) x AR136704 (1-1379)

Qy 2 11eAnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnIleTyrAlaThrPheMet 21
Db 291 GTGAATCAATCATCTACATGTTGGAAGTACCACTTACCAATACGCACTTTCTG 350
Qy 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeu 41
Db 351 AATGATCTTCGTATGAAGCAAGATCCAGTTTAAATGCTATGGAATACCAATGCTG 410
Qy 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
Db 411 CCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 470
Qy 62 ThrIleThrIleuLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
Db 471 ACCATCACTTAATGCTGAGACGAAACAAATTTGATGAGGGGATTTCTGATCCCTT 530

QY 82 AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
DB 531 GAAACCAATTAATGATGCTGATTCATATCTTAATGATATCTCAGGTACTGAACGCAAGAT 530
QY 102 ValGluAsnThrLeuCysSerSerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
DB 591 GTAGAGACTACTCTTTGGCCCAATTCGCTGTGTAGTAAACATMAACTTTGAT 650
QY 122 SerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAsnGluValGluLeu 141
DB 651 AGTCGATATCCAACTTGGAAATCAAAAGCGAGTAAATCAAGAACTCAGTCCAACTG 710
QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPheProVal 161
DB 711 GGAATTCAAATACTCGACAGTAAATATGGAAGATTTCTGAGTGATGATCATTCACTGAG 770
QY 162 LysThrGluAlaPhePheLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 181
DB 771 AAAACGAAAGCCGAATTCCTAATGTGTAGCCATCAAAATGGTATCAGAGCAGCAAGATTC 830
QY 182 LysTyrIleGluAsnGluValLysThrAsnPheAsnArgAlaPheTyrProAspProLys 201
DB 831 AAGTACATAGAGAACTCAGTGAAACTAATTTTAACAGACATTCAACTTAATCCCAA 890
QY 202 ValIleAsnLeuGluGluLysTyrGlyLysIleSerGluAlaIleHisAsnAlaLysAsn 221
DB 891 GTACTTAATTTGCAAGAGACATGGGGTAAATTTCAACAGCAATTCATGATGCCAAGAT 950
QY 222 GlyAlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrLysTyrPileValLeu 241
DB 951 GGAGTTTACCCCAACCTCTCGAGCTAGTGATGCCAGTGTGCCAAGTGATAGTTTG 1010
QY 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsnGlyThrCysGln 261
DB 1011 AGAGTGAATGAATCAAGCTGATGACACTTAAACTACGTTGGTGGAGCTGTGAG 1070
QY 262 ThrThr 263
DB 1071 ACNACT 1076

Search completed: April 9, 2006, 07:31:35
Job time : 6007.59 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 9, 2006, 00:56:13 ; Search time 697.998 Seconds
(without alignments)
251.204 Million cell updates/sec

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Perfect score: 1357
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Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 4996997 beqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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-OUTFMT=p2ts -NORM=ext -HEADP12Z=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03h
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-WARN TIMEOUT=30 -THRAIDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELBEXT=7

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13: geneseqn2004a:*
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15: geneseqn2005a:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

SUMMARIES						
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1	1357	100.0	792	6	AAD47716	Aad47716 Pokeweed
2	1352	99.6	945	6	AAD47715	Aad47715 Pokeweed
3	1312	96.7	1092	6	AAD47729	Aad47729 Pokeweed
4	1052	77.5	882	2	AAT99556	Aat99556 Phytolacc

5	1050	77.4	1379	3	AAZ45197	Aaz45197	Wild-type
6	1050	77.4	1379	6	AAZ59220	Aaz59220	Pokeweed
7	1050	77.4	1379	6	AAZ42738	Aad42738	Pokeweed
8	1050	77.4	1379	10	ADJ05787	Adj05787	DNA encod
9	1048	77.2	1378	12	ADG76061	Adg76061	American
10	1047	77.2	1379	4	AAC87929	Aac87929	P. american
11	1044	76.9	1164	11	ADM74765	Adm74765	HIV-1 inh
12	1044	76.9	1195	2	AAO56672	Aao56672	Sequence
13	1042	76.8	1378	6	AAAD42735	Aad42735	Pokeweed
14	1042	76.8	1379	3	AAZ59221	Aaz59221	Variant P
15	1041	76.7	1164	11	ADM74751	Adm74751	HIV-1 inh
16	1034	76.2	1195	2	AAQ81457	Aaq81457	Phytolacc
17	1014.5	74.8	2472	2	AAQ33967	Aaq33967	Pokeweed
18	977.5	72.0	2369	2	AAQ39557	Aaq39557	Phytolacc
19	977.5	72.0	2369	2	ABA96543	Ab96543	Phytolacc
20	862.5	63.6	918	2	AAQ64893	Aaq64893	Antiviral
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22	793	58.4	455	6	AAAD42717	Aad42717	Pokeweed
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24	453	33.4	934	3	AAZ45198	Aaz45198	Wild-type
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27	349	25.7	964	3	AAZ61125	Aaz61125	DNA encod
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29	349	25.7	999	3	AAZ61122	Aaz61122	DNA encod
30	349	25.7	999	3	AAZ61119	Aaz61119	DNA encod
31	344.5	25.4	863	2	ABA96547	Ab96547	Cloning v
32	342	25.2	864	1	AAAN1504	Aan1504	DNA of r
33	341	25.1	804	2	AAQ38936	Aaq38936	Saporin c
34	341	25.1	804	2	AAQ85385	Aaq85385	Saporin c
35	341	25.1	804	2	AAQ98042	Aaq98042	M13mp18-G
36	341	25.1	804	2	AAT17964	Aat17964	Saporin c
37	341	25.1	804	3	AAAI2862	Aai12862	Saporin D
38	341	25.1	804	9	ACD67205	Adc67205	Common so
39	341	25.1	804	10	ADC34589	Adc34589	Common so
40	341	25.1	804	10	ADH92013	Adh92013	DNA encod
41	340	25.1	765	3	AAAI2895	Aai12895	Mammalian
42	340	25.1	765	9	ACD27612	Adc27612	Common so
43	340	25.1	765	10	ADC34645	Adc34645	Mammalian
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45	340	25.1	763	2	AAT18231	Aat18231	Amplified

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ID	AA042716 standard; DNA; 792 BP.
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AC	
AA042716;	
XX	
DT	15-NOV-2002 (first entry)
XX	
DB	Pokeweed mature PAP-S protein encoding DNA.
XX	
XX	Necrotic effect; transgenic plant; antiviral pro
KW	gene; db.
XX	
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OS	Phytolacca americana.
XX	
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FT	complement(436..462)
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FT complement(765..792)
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XX MO200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001MO-GB004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX Thomas CR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX WPI; 2002-489891/52.
XX P-PSDB; AAE25919.
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX PT which acts in response to application of specific stimulus to plant.
XX
XX Claim 2; Page 76; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
XX CC specific cells of a plant. The method involves transforming the plant
XX CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX CC PAP', PAPI and PAP-S, where the gene(s) comprises a promoter which acts
XX CC in response to the application of a specific stimulus to the plant so as
XX CC to facilitate expression of the pokeweed antiviral protein in specific
XX CC cells of the plant. The method is useful for inducing a necrotic effect
XX CC in specific cells of a plant. The present sequence is pokeweed mature PAP
XX CC -S protein encoding DNA
XX
XX Sequence 792 BP; 268 A; 161 C; 151 G; 212 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 2.03e-141 Length: 792
XX Score: 1357.00 Matches: 263
XX Percent Similarity: 100.0% Conservative: 0
XX Best Local Similarity: 100.0% Mismatch: 0
XX Query Match: 100.0% Indels: 0
XX DB: 6 Gaps: 0
XX
XX US-09-978-274A-4 (1-263) x AAD42716 (1-792)
XX
XX 1 MetIleasnthrllethrpheapalaglYAsnAlaThrlleasnyTYrAlaThrPhe 20
XX 1 ATGATTAATACGATCACCCTTGATGCTGGAATGCCACATTAACAATATGCCACCTTT 60
XX
XX 21 MetGluSerleuArganglnAlaLYAspProLYleuLYscYTYrGlyIlePromet 40
XX 61 ATGAAATCTCTTGATATCAAGGAAAGATCCAAATAAAGCTATGACATACCAATG 120
XX
XX 41 LeuProAspThrAsnSerThrProLYsTYrLeuLeuValLYleuGlnGlyAlaAsnLeu 60
XX 121 CTACCTGATCTATTCGATCGACCCCTTAAGTACTTATGCTTAAGCTCCAAAGGAGCAACCTA 180
XX
XX 61 LYsThrlleThrLeuMetleuArgArgAsnAsnLeuTYrValMetGlyTYrSerAspPro 80
XX 181 AAAACCATTAACATAATGCTGAGACGAAATTAACCTTAAGCTGANTGGCTATTCGATCCC 240
XX
XX 81 PheAsnGlyAsnLYsCYsArgTYrHisIlePheAsnAspIleThrSerThrGluArgThr 100
XX 241 TTCATATGGCAATATAGTCTGCTTACATATATTTAATGATATTAACAAGCACCGAAGCACT 300
XX
XX 101 AspValGluAsnThrleuCYsSerSerSerSerSerArgValAlaMetSerIleAsnTYr 120
XX 301 GATGTGAGAAATCTTGTGCTCAAGTTCTAGTTCTCGTGTGCAMGTCCATTAACTAC 360
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QY 121 AsnSerleuTYrProThrMetGluLYsLYsAlaGluValAsnSerArgAsnGlnValGln 140
DB 361 AATAGCTATATTCGACCAATGAGAAAGCAAGGAAATTAACATCAAGAAATCAAGTCCAA 420
QY 141 LeuGlyIleGlnIleleuSerSerAspIleGlyLYsIleSerGlyValAspSerPhePro 160
DB 421 TTGGGAATTCAAATACACAGCAGTGCATTTGAAAAATCTCTGAGATTGATTCCTCCCT 480
QY 161 VallyeThrcGluAlaPhePheleuLeuValAlaIleGlnMetValSerGluAlaAlaArg 180
DB 481 GTAAAAAAGTGAAGCTTTTCTTACTGCTGATGCCATCCAAATGATTCAGAGGACGCCGA 540
QY 181 PheLYsTYrIleGluAsnGlnValLYsThrAsnPheAsnArgAlaPheTYrProAspPro 200
DB 541 TTCAGATACATAGAGAACCAAGTCAGACATTAATTTAATAGACATTCCTGATCCCTCC 600
QY 201 LYsValIleAsnleuGlnGluLYsTYrGlyLYsIleSerGluAlaIleHisAsnAlaLYs 220
DB 601 AAAGTAAATTAACTTGAGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCAATGCCAAG 660
QY 221 AsnGlyValAlaLeuProLYsProleuGluLeuValAspAlaLYsGlyThrlYsTPRIleVal 240
DB 661 AATGGGGCTTTACCCAAACCACTTGAGCTAGTGATGCCAAAGATACCAAGTGGATAGCTT 720
QY 241 LeuArgValAspGluIleAsnArgAspValAlaLeuLeuLYsTYrValAsnGlyThrCYs 260
DB 721 CTTAGAGTGAATGAATCAATCAATCGTATGTCGACTCTTAAAGTACGTAAATGAGAACCTGT 780
QY 261 GlnThrThr 263
DB 781 CAGACAACT 789
XX
XX RESULT 2
XX AAD42715
XX ID AAD42715 standard; DNA; 945 BP.
XX
XX AC AAD42715;
XX
XX DT 15-NOV-2002 (first entry)
XX
XX DE Pokeweed pro-PAP-S protein encoding DNA.
XX
XX KM Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
XX gene; ds.
XX
XX OS Phytolacca americana.
XX
XX FH Key
XX FH Location/Qualifiers
XX FT 1..945
XX FT /*tag= a
XX FT /product= "Pro-PAP-S protein"
XX FT primer_bind
XX FT 1..24
XX FT /*tag= b
XX FT /bound_moiety= "Primer PS1BF"
XX FT complement(735..776)
XX FT /*tag= c
XX FT /bound_moiety= "Primer PSXDR"
XX FT 736..777
XX FT primer_bind
XX FT /*tag= d
XX FT /bound_moiety= "Primer PSXDF"
XX FT 750..759
XX FT /*tag= e
XX FT /note= "Sequence replacing removed XbaI site"
XX FT primer_bind
XX FT /*tag= f
XX FT /bound_moiety= "Primer PS2BR"
XX
XX MO200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001MO-GB004593.
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XX Inducing necrotic effect in specific cells of plant by transforming plant
PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT which acts in response to application of specific stimulus to plant.
XX
XX Disclosure, Page 83; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
CC specific cells of a plant. The method involves transforming the plant
CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
CC in response to the application of a specific stimulus to the plant so as
CC to facilitate expression of the pokeweed antiviral protein in specific
CC cells of the plant. The method is useful for inducing a necrotic effect
CC in specific cells of a plant. The present sequence is a fusion DNA. This
CC sequence comprises pokeweed pro-PAP-S DNA, rice cytochrome delta D86 DNA,
CC and Tobacco Etch virus (TEV) N1A protease cleavage site (PCS). (Updated
CC on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 1092 BP; 369 A; 195 C; 222 G; 306 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 3,29e-136 Length: 1092
Score: 1312.00 Matches: 255
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 96.7% Indels: 0
DB: 6 Gaps: 0
US-09-978-274a-4 (1-263) x AAD42729 (1-1092)
QY 1 MetIleAnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPhe 20
DB 1 ATGATAAATACGATCACTTGTAGTGTGAATGCCACATTAACAAATATGCCACTTT 60
QY 21 MetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrTgLyIleProMet 40
DB 61 ATGGAATCTCTTGTAATCAAGCGAAGAAATCCAAATCAAAATGCTATGCGATACCAATG 120
QY 41 LeuProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeu 60
DB 121 CTACCTGATCTAATTCGACCCCTTAAGTACTTATGTTAAGCTCCAAAGTGCAAACTTA 180
QY 61 LysThrIleThrLeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspPro 80
DB 181 AAACACCTTACATTAATGCTGAGAGCAAAATTAACGTAAAGGCTTATTCGATCCC 240
QY 81 PheAsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThr 100
DB 241 TTCAATGGCAATAGTGTCTGTTACCATATTTATGATATTTACMACCGCAACGCACT 300
QY 101 AspValGluAsnThrLeuCysSerSerSerSerArgValAlaMetSerIleAsnTyr 120
DB 301 GATGTGGAAATATCTTTCTGCTCAAGTTCTAGTTCCTGCTGTTGCCAATGCTTAATAC 360
QY 121 AsnSerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAsnGlnValGln 140
DB 361 AATAGCTTATATCCGACCATGAGAAAGAAAGCAAGAAATTAACCAAGAAATCAAGTCCA 420
QY 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPhePro 160
DB 421 TTGGGAATTCMAATATACACAGACAGCATTTGGAAAAATCTCTGAGATTGATTCACTCC 480
QY 161 ValIleThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArg 180
DB 481 GTAAAAATCAGAGCTTTTCTTACTGCTAGCCATCCAAATGGTTTACAGAGCCGCA 540
QY 181 PheLysTyrIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyrProAspPro 200
DB 541 TTCAAGTACATAGAGAACCAAGTCAAGACTAATTTTAAATGAGCATTCACCGTGAATCC 600
QY 201 LysValIleAsnLeuGluGlyTyrGlyLysIleSerGluAlaIleHisAsnAlaLys 220
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DB 601 AAGTAATTAATCTTGGAGAGAAAGTGGGCAAAATCTCTGAGCAATTCACAAATGCCAAG 660
QY 221 AsnGlyValLeuProLysProLysGluLeuValAspAlaLysGlyThrLysTrpIleVal 240
DB 661 AATGGGGCTTACCCAAACCACTTGAAGTGAATGCGCAAAAGTACCAAGTGAATGTT 720
QY 241 LeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyr 255
DB 721 CTTAGAGTGAATGAATCAATCGTGAATGTGCACTCTTAAAGTAC 765
RESULT 4
AAT9556
ID AAT9556 standard; DNA; 882 BP.
XX
XX AAT9556;
AC
AC 17-OCT-2003 (revised)
DT 08-JUN-1998 (first entry)
XX
XX Phytoacca insularis antiviral protein gpi2 gene.
DE
XX Antiviral protein; gpi2 gene; virucide; transgenic plant;
KM virus resistance; immunoconjugate; AIDS; cancer; therapy; ss.
XX Phytoacca insularis; Nakai.
FH
FH Key Location/Qualifiers
FT CDS 1..882
FT /*tag= a
FT /trans_except= (pos:715..717, aa:11e)
FT
FT EP808902-A2.
XX
XX 26-NOV-1997.
PD
XX
XX 30-SEP-1996; 96EP-00307159.
PF
XX
XX 22-MAY-1996; 96KR-00017404.
PR
XX
XX (JINR-) JIN RO LTD.
PA
XX Moon Y, Choi J, Yun Y, Jin J, Hong E, Lee J, Choi K, Lee J,
PI Song S, Choi Y, Kim C, Kim M;
XX
XX WPI; 1998-001788/01.
DR
DR P-PSDB; AAW6773.
XX
XX Antiviral proteins of Phytoacca insularis Nakai and their genes - useful
PT in plant antiviral agents and immunoconjugates for the treatment of AIDS
PT and cancer.
XX
XX Claim 2; Page 10-12; 26pp; English.
XX
XX This polynucleotide comprises the coding region of the Phytoacca
CC insularis Nakai gene coding for a 32.8 kDa novel antiviral protein
CC designated gpi2 (see AAW6773). The gpi2 gene was isolated from leaf
CC genomic DNA by PCR amplification (see AAT9558-59). Another gene (see
CC AAT9557), encoding a 35.7 kDa protein (see AAW6774) designated gpi50,
CC has also been isolated from P. insularis Nakai. Also claimed are vectors
CC encoding these antiviral proteins and host cells transformed or
CC transfected with these vectors. E. coli XL1-Blue MRF' gpi2 (KCM-10080)
CC host cells are claimed, as is a process for preparing antiviral protein
CC by culturing these cells and purifying the protein from inclusion
CC bodies. The antiviral proteins and recombinant proteins inhibit protein
CC synthesis. They can be used as active ingredients of antiviral agents of
CC plant viruses, and employed in the manufacture of immunoconjugates for
CC the treatment of AIDS and cancer. The isolated genes can be used in the
CC breeding of transgenic plants having viral resistance. (Updated on 17-OCT
CC -2003 to standardise OS field)
XX
XX Sequence 882 BP; 301 A; 164 C; 174 G; 243 T; 0 U; 0 Other;
SQ
Alignment Scores:
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QY 22 GluSerLeuArgbAnGlnAlaIySaPProLyLeuIyCyTyGlyIleProMetLeu 41
DB 351 AATGATCTTGTATGAGGAAAGATCCAAAGTTAAATGATGGAATACCAATGCTG 410
QY 42 ProAspThrAsnSerThrProLySTyRLeuLeuValIleuGlnIleValaAsnLeuIyS 61
DB 411 CCNATPACAAATACAAATCCAAAGTACGTGTGTGAGCTCCAAAGTTCAAAATAAAAA 470
QY 62 ThrIleThrLeuMetLeuArgArgAsnAsnLeuTyRValMetGlyTyRSeArpProPhe 81
DB 471 ACCATCACCTAATGCTGAGACGAAACAATTTGATGTATGCTTATCTGATCCCTTT 530
QY 82 AsnGlyAsnLysCyArGtyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
DB 531 GAAACCAATAAATAGTGTACCATTAATCAATATCTCAAGTATCCAAAGTCCCAAGAT 590
QY 102 ValGluAsnThrLeuCySeSerSerSerSerArgValAlaMetSerIleAsnTyRAsn 121
DB 591 GTRAGACTACTCTTTGGCCCAATGCGAATTCGTGTGTATGTAATAAACAATAACTTTGAT 650
QY 122 SerLeuTyRProThrMetGluLySAlaGluValaAsnSerArgbAnGlnIleu 141
DB 651 AGTCGATATCCAAATTCGATGGAATCAAAAGCGAGTAATAATCAAGAAGTCCAGTCCAACTG 710
QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLySileSerGlyValaAspSerPheProval 161
DB 711 GGAATTCCAATACTCCACAGTAATATGGAAAGATTTCTGAGATGATGTCATTCACCTGAG 770
QY 162 LysThrGluAlaPhePheLeuLeuValaIleGlnMetValSerGluAlaIleArgPhe 181
DB 771 AAAACCGAAGCCGAATTCCTATTGTAGCATCAATCAATGATCAAGGCAAGATTC 830
QY 182 LysTyRileGluAsnGlnValIySThrAsnPheAsnArgAlaPheTyRProAspProLyS 201
DB 831 AGTACATAGAGATCAGGTGAAACCTAATTTTAAACAGACATTCACCTAATCCCAAA 890
QY 202 ValIleAsnLeuGlnGluLySTyRgLySileSerGlnAlaIleHisAsnAlaIySaP 221
DB 891 GATCTTAATTTTGCACAGACATGGGGTAAATGATTCAACAGCAATTCATGATGCCAAGAT 950
QY 222 GlyAlaLeuProLySProLeuGlnIleuValaAspAlaIyGlyThrIySTyRProIleValIleu 241
DB 951 GGAATTTTACCCAAACCTCTCGAGCTAGTGATGCCAGTGCTCCAAAGTGAATGCTG 1010
QY 242 ArgValaAspGluIleAsnArgbAspValaIleLeuLeuLySTyRValaAsnGlyThrCySgln 261
DB 1011 AGAGTGATGAGAAATCAAGCTGATGTAGACCTTAAACTACGTTGGTGGAGCTGTGAG 1070
QY 262 ThrThr 263
DB 1071 ACAACT 1076
RESULT 6
AAZ59220
ID AAZ59220 standard; cDNA; 1379 BP.
XX
XX AAZ59220;
XX
XX 20-APR-2000 (first entry)
XX
XX Pokeweed antiviral protein coding sequence spring leaf form.
XX
XX Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
XX resistance; potato virus X; potato virus Y; potato leaf roll virus;
XX tuber; ss.
XX
XX Phycolacca americana.
XX
XX US6015940-A.
XX
XX 18-JAN-2000.
XX
XX 07-APR-1992; 92US-00865169.
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XX
XX 07-APR-1992; 92US-00865169.
XX
XX (MONS ) MONSANTO CO.
XX
XX Kaniewski WK, Turner NE, Lodge JK;
XX
XX WPI; 2000-126326/11.
XX
XX
XX Production of transgenic potato plants or tubers expressing pokeweed
XX antiviral protein which are resistant to potato virus X or Y.
XX
XX Claim 6; Fig 4; 30pp; English.
XX
XX This is the coding sequence for the spring leaf form of the pokeweed
XX antiviral protein (PAP) which is used to generate transgenic potato
XX plants. PAP is able to confer resistance to infection by potato virus X
XX (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in the
XX potato plant or tuber expressing PAP
XX
XX
XX Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 7,43e-107 Length: 1379
XX Score: 1050.00 Matches: 200
XX Percent Similarity: 87.0% Conservative: 28
XX Best Local Similarity: 76.3% Mismatches: 34
XX Query Match: 77.4% Indels: 0
XX DB: 3 Gaps: 0
XX
XX US-09-978-274A-4 (1-263) x AAZ59220 (1-1379)
QY 2 IleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyRAlaThrPheMet 21
DB 291 GTGAATACATCATCTACATGTTGAGAGTACCAATACCAATACCAATCTTTCTG 350
QY 22 GluSerLeuArgbAnGlnAlaIySaPProLyLeuIyCyTyGlyIleProMetLeu 41
DB 351 AATGATCTTGTATGAGGAAAGATCCAAAGTTAAATGATGGAATACCAATGCTG 410
QY 42 ProAspThrAsnSerThrProLySTyRLeuLeuValIleuGlnIleValaAsnLeuIyS 61
DB 411 CCNATPACAAATACAAATCCAAAGTACGTGTGTGAGCTCCAAAGTTCAAAATAAAAA 470
QY 62 ThrIleThrLeuMetLeuArgArgAsnAsnLeuTyRValMetGlyTyRSeArpProPhe 81
DB 471 ACCATCACCTAATGCTGAGACGAAACAATTTGATGTATGCTTATCTGATCCCTTT 530
QY 82 AsnGlyAsnLysCyArGtyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
DB 531 GAAACCAATAAATAGTGTACCATTAATCAATATCTCAAGTATCCAAAGTCCCAAGAT 590
QY 102 ValGluAsnThrLeuCySeSerSerSerSerArgValAlaMetSerIleAsnTyRAsn 121
DB 591 GTRAGACTACTCTTTGGCCCAATGCGAATTCGTGTGTATGTAATAAACAATAACTTTGAT 650
QY 122 SerLeuTyRProThrMetGluLySAlaGluValaAsnSerArgbAnGlnIleu 141
DB 651 AGTCGATATCCAAATTCGATGGAATCAAAAGCGAGTAATAATCAAGAAGTCCAGTCCAACTG 710
QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLySileSerGlyValaAspSerPheProval 161
DB 711 GGAATTCCAATACTCCACAGTAATATGGAAAGATTTCTGAGATGATGTCATTCACCTGAG 770
QY 162 LysThrGluAlaPhePheLeuLeuValaIleGlnMetValSerGluAlaIleArgPhe 181
DB 771 AAAACCGAAGCCGAATTCCTATTGTAGCATCAATCAATGATCAAGGCAAGATTC 830
QY 182 LysTyRileGluAsnGlnValIySThrAsnPheAsnArgAlaPheTyRProAspProLyS 201
DB 831 AGTACATAGAGATCAGGTGAAACCTAATTTTAAACAGACATTCACCTAATCCCAAA 890
QY 202 ValIleAsnLeuGlnGluLySTyRgLySileSerGlnAlaIleHisAsnAlaIySaP 221
```

Db 891 GTACTTAATTGCAAGACATGGGGTAAAGATTCAACGCAATTCATGATCCCAAGAT 950
Qy 222 GAlaAlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrLysTrpIleValLeu 241
Db 951 GGAATTATACCAAACTCTCGAGCTAGAGTGCAGTGTGCCAAGGAGTATGTGTG 1010
Qy 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTrpValAsnGlyThrCysGln 261
Db 1011 AGAGTGATGAATCAAGCTGATGTAGACTTTAACTACGTTGGTGGAGCTGTGAG 1070
Qy 262 ThrThr 263
Db 1071 ACAACT 1076
RESULT 7
AAD42738
ID AAD42738 standard; DNA; 1379 BP.
XX AAD42738;
AC
XX
DT 15-NOV-2002 (first entry)
XX
DB Pokeweed PAP' DNA #1.
XX
KM Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds.
XX
OS Phytolacca americana.
XX
FH Key Location/Qualifiers
FT misc_feature 290..1076
FT /tag= a
FT /note= "Mature PAP' sequence"
XX
PN WO200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-GB004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
PA (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX
XX WPI; 2002-489891/52.
XX
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
XX PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX PT which acts in response to application of specific stimulus to plant.
XX
XX
XX Claim 5; Page 86; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
XX CC specific cells of a plant. The method involves transforming the plant
XX CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX CC PAP', PAPI and PAP-S, where the gene(s) comprises a promoter which acts
XX CC in response to the application of a specific stimulus to the plant so as
XX CC to facilitate expression of the pokeweed antiviral protein in specific
XX CC cells of the plant. The method is useful for inducing a necrotic effect
XX CC in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX
SO Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 7.43e-107 Length: 1379
Score: 1050.00 Matches: 200
Percent Similarity: 87.0% Conservative: 28
Best Local Similarity: 76.3% Mismatches: 34
Query Match: 77.4% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-4 (1-263) x AAD42738 (1-1379)
Qy 2 IleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTrpAlaThrPheMet 21
Db 291 GTGATATCAATCACTTACCAATGTTGAAGTACCAACATTACCAATAGCCACTTTTCG 350
Qy 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTrpGlyIleProMetLeu 41
Db 351 AATGATCTCTTATGAAAGCCAAAGATCCAACTTTAAATCTATGAAATACCAATGCTG 410
Qy 42 ProAspThrAsnSerThrProLysTrpLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
Db 411 CCCAATACAAATATACCAATCCAAAGTACGTTGGTGTGATCCAAAGTTCCAAATAAAA 470
Qy 62 ThrIleThrLeuMetLeuArgAspAsnLeuTrpValMetGlyTrpSerAspProPhe 81
Db 471 ACCATCACTAAATGCTGAGAGCAAAACAATTGTATGTAGAGGGTTATTCGATCCCTTT 530
Qy 82 AsnGlyAsnLysCysArgTrpHisIlePheAsnAspIleThrSerThrGluThrAsp 101
Db 531 GAAACCAATTAATGTCTTACCAATCTTTATGATATCTCAGGTAAGTGAAGCCCAAGT 590
Qy 102 ValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTrpAsn 121
Db 591 GTAGAGACTACTCTTGGCCAAATGCCAATCTCTGTTAGTAAATAACATTAACCTTTGAT 650
Qy 122 SerLeuTrpProThrMetGluLysValAlaGluValAsnSerArgAsnGlnValGlnLeu 141
Db 651 AGTCGATATTCACAACTTGGAATCAAAAGCCGAGATGAATAAATCAAGAAAGTCAGTCCAC 710
Qy 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPheProVal 161
Db 711 GGAATTCAAATCTCGACAGATTAATTTGGAAGAGTTCTGAGATGATCTCACTGAG 770
Qy 162 LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 181
Db 771 AAACCCGAAAGCCGAATCTTATGTTGTAGCCATACAAATGATATCAGAGGAGCAAGATTC 830
Qy 182 LysTrpTrpIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTrpProAspProLys 201
Db 831 AAGTACATATGAGATCGATGTAATACTTAATTTTAAAGAGATCAACCCCAATCCCAAA 890
Qy 202 ValIleAsnLeuGluGluLysTrpGlyLysIleSerGluAlaIleHisAsnAlaLysAsn 221
Db 891 GTACTTAATTGCAAGACATGGGGTAAAGATTTCACACAGCAATTCATGATCCCAAGAT 950
Qy 222 GAlaAlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrLysTrpIleValLeu 241
Db 951 GGAATTATACCAAACTCTCGAGCTAGAGTGCAGTGTGCCAAGGAGTATGTGTG 1010
Qy 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTrpValAsnGlyThrCysGln 261
Db 1011 AGAGTGATGAATCAAGCTGATGTAGACTTTAACTACGTTGGTGGAGCTGTGAG 1070
Qy 262 ThrThr 263
Db 1071 ACAACT 1076
RESULT 8
AD105787
ID AD105787 standard; DNA; 1379 BP.
XX
XX AD105787;
XX
XX 15-APR-2004 (first entry)
XX
XX
XX DNA encoding the wild-type pokeweed antiviral protein.
XX
XX ribosome depurination; antifungal; antiviral; virucide; anti-HIV;
XX KW cytostatic; immunosuppressive; agricultural biotechnology; pharmaceuticals;
XX KW medicine; cancer; AIDS; viral infection; autoimmune disease; T-cell;
XX KW B-cell; transgenic; plant; wild-type; pokeweed antiviral protein; gene;
XX ds.

XX PhytoIacca americana.
OS
XX
XX Key Location/Qualifiers
FH CDS 225..1166
FT //tag= a
FT /product= "wild-type pokeweed antiviral protein"
XX
XX MO200262952-A2.
XX
XX 15-AUG-2002.
XX
XX 01-FEB-2002; 2002MO-US002792.
XX
XX 02-FEB-2001; 2001US-0266396P.
XX
XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Turner NE, Hudak KA, Parikh B;
XX WPI; 2003-15656/15.
XX P-PSDB; ADI05788.
XX
XX New Pokeweed Antiviral Protein (PAP) mutant that is less toxic than wild-
PT type PAP, useful in agricultural biotechnology or in the fields of
PT pharmaceuticals and medicine, e.g. treating cancer, AIDS, viral infection
PT or autoimmune disease.
XX
XX
XX Disclosure; SEQ ID NO 1; 51bp; English.
XX
XX The invention relates to a novel Pokeweed Antiviral Protein (PAP) mutant
CC that is less toxic than wild-type PAP and exhibits ribosome depurination
CC activity, where the mutant is a central domain mutant or N-terminal
CC domain mutant. The PAP mutants have the following activities: antifungal,
CC antiviral, vincristine, anti-HIV, cytostatic and immunosuppressive. The PAP
CC mutants are useful in agricultural biotechnology as well as in the fields
CC of pharmaceuticals and medicine. The PAP mutants and methods are useful in
CC treating mammals with cancer, AIDS, viral infection or autoimmune
CC diseases associated with proliferations of unwanted T-cells or B-cells.
CC The transgenic plants are useful in exhibiting resistance to a broad
CC spectrum of plant pests e.g. viruses and fungi. This polynucleotide
CC sequence represents the DNA encoding the wild-type pokeweed antiviral
CC protein of the invention.
XX
XX
SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
XX
XX
Alignment Scores:
Pred. No.: 7 43e-107 Length: 1379
Score: 1050.00 Matches: 200
Percent Similarity: 87.0% Conservative: 28
Best Local Similarity: 76.3% Mismatches: 34
Query Match: 77.4% Indels: 0
DB: 10 Gaps: 0
US-09-978-274A-4 (1-263) x ADI05787 (1-1379)
QY 2 IleaSnThrlleThrPheAepAlaGlyAsnAlaThrlleAsnlySTyAlaTrnPhemec 21
DB 291 GTGAATACATCATCATCAATGTTGGAAGTACCAACCATTTGCAAAATACGACATTTCTG 350
QY 22 GluSerleuArganGlnAlaLysAspProlyleuLecySTyrglyleProMetleu 41
DB 351 AATGATCTTCGTATATGAAGGAAAGATCCAAAGTTTAAAGCTATGGAATACCAATGCTG 410
QY 42 ProAepThrAsnSerThrProlySTyLeuLeuVallyleuGlnGlyAlaAsnleuLys 61
DB 411 CCCAATACAAATACCAATCCAAAGTACGTCTGCTGAGCTCCAAAGTTTCAAAATAAAAA 470
QY 62 ThrlleThrlleuLecleuArganGlnAlaLysAspProlyleuLecySTyrglyleProMetleu 81
DB 471 ACCATCACACTAATGCTGAGACGAAACAAATTTGATGTGATGGGTATTCGATCCCTT 530
QY 82 AaNglyAaenlyeCyAaGrgTyrlleSTlePheAaenAepIleThrSerThrlGuaTgThraP 101

DB 531 GAAACCAATAAATGCTTACCATCTTAATGAATCTCAGGTAAGTGAACCCCAAGAT 590
QY 102 ValGluAsnThrlleuCySerSerSerSerSerSerArgValAlaMetSerIleAenTyAsn 121
DB 591 GTAGAGACTACTCTTTCGCCAATTCCTGCTGATGAATAAACAATAACTTTGAT 650
QY 122 SerleuTyProThrMetGluLysLysAlaGluValAsnSerArganGlnAlaGlnleu 141
DB 651 AGTCATATTCAAATTCGATTCGAAAGCGGAGTAAATCAAGAGTCAAGTCCAACTG 710
QY 142 GlyTlleGlnIleuSerSerSerAepIleGlyLysIleSerGlyValAspSerPheProVal 161
DB 711 GGAATTCAAATTAATCTCCACGTAATATTTGAAAGATTTCTGAGATGATCATTCAC 770
QY 162 LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAargPhe 181
DB 771 AAAACCGAAGCCCAATTCCTATTGTGAGCCATCAAAATGATCAAGGCGCAAGATTC 830
QY 182 LysTyrlleGluAnGlnValLysThrAsnPheAsnArgAlaPheTyProAepProlys 201
DB 831 AAGTACATAGAGATCAGGTGAAGAACTAATTTTAAACAGGCAATTCAAACCTAATCCAA 890
QY 202 ValIleAenleuGluGluLysTyrglyLysIleSerGluAlaIleHsaenAlaLysAsn 221
DB 891 GTACTTAATTTGCAAGAGACATGGGGTAAAGATTTCAAACGCAATTCATGATGCCAAGAT 950
QY 222 GlyAlaLeuProlyProleuGluLeuValAspAlaLysGlyThrllySTPrlleValleu 241
DB 951 GGAATTTTACCCAAACCTCTCGAGCTAGAGGAGCCAGTGGTCCAAAGTGAATGCTTG 1010
QY 242 ArgValAspGluIleAaenArgPheValAlaLeuLysTyValAaNglyThrCySgln 261
DB 1011 AGAGTGATGAATCAAGCCTGATGTAGCACTTTAAACTACGTTGGTGGAGCTGTGAG 1070
QY 262 ThTrThr 263
DB 1071 ACAACT 1076
RESULT 9
ADG76061
ID ADG76061 standard; DNA; 1378 BP.
XX
XX ADG76061;
XX
XX 11-MAR-2004 (first entry)
XX
XX DE American pokeweed antiviral protein (PAP) DNA Segid 1.
XX
XX KW gene; ds; pokeweed antiviral protein; PAP; HIV-1; anti-HIV; antiviral;
KM nucleoside analogue inhibitor; viral protease inhibitor; viral infection;
KM American pokeweed; retroviral.
XX
XX OS PhytoIacca americana.
XX
XX PN WO2003106479-A2.
XX
XX PD 24-DEC-2003.
XX
XX PF 17-JUN-2003; 2003MO-US019141.
XX
XX PR 17-JUN-2002; 2002US-0389649P.
XX
XX PA (PARK-) PARKER HUGHES INST.
XX
XX PI Uckun FM;
XX
XX DR WPI; 2004-082156/08.
XX
XX DR P-PSDB; ADG76064.
XX
XX PT Novel modified pokeweed antiviral protein useful for inhibiting viral
PT replication, for inducing depurination of viral RNA, or for treating
PT viral infection in subject.

XX Example 2; SEQ ID NO 1; 62pp; English.

CC This invention relates to novel modified pokeweed antiviral proteins
CC (PAPs). Specifically, it refers to modifications relative to wild-type
CC PAP that confer increased activity towards viral RNA, particularly
CC retroviral RNA such as HIV-1 and drug resistant HIV-1. Furthermore,
CC modified PAP also exhibits decreased activity towards ribosomal RNA,
CC relative to wild-type PAP. The present invention describes a molecular
CC model of PAP-RNA interactions that have been used for the rational
CC redesign of PAP mutants with potent anti-HIV activity, where
CC modifications have been introduced in regions other than the active site.
CC Accordingly, these mutants represent antiviral agents that can work as
CC nucleoside analogue inhibitors of reverse transcriptase, as well as viral
CC protease inhibitors that can be used for treating viral infections. As
CC such, they are useful for inhibiting viral replication and for
CC deactivating viral RNA. This polynucleotide sequence is the DNA encoding
CC the wild type american pokeweed antiviral protein (PAP) of the invention.
XX

Alignment Scores:

Pred. No.: 1.24e-106 Length: 1378
Score: 1048.00 Matches: 200
Percent Similarity: 87.0% Conservative: 28
Best Local Similarity: 76.3% Mismatches: 34
Query Match: 77.2% Indels: 0
DB: 12 Gaps: 0

US-09-978-274a-4 (1-263) x ADG76061 (1-1378)

QY 2 Ileaanthrillethrpheaspalaglyasnaalathrilleasmytyralathrphemet 21
DB 290 GTGATACATCATCTACATAGTTGGAGTAGTACCATAGCAATAGCCACTTTCTG 349
QY 22 GluserleuatgansnglialalyaspProlysleuysCytytylytleprowleu 41
DB 350 AATGATCTTCGTATGAGCAAGATCCAAATTAATGCTAATGATACCAATGCTG 409
QY 42 ProaspthraensethrProlytyrleuValysleuGlnGlyAlaasleuys 61
DB 410 CCAATACCAATACCAATCAAGATGCTGTGGTGGTCCCAAGGTTCAATTAATAA 469
QY 62 ThrillethraemleuArgArgasnaenleuTyValmetGlyTyrSerAspProph 81
DB 470 ACCATCACACTAATCTGAGAGCAATTTGATGATGGGTTATTCGATCCCTT 529
QY 82 AsnglyanlyCyatgytyrhisllephasnaenlethrsertthrgluarthrAsp 101
DB 530 GAAACCAATAATATGCTTACCATATCTTTATGATATCTCAGGACTGAAAGCCAA 589
QY 102 ValgluabanthrleuCySerSerSerSerSerArgValAlametSerilleasntyrAsn 121
DB 590 GTAGAGACTACTCTTTGCCCAATGCCAATCTCGTGTATTAATAAACATTAACCTTGCAT 649
QY 122 SerleutytyrProthrmetyrleuValysleuValaJaenserArgasnglValGlnleu 141
DB 650 AGTGAATATCCAACTTGCATTCGAATCAAAAGCGGAGTAAATCAAGAGTCAGCTCAACTG 709
QY 142 GlylleeglnleuSerSerAspilleGlylyslleSerglyValasSerpheProval 161
DB 710 GGAATTCAAATACCTCGACAGTAATATTGGAAGAATTTCTGAGAGGATGATTCACCTGAG 769
QY 162 LysethrgluAlaphepethleuValaAlleGlnmetValSergluAlaAlaArgphe 181
DB 770 AAAACCGAAGCGGAATTCCTATGGTATCCCAATCAATGATATCGAAGGCGCAAGATTC 829
QY 182 LysTyrlleegluanglVallyeThrasnaPhasnaArgAlaPheTyProaspProlys 201
DB 830 AAGTACATATAGAGATCGGTGAAAATCTAATTTTAACAGAGATTCACACCTTAATCCCAA 889
QY 202 VallleasntleugluGlylytyrGlylyslleSergluAlaAlleHlaasnaAlalyaAn 221

DB 890 GTACTTAATTTGCAAGAGACATGGGGTAAAGATTTCACAGCAATTCATGATGCCAAGAT 949
QY 222 GlyAlaLeuProlysProleuGlnleuValaspaAlaAlaAlaAlaAlaAlaAlaAla 241
DB 950 GGAATTTTAAACCAACCTCTGAGCTGATGATGCACTGATGATGATGATGATGATGATG 1009
QY 242 ArgValaAspGlnleuAlaAsnaArgAspValAlaAlaAlaAlaAlaAlaAlaAlaAla 261
DB 1010 AGAGTGATGAAATCAACCTGATGATGATGATGATGATGATGATGATGATGATGATG 1069
QY 262 ThrThr 263
DB 1070 ACAACT 1075

RESULT 10

AA087929
ID AAC87929 standard; DNA; 1379 BP.

AC AAC87929;

DT 06-MAR-2001 (first entry)

DE P. americana pokeweed antiviral protein encoding DNA SEQ ID NO:1.

XX PhytoLacca americana; pokeweed; pokeweed antiviral protein; PAP; cancer;
XX bioherapeutic; fusion protein; immunconjugate; mutant; cytostatic;
XX anti-HIV; human immunodeficiency virus; AIDS; leukemia; lymphoma;
XX brain tumour; neuroblastoma; soft tissue sarcoma; osteosarcoma; ss.
XX PhytoLacca americana.

XX Key Location/Qualifiers

FT CDS 225..1166

FT /*tag= a /product= "pokeweed antiviral protein (PAP)"

PN US6146628-A.

PD 14-NOV-2000.

XX 11-JUL-1995; 95US-00501253.

XX 11-JUL-1995; 95US-00501253.

XX (MNU) UNIT MINNESOTA & RUTGERS.

XX (UTNE-) UNIT STATE NEW JERSEY.

XX Uckun FM, Tumer NE;

XX WPI: 2001-040422/05.

XX P-PSDB; MAB36500.

XX Immunconjugates useful for treating cancer and acquired immunodeficiency
XX syndrome, comprises mutant pokeweed anti-viral protein and a targeting
XX moiety that binds a cell surface receptor.

XX Disclosure; Col 47-50; 32pp; English.

XX The present invention describes a fusion protein or an immunconjugate
XX (I), comprising mutant Pokeweed Anti-viral protein (PAP) having an amino
XX acid substitution at residue 75, 97 or 176 of native PAP and a targeting
XX moiety that binds a cell surface receptor. (I) can have cytostatic and
XX anti-HIV activities, and is an inhibitor of cellular RNA or protein
XX synthesis. (I) is useful for treating AIDS and cancers including
XX leukemia, lymphoma, a brain tumour, neuroblastoma, osteosarcoma, soft
XX tissue sarcoma, breast, prostate, ovarian, testicular, melanoma, lung, or
XX colon cancer. Immunconjugates prepared using PAP mutants exhibit an
XX improved therapeutic index over immunconjugates containing either wild-
XX type PAP or variant PAP. The present sequence encodes the wild-type PAP,
XX which is given in the exemplification of the present invention
XX Sequence 1379 BP; 488 A; 234 C; 268 G; 389 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,61e-106 Length: 1379
 Score: 1047.00 Matches: 199
 Percent Similarity: 87.0% Conservative: 29
 Best Local Similarity: 76.0% Mismatches: 34
 Query Match: 77.2% Indels: 0
 DB: 4 Gaps: 0

US-09-978-274A-4 (1-263) x AAC87929 (1-1379)

```

QY      2  ILAENThrlleThrPheAapAlaGlyAapAlaThrIleAenlyTyraIaThrPheMet 21
DB      291  GTAAATACAAATCAATCTTGAAGTGGAAAGTACCAATTAAGCAAAATCGCCACTTTTCTG 350
QY      22  GluSerleuArgAnglnAlaYsaPProlySleuYsCyTyrgIyIleProMetLeu 41
DB      351  AATGATCTTCGTATGAAGGAAAGATCCAAAGTTTAAATGCTATGGAATACCAATGCTG 410
QY      42  ProAapThrAenSerThrProlySTyLeuLeuValIleSerglnIyAlaAenLeuYs 61
DB      411  CCCAATACAAATCAAAATCCAAAGTACGTGTGGTTCAGCTCCAAAGGTTCAAAATAAAAA 470
QY      62  ThrIleThleuMetLeuArgAenAenLeuTyraIaMetGlyTyrsSerAapProPhe 81
DB      471  ACCATCACTAATGCTGAGACGAAACAAATTTGTATGTGATGGTTATTTCTGATCCCTTT 530
QY      82  AenGlyAenlyCyAargTyrsIlePheAapAlaThrIleSerThrgIuArgThnAsp 101
DB      531  GAAACCAATTAATGTGCTTCCATATCTTTAATGATATCTCAAGTACTGAACGCCAAGAT 590
QY      102  ValGlyAenThreucCySerSerSerSerSerArgValAlaMetSerIleAenTyraSn 121
DB      591  GTAGAGACTACTCTTTGGCCCAATGCCCAATTCGTGTGTGTAAACATTAACCTTGAT 650
QY      122  SerLeuTyrrProThrMetGlyulYblyAlaGlyValAenSerArgAenGlnValGlnLeu 141
DB      651  AGTCGATATCCAAATTTGGAATCAAAAACGGAGATAAATCAAGAAATCGAGTCCAACTG 720
QY      142  GlyIleGlnIleuSerSerAapIleGlyIleSergIyValAaSerPheProVal 161
DB      711  GGAATTCAAATATCTCCACAGATTAATTTGAAAGATTTCTGAGTGAATGTCATTCACCTGAG 770
QY      162  TySThrGlnAlaPhePheLeuLeuValAlaIleGlnMetValSergIuAlaAargPhe 181
DB      771  AAAACCAAGCCCAATTCCTATTGTGTAGCATCAATGTGTATCAGAGCGACAGCAAGATTC 830
QY      182  TySTyrrIleGlnAenGlnValIleTyThraPheAapAlaPheTyrrProAapProlyS 201
DB      831  AAGTACATAGAGATCAAGGTGAAACTTAATTTTAACGAGCAATTCACCTTAATCCCAAA 890
QY      202  ValIleAenLeuGlnGlyulYblySTyrgIyIleSergIuAlaIleHisAenAlaYsaSn 221
DB      891  GTRACTTAATTTGCAAGAGACATGGGGTAAGATTTCAACAGCAATTCATGATGCCAAGAT 950
QY      222  GlyAlaLeuProlySProLeuGlnLeuValAaPAlaYsGlyThrySTyrrIleValLeu 241
DB      951  GGGATTTTACCCAAACCTCTCGAGTATGATGATGCCAGTGGTCCAAAGTATGATGCTTG 1010
QY      242  ArgValAapGlnIleAenArgAapValAlaLeuLeuYsTyraIaengIyThrCyGln 261
DB      1011  AAGGTGGAATGAATCAAGCTGATGTAGCACTCTTAACATACGTGGTGGAGACTGTCAG 1070
QY      262  ThnThr 263
DB      1071  ACAACT 1076

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RESULT 11

ADM74765
 ADM74765 standard; cDNA; 1164 BP.

AC ADM74765;
 XX
 DT 03-JUN-2004 (first entry)

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XX      DE      HIV-1 inhibition activity related Tat cDNA.
XX      KW      human immunodeficiency virus; HIV-1; tumour; plant;
XX      KW      Chinese phytiolacca leaf; trans-acting activation factor; Tat; mutant;
XX      KW      gene; ss.
XX      OS      Human immunodeficiency virus 1.
XX      FT      Key
XX      FT      CDS
XX      FT      Location/Qualifiers
XX      FT      2..943
XX      FT      /*tag= a
XX      FT      /product= "Tat HIV-1 protein"
XX      CN1400220-A.
XX      PD      05-MAR-2003.
XX      XX
XX      PP      02-AUG-2001; 2001CN-00123911.
XX      PR      02-AUG-2001; 2001CN-00123911.
XX      PA      (PBRC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
XX      PI      Peng X, Bai L, Yin B,
XX      DR      WPI; 2003-469263/45.
XX      DR      P-PSDB; ADM74766.
XX      PT      Two kinds of cDNA with actively capable of extensively inhibiting HIV and
XX      PS      its expression, separation and purification method in protokaryon.
XX      PS      Example 9; Page 11-12; 17pp; Chinese.
XX      CC      The present invention relates to two kinds of cDNA which can inhibit
XX      CC      human immunodeficiency virus (HIV-1) activity, including separation clone
XX      CC      of two kinds of cDNA, external mutation, fusion expression in prokaryotes
XX      CC      and application of the cDNA in preparation of preparation for curing the
XX      CC      virus and tumours. One of the described cDNAs is obtained by separation
XX      CC      and cloned from a plant Chinese phytiolacca leaf, and one from the trans-
XX      CC      acting activation factor (Tat) mutant coded by human immunodeficiency
XX      CC      virus HIV-1 gene. This polynucleotide sequence represents the Tat cDNA
XX      CC      used in the HIV-1 inhibition activity of the invention.
XX      SQ      Sequence 1164 BP; 403 A; 203 C; 218 G; 340 T; 0 U; 0 Other;

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Alignment Scores:

Pred. No.: 2.75e-106 Length: 1164
 Score: 1044.00 Matches: 199
 Percent Similarity: 87.0% Conservative: 29
 Best Local Similarity: 76.0% Mismatches: 34
 Query Match: 76.9% Indels: 0
 DB: 11 Gaps: 0

US-09-978-274A-4 (1-263) x ADM74765 (1-1164)

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QY      2  ILAENThrlleThrPheAapAlaGlyAapAlaThrIleAenlyTyraIaThrPheMet 21
DB      68  GTAAATACAAATCAATCTTGAAGTGGAAAGTACCAATTAAGCAAAATCGCCACTTTTCTG 127
QY      22  GluSerleuArgAnglnAlaYsaPProlySleuYsCyTyrgIyIleProMetLeu 41
DB      128  GATTAATCTTCGTATGAAGGAAAGATCCAAAGTTTAAATGCTATGGAATACCAATGCTTG 167
QY      42  ProAapThrAenSerThrProlySTyLeuLeuValIleSerglnIyAlaAenLeuYs 61
DB      188  CCCAATACAAATCAATCCAAAGTACGTGTGGTTCAGCTCCAAAGGTTCAAAATAAAAA 247
QY      62  ThrIleThleuMetLeuArgAenAenLeuTyraIaMetGlyTyrsSerAapProPhe 81
DB      248  ACCATCACTAATGCTGAGACGAAACAAATTTGTATGTATGGCTATTTCTGATCCCTTT 307
QY      82  AenGlyAenlyCyAargTyrsIlePheAapAlaThrIleSerThrgIuArgThnAsp 101

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Db      308 GATACCAATAGTGTGTTACCATATCTTAGTATATCTCAGTACGACGCAAGAT 367
Qy      102 ValGluGlnThrLeuCySerSerSerSerSerArgValAlaMetSerIleAsnThr 121
Db      368 GTAGAGTACTCTTGTCCCAATCTCTGTAGTAAACATTAACATATATAT 427
Qy      122 SerLeuTyProThrMetGluLeuValysAlaGluValaSerArgAsnGluValGlnLeu 141
Db      428 AGTGATATCCAACTTGGAAATCAAAACGGAGTAAATCAAGAGTCAAGTTCACCTG 487
Qy      142 GlyIleGlnIleLeuSerSerSerIleGlyIleSerGlyValaSerPheProVal 161
Db      488 GGAATTCAAATATCTGACATATATGAAAGATTTCTGGAGTACATTCATCTGAG 547
Qy      162 LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaPhe 181
Db      548 AAAACCGAAGCCGAATTCCTACTGACCAATCAAAATGATATCAAGGCAAGATTC 607
Qy      182 LysTyrlleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyProAspProlys 201
Db      608 AAGTACATAGGGAATCAGGTGAAAATTTTAAACAGATTCATCTATCTCCAA 667
Qy      202 ValIleAsnLeuGluGluLysTyrlleSerGluAlaIleHisAsnAlaLysAsn 221
Db      668 GTACTTATTTGGAAGACATGGGGTAAATTTCTACAGCAATTCATGATGCCAAGAT 727
Qy      222 GlyAlaLeuProLysProLeuGluLeuValAsnAlaLysGlyThrLysTrpIleValLeu 241
Db      728 GGAATTTTACCAAACTCTGAGCTAGTGAATGCCAGTGTGCCAAGTGAATGTGTG 787
Qy      242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrlleValaSerGln 261
Db      788 AGACTGATGATATCAAGCTGATGTAGCACTTAAACTACGTTGGTGGAGCTGCCAA 847
Qy      262 ThrThr 263
Db      848 ACAACT 853

RESULT 12
ID      AA056672 standard; cDNA; 1195 BP.
AC      AA056672;
XX
XX      16-OCT-2003 (revised)
DT      25-MAR-2003 (revised)
DT      04-SEP-1994 (first entry)
XX
XX      Sequence of Phytoacta antiviral protein (PAP) cDNA.
XX      Antiviral protein; PAP; virus-resistance; transgenic plant; ss.
XX
XX      Phytoacta americana; L.
XX
XX      Key      Location/Qualifiers
XX      CDS      33..974
XX      FT      /*tag= a
XX      PN      EP585554-A1.
XX      PD      09-MAR-1994.
XX      PF      30-JUN-1993; 93EP-00110445.
XX      PR      16-AUG-1992; 92KR-00014895.
XX      PA      (JINR-) JIN RO LTD.
XX      PI      Kim M, Lee K, Jeong H, Choi K, Moon Y, Jeon H;
XX      WPI, 1994-076002/10.
XX      P-PSDB; AAR48548.
DR

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XX      Expression vector for phytoacta antiviral protein - used for producing
PT      transgenic virus-resistant plants and for producing the antiviral agent.
XX
XX      Disclosure; Fig 1; 15pp; English.
XX
XX      To isolate PAP gene, total cellular mRNA was purified from leaves of
CC      Phytoacta americana L. obd. in Korea. A cDNA library was constructed.
CC      The PAP gene was selected by immunoscreening employing anti-PAP antibody.
CC      A deletion mutant was prepd. from the isolated PAP gene, and the DNA
CC      sequence of the PAP gene was determined. (Updated on 25-MAR-2003 to
CC      correct PW field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ      Sequence 1195 BP; 420 A; 201 C; 230 G; 344 T; 0 U; 0 Other;

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US-09-978-274A-4 (1-263) x AA056672 (1-1195)

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Alignment Scores:
Pred. No.:      2,85e-106      Length:      1195
Score:          1044.00      Matches:      199
Percent Similarity: 86.6%      Conservative: 28
Best Local Similarity: 76.0%      Mismatches: 35
Query Match:      76.9%      Indels:      0
DB:              Gaps:      0

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Qy      2 IleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrlleThrPheMet 21
Db      99 GGTAAATCAATCATCTCAATGTTGAAGTGAATGCCATTTGCAATTCGCACTTTCTG 158
Qy      22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCySerTyrlleProMetLeu 41
Db      159 AATGATCTCTGATATGAAGCAAGATCCAGTTTAAATGCTATGAAATCCAAATGCTG 218
Qy      42 ProAspThrAsnSerThrProLysTyrlleLeuValLysLeuGlnGlyAlaAsnLeuLys 61
Db      219 CCCAATCAAAATCAATCCAAAGTACGTGTGTTGAGTCCCAAGGTTCCAAATTAATAA 278
Qy      62 ThrIleThrLeuMetLeuArgAsnAsnLeuTyrlleMetGlyTyrlleSerAspProPhe 81
Db      279 ACCATCAACATTAATGCTGAAGCAAGCAATTTGATGTGATGATTTTCATCCCTTT 338
Qy      82 AsnGlyAsnLysCySerTyrlleIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db      339 GAAACCACTTAATGCTTACCAATCTTTATATATCTCAGTATCTGAAGCCCAAGAT 398
Qy      102 ValGluAsnThrLeuCySerSerSerSerSerArgValAlaMetSerIleAsnTyrlle 121
Db      399 GTAGAGACTACTCTTGTCCCAATGCAATTTCTGTGATGAATAAACAATTAACCTTGAT 458
Qy      122 SerLeuTyProThrMetGluLysValaGluValaSerArgAsnGlnValGlnLeu 141
Db      459 AGTCGATATCCAACTTGGAAATCAAAACGGAGTAAATCAAAAGTCAAGTCCAACTG 518
Qy      142 GlyIleGlnIleLeuSerSerSerIleGlyIleSerGlyValaSerPheProVal 161
Db      519 GGAATTCAAATATCTCGAAGATTAATTTGAAGATTTCTGAGAGTCAATTCACGAG 578
Qy      162 LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaPhe 181
Db      579 AAAACCGAAGCCGAATTCCTATTTGTAGCCATCAATGTATCAAGAGCAAGCAATTC 638
Qy      182 LysTyrlleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyProAspProLys 201
Db      639 AAGTACATAGGGAATCAGGTGAAAATTTTAAACAGATTCCAACCTTAATCCCAA 698
Qy      202 ValIleAsnLeuGluGluLysTyrlleSerGluAlaIleHisAsnAlaLysAsn 221
Db      699 GTACTTATTTGCAAGAGATGGGTAAATTTTCAAGCAATTCATGATGCCAAGAT 758
Qy      222 GlyAlaLeuProLysProLeuGluLeuValaLysGlyThrLysTrpIleValLeu 241
Db      759 GGAATTTTACCAAACTCTGAGCTAGTGAATGCCAGTGTGCCAAGTGAATGTGTG 818

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Qy      242 ArgValAspGluIleAsnArgAspValAlaLeuLeuYrYrValaEnglyThrCyGln 261
Db      819 AGAGTGGATGAATAATCAAGCTGATGATGACACTTAAACTGTTGGTGGAGCTGTCAAG 878
Qy      262 ThrThr 263
Db      879 ACAACT 884

RESULT 13
AAD42739
AAD42739 standard; DNA; 1378 BP.
XX
AC      AAD42739;
XX
DT      15-NOV-2002 (first entry)
XX
DE      Pokeweed PAP' DNA #2.
XX
KM      Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds.
XX
OS      Phytolacca americana.
XX
FH      Key      Location/Qualifiers
FT      misc_feature      290..1076
FT      /tag=a
FT      /note="Mature PAP' sequence"
XX
PN      MO200233107-A2.
XX
PD      25-APR-2002.
XX
PF      15-OCT-2001; 2001MO-GB004593.
XX
PR      14-OCT-2000; 2000GB-00025217.
XX
PA      (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
PI      Thomas CR, Mepherston MJ, Atkinson HU, Neelam A;
XX
DR      WPI; 2002-489891/52.
XX
PT      Inducing necrotic effect in specific cells of plant by transforming plant
PT      with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT      which acts in response to application of specific stimulus to plant.
XX
PS      Claim 5; Page 86-87; 87pp; English.
XX
CC      The invention relates to a method of inducing a necrotic effect in
CC      specific cells of a plant. The method involves transforming the plant
CC      with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC      PAP', PAPI and PAP-S, where the gene(s) comprises a promoter which acts
CC      in response to the application of a specific stimulus to the plant so as
CC      to facilitate expression of the pokeweed antiviral protein in specific
CC      cells of the plant. The method is useful for inducing a necrotic effect
CC      in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX
SQ      Sequence 1378 BP; 488 A; 234 C; 269 G; 387 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      5 79e-106      Length:      1378
Score:      1042.00      Matches:      199
Percent Similarity:      86.6%      Conservative:      28
Best Local Similarity:      76.0%      Mismatches:      35
Query Match:      76.8%      Indels:      0
DB:      6      Gaps:      0

US-09-978-274A-4 (1-263) x AAD42739 (1-1378)
Qy      2 IleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnYrYrAlaThrPheMet 21
Db      291 GTGAAATACATCATCTACATGTTGGAGATACCAACATTGCAAAATACGCACTTTTCGG 350
Qy      22 GluSerLeuArgAsnGlnAlaValAspProLeuLeuYrCySerGlyIleProMetLeu 41

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Db      351 AATGATCTTCGTATGATGAAGCAAGATCCAAAGTTTAAATGCTATGGAATACCAATGCTG 410
Qy      42 ProAspThrAsnSerThrProYrYrLeuLeuValIleLeuGlnGlyAlaAsnLeuYr 61
Db      411 CCCAATACAAATACAAATCCAAAGCAGTGTGGTGAAGCTCCAAAGGTTCAAAATAAAAA 470
Qy      62 ThrIleThrLeuMetLeuArgAsnAsnLeuYrValMetGlyYrSerAspProPhe 81
Db      471 ACCATCACTAATATGCTGAGAACCAAACTTTGTATGTATGGTTATTTCTGATCCTTT 530
Qy      82 AsnGlyAsnYrCySerArgYrHsiIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db      531 GAAACCAATAAATGTCGTACATATCTTAATGATATCTCAGTACTGAACGCCAAGAT 590
Qy      102 ValGluAsnThrLeuYrCySerSerSerSerSerArgYrValAlaMetSerIleAsnYrAsn 121
Db      591 GTAGAGACTACTCTCTTGGCCCAATGCCAATTCGTGTAGTAAACATTAACCTTTGAT 650
Qy      122 SerLeuYrProThrMetGluYrSlyAlaGluValAsnSerArgAsnGlnValGlnLeu 141
Db      651 AGTCGATATCCAACTTGGAAATCAAAAGCGAGTAAATCAAGAACTCAGTCCAACTG 710
Qy      142 GlyIleGlnIleLeuSerSerAspIleGlyYrIleSerGlyValAspSerPheProVal 161
Db      711 GGAATTCAAATACTCGACGATATATTTGAAAGATTTCTGAGTGTGATCATTCACCTGAG 770
Qy      162 LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaIleArgPhe 181
Db      771 AAAACCGAAGCCCAATTCCTATTGTGTAGCCATCAAAATGGTATCAAGGCAAGAAATTC 830
Qy      182 LysYrIleGluAsnGlnValIleYrThrAsnPheAsnArgAlaPheYrProAspProYr 201
Db      831 AAGTACATAGAGATCAGTGGAATTAATTTTAACAGAGCATTCAAACCTTAATCCAA 890
Qy      202 ValIleAsnLeuGluGluYrYrGlyYrIleSerGluAlaIleHsiAsnAlaYrAsn 221
Db      891 GTACTTAATTTGCAGAGACATGGGTTAAGATTTCAAACGAAATCATGATGCCAAGAA 950
Qy      222 GluAlaLeuProYrAspProLeuGluLeuValAspAlaIleGlyThrYrSerPheIleVal 241
Db      951 GAGGTTTACCCCAACCTCTCGAGCTAGTGAGCCAGTGAGTCCAAAGTGTGATGTG 1010
Qy      242 ArgValAspGluIleAsnArgAspValAlaLeuLeuYrYrValaEnglyThrCyGln 261
Db      1011 AGAGTGGATGAATAATCAAGCTGATGATGACACTTAAACTAGCTGTGTGGAGCTGTCAAG 1070
Qy      262 ThrThr 263
Db      1071 ACAACT 1076

RESULT 14
AAZ59221
AAZ59221 standard; cDNA; 1379 BP.
XX
AC      AAZ59221;
XX
DT      20-APR-2000 (first entry)
XX
DE      Variant pokeweed antiviral protein spring leaf form coding sequence.
XX
KM      Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
XX      resistance; potato virus X; potato virus Y; potato leaf roll virus;
XX      tuber; ss.
XX
OS      Phytolacca americana.
XX
PN      US6015940-A.
XX
PD      18-JAN-2000.
XX
PF      07-APR-1992; 92US-00865169.
XX

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PR 07-APR-1992; 92US-00865169.
XX (MONS ) MONSANTO CO.
XX PI Kaniewski WK, Turner NE, Lodge JK;
XX WP1; 2000-126326/11.
XX Production of transgenic potato plants or tubers expressing pokeweed
PT antiviral protein which are resistant to potato virus X or Y.
XX
PS Claim 7; Fig 5; 30bp; English.
XX
CC This is the coding sequence for a variant spring leaf form of the
CC pokeweed antiviral protein (PAP') which is used to generate transgenic
CC potato plants. PAP' is able to confer resistance to infection by potato
CC virus X (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in
CC the potato plant or tuber expressing PAP'. PAP' varies from PAP
CC (AAZ59220) by mutations L20R and Y49H
XX
SQ Sequence 1379 BP; 489 A; 234 C; 269 G; 387 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.8e-106 Length: 1379
Score: 1042.00 Matches: 199
Percent Similarity: 86.6% Conservative: 28
Best Local Similarity: 76.0% Mismatches: 35
Query Match: 76.8% Indels: 0
DB: 3 Gaps: 0

US-09-978-274A-4 (1-263) x AAZ59221 (1-1379)

QY 2 ILeAsnThrlleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMet 21
DB 291 GTGAATCAATCATCTACAAATGTTGAAAGTCCACCAATTAACCAATTCCTTTCGG 350
QY 22 GluSerLeuArgAsnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeu 41
DB 351 AATGATCTTCGTATGAAGCAAGATCCAAAGTTTAAATCTATGGAATCCAAATGCTG 410
QY 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
DB 411 CCCAATCAATATCAATATCCAAAGCAGTGTGTTGAGTCCCAAGGTTCAAAATTAATAA 470
QY 62 ThrIleLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
DB 471 ACCATCACTAATCTGAGAGCAAAACAATTTGATGAGGTATTCGATCCCTTT 530
QY 82 AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
DB 531 GAAACCAATTAATGCTGTTACCAATATCTTTATGATATCTCAGGTAATCGAACCAAGAT 590
QY 102 ValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
DB 591 GTAGAGCTACTCTCTTCCCAAAATGCCAATTCGTGTGATTAATAAACATTAATCTTGAT 650
QY 122 SerLeuTyrProThrMetGluLysValGluValAsnSerArgAsnGlnValGlnLeu 141
DB 651 AGTCGATATCCAAATGGAATCAAAAGCGGAATCAAAATCAAAAGCGAGTCCAACTG 710
QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAlaSerPheProVal 161
DB 711 GGATTCAAATATCTCGACATTAATTTGAAAGATTTCTGAGAGTATCTATTCACGAG 770
QY 162 LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaAspPhe 181
DB 771 AAAACCGAAGCCGAATTCCTAATGTTGATCCATCAAAATGATATGAGGCGCAAGATTC 830
QY 182 LysTyrIleGlnValAsnGlnValLysThrAsnPheAsnArgAlaPheTyrProAspProLys 201
DB 831 AAGTACATTAAGATTCAGGTCAAAATCTAATTTTAAACAGAGCATTCAAACCTTAATCCAAA 890
QY 202 ValIleAsnLeuGlnGluLysTyrGlyLysIleSerGluAlaIleHisAsnAlaLysAsn 221

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DB 891 GTACTTAATTTGCAAGAGACATGGGCTAAGTTTCAACAGCAATTCATGATGCCAAGAT 950
QY 222 GlyAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyTyrLysTyrIleValLeu 241
DB 951 GGAGTTTACCCAAACCTCTCGAGCTAGTGCAGTGTGCTCAAGTGTGATGTGTG 1010
QY 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsnGlyTyrCysGln 261
DB 1011 AGAGTGAATGAATCAAGCCTGATGTAGCACTTTAAACTACGTGTGGAGCTGTGAG 1070
QY 262 ThrThr 263
DB 1071 ACAACT 1076

RESULT 15
ADM74751
ID ADM74751 standard; cDNA; 1164 BP.
XX
AC ADM74751;
XX
DE 03-JUN-2004 (first entry)
XX
DE HIV-1 inhibition activity related cDNA.
XX
KW human immunodeficiency virus; HIV-1; tumour; plant;
KW Chinese phytoleuca leaf; trans-acting activation factor; Tac; mutant;
KW gene; ss.
XX
OS Human immunodeficiency virus 1.
XX
FH Key Location/Qualifiers
FT CDS 1..1164
FT /*tag= a
FT /product= "HIV-1 related protein"
XX
XX CN1400220-A.
XX
XX 05-MAR-2003.
XX
XX 02-AUG-2001; 2001CN-00123911.
XX
XX 02-AUG-2001; 2001CN-00123911.
XX
XX 02-AUG-2001; 2001CN-00123911.
XX
XX (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
XX
XX Peng X, Bai L, Yin B;
XX
XX WP1; 2003-469263/45.
XX
XX P-PSDB; ADM74752.
XX
XX Two kinds of cDNA with activity capable of extensively inhibiting HIV and
XX its expression, separation and purification method in protokaryon.
XX
XX Example 8; Page 9-10; 17pp; Chinese.
XX
XX The present invention relates to two kinds of cDNA which can inhibit
XX human immunodeficiency virus (HIV-1) activity, including separation clone
XX of two kinds of cDNA, external mutation, fusion expression in prokaryons
XX and application of the cDNA in preparation of preparation for curing the
XX virus and tumours. One of the described cDNAs is obtained by separation
XX and cloned from a plant Chinese phytoleuca leaf, and one from the trans-
XX acting activation factor (Tac) mutant coded by human immunodeficiency
XX virus HIV-1 gene. This polynucleotide sequence represents a cDNA used in
XX the HIV-1 inhibition activity of the invention.
XX
SQ Sequence 1164 BP; 379 A; 239 C; 248 G; 298 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.94e-106 Length: 1164
Score: 1041.00 Matches: 198
Percent Similarity: 87.0% Conservative: 30
Best Local Similarity: 75.6% Mismatches: 34

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Query Match: 76.7% Indels: 0
DB: 11 Gaps: 0

US-09-978-274A-4 (1-263) x ADM74751 (1-1164)

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QY      2  ILeaenThrllethrPheAspAlaGlyAsnAlaThrIleasnlyTyraIatThrPheMet 21
DB      289 GTGAAATACAAATCAATCTCAATGTTGGAAAGTACCACCAATTAAGCAATAGCCACATTTCTG 348
QY      22  GluSerleuArgAsnGlnAlaLysAspProLysleuLysCysTyrglyIleProMetLeu 41
DB      349 GATATATTTGCTATGATGAGGAAAGATCCAACTTAATAAGCTATGGAATACCAATGTTG 408
QY      42  ProAspThrAsnSerThrProLysTyrlleuLeuValLysleuGlnGlyAlaAsnleuLys 61
DB      409 CCCAATACAAATCCAAATCCAAAGTACGTGTGTTGAGCTCCAAAGTTCAATATAAAAA 468
QY      62  ThrIleThrleuMetLeuArgAsnAsnleuTyraIleMetGlyTyrsAspProPhe 81
DB      469 ACCATCAGACTAATGCTGAGAGACGAAACAATTTGTATGTGATGGGCTATTCTGATCCCTTT 528
QY      82  AsnGlyAsnLysCysArgTyraIlePheAsnAspIleThrSerThrGluArgThrAsp 101
DB      529 GATACCAATTAAGTCTGCTTACCATATCTTTAGTATCTCAGGCTAGAAACGCAAGAT 588
QY      102 ValGluAsnThrleuLysSerSerSerSerSerArgValAlaMetSerIleAsnTyraSn 121
DB      589 GTAGAGACTACTGTTGCCCAATCCCAATCTCGTGTAGTAAACATTAATCTATGAT 648
QY      122 SerleuTyrrProThrMetGluLysValGluValAsnSerArgAsnGlnValGlnleu 141
DB      649 AGTCGATATCCAACTTGGAAATCAAAAGCGGAGTAAATCAAGAACTCAAGTTCAACTG 708
QY      142 GlyIleGlnIleleuSerSerAspIleGlyLysIleSerGlyValAspSerPheProVal 161
DB      709 GGAATTCAAATTAATCTCGACATTAATTTGAAAGATTTCTGAGTGAAGCTATTCACAG 768
QY      162 LysThrGluAlaPhePheleuLeuValAlaIleGlnMetValSerGluAlaIaArgPhe 181
DB      769 AAAACCGAAGCCGAATTCCTACTGTTGTCATCAAAATGATCAAGAGCGACGAAGATTC 828
QY      182 LysTyrrIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyrrProAspProLys 201
DB      829 AAGTACATAGGGGATCGAGTGAAGAACTTAATTTTAACAGACATTCATCTTAATCCCAA 888
QY      202 ValIleAsnleuGluGluLysTyrrGlyLysIleSerGluAlaIleHisAsnAlaLysAsn 221
DB      889 GTACTTAAATTTGGAAGAGACATGGGGTAAATTTCTACAGCAATTCATGATGCCAAGAT 948
QY      222 GlyAlaLeuProLysPProleuGluLeuValAspAlaLysGlyThrLysTrpIleValLeu 241
DB      949 GGAATTTTACCCAAACCTCTCGAGCTAGTGATGCCAGTGCCAAAGTGATAGTGTG 1008
QY      242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyraIleAsnGlyThrCysGln 261
DB      1009 AAGAGTGAAATGATCAAGCTGATGTAGCACTCTTAACATACGTGTGGTGGAGCTGCCAA 1068
QY      262 ThrThr 263
DB      1069 ACAAAT 1074
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Search completed: April 9, 2006, 02:22:32
Job time : 703.998 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 9, 2006, 01:41:02 ; Search time 4779.97 Seconds
(without alignments)
2574.284 Million cell updates/sec

Title: US-09-978-274A-4

Perfect score: 1357

Sequence: 1 MINTTFDAGNATINKYATF.....DEINRDVALTKYVNGTCQTT 263

Scoring table: BIOSUM62
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Ygapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=EST -QFMT=faa2lap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biolum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=400 -THR.SCOR=50 -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pic -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=shs807
-USR=US0978274.@CGN.1.1.9564.@runat_07042006_173034_28424 -NCPU=6 -ICPU=3
-NO MMAD -NEG.SCOR=50 -WAIT -DSBLOCK=100 -LONGLOG -DEV.TIMEOUT=120
-MAIN.TIMEOUT=30 -THRAUD=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
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2: gb_est2:*
3: gb_est3:*
4: gb_hlc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsa1:*
10: gb_gsa2:*
11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	335.5	24.7	829	7	CN782289 EST00385
2	266.5	19.6	993	2	BE035039 MM02A03 M
3	266.5	19.6	1021	2	BE036639 MP03B03 M
4	263.5	19.4	1033	2	BE036541 MP01B07 M
5	266.5	18.9	816	2	BE035038 MM02A01 M
6	251.5	18.5	639	2	BE037217 MP18B02 M
7	248.5	18.3	837	1	AM053634 L30-1401T

8	245	18.1	649	6	CA838757
9	245	18.1	649	6	CA839330
10	245	18.1	661	6	CA835532
11	245	18.1	671	6	CA839511
12	245	18.1	689	6	CA833333
13	245	18.1	689	6	CA833383
14	239	17.6	841	7	CO121195
15	235	17.3	903	7	CO103587
16	225	16.6	639	6	CA838855
17	217.5	16.0	1038	2	BE033546
18	187	13.8	498	5	BQ588134
19	172.5	12.7	811	2	BE034055
20	171.5	12.6	489	2	BE130330
21	164.5	12.1	662	6	CF227046
22	164	12.1	661	6	CF227047
23	152	11.2	698	6	CA838926
24	151	11.1	405	8	T24255
25	150.5	11.1	267	1	AA856221
26	149.5	11.0	665	6	CF227084
27	149	11.0	671	7	CN846973
28	142	10.5	659	7	CN848288
29	140.5	10.4	658	5	BQ583480
30	138.5	10.2	603	5	BQ590856
31	134	9.9	601	6	CA198032
32	130.5	9.6	659	5	BQ584743
33	128	9.4	1094	4	AY105813
34	126	9.3	420	6	CF227009
35	126	9.3	678	6	CA840373
36	125.5	9.2	677	6	CA174183
37	125.5	9.2	680	6	CA198271
38	124	9.1	546	5	BQ588856
39	124	9.1	546	6	CA838446
40	123	9.1	497	5	BQ488214
41	123	9.1	621	7	CV052755
42	120	8.8	644	4	CA838401
43	118.5	8.7	346	5	BQ584811
44	117.5	8.7	614	7	CN846558
45	115	8.5	649	7	CN948289

ALIGNMENTS

RESULT 1
CN782289 829 bp mRNA linear EST 21-MAY-2004
LOCUS CN782289
DEFINITION EST00385 cgeed Chenopodium quinoa cDNA clone S02022 5' similar to
antiviral ribosome-inactivating protein CAP30B [Chenopodium album],
mRNA sequence.
ACCESSION CN782289
VERSION CN782289
KEYWORDS
SOURCE CN782289.1 GI:47561753
ORGANISM
EST.
Chenopodium quinoa (quinoa)
Chenopodium quinoa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Chenopodium.
1 (bases 1 to 829)
Coles,N.D., Coleman,C.E., Christensen,S.A., Jellin,E.N.,
Stevens,M.R., Bonifacio,A., Rojas-Beltran,J.A., Fairbanks,D.J. and
Maughan,P.J.
Development and use of an expressed sequenced tag library in quinoa
(Chenopodium quinoa Willd.) for the discovery of single nucleotide
polymorphisms
Plant Sci. 168 (2), 439-447 (2005)
Contact: Coleman, Craig R.
Department of Plant and Animal Sciences
Brigham Young University
275 WTB, Brigham Young University, Provo, UT 84602, USA
Tel: (801) 422-5145
Fax: (801) 422-0008
Email: craig.coleman@byu.edu
Plate: 02 row: J column: 22
Seq primer: M13 Forward

JOURNAL COMMENT

High quality sequence stop: 829.

FEATURES
Location/Qualifiers

1..829
/organism="Chenopodium quinoa"
/mol_type="mRNA"
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/lab_host="XL-1 Blue"
/clone_lhb="cgseed"
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ORIGIN

Alignment Scores:

Pred. No.: 5,41e-31 Length: 829
Score: 335.50 Matches: 92
Percent Similarity: 53.54 Conservative: 39
Best Local Similarity: 37.64 Mismatches: 95
Query Match: 24.74 Indels: 19
DB: 7 Gaps: 8

US-09-978-274A-4 (1-263) x CN782289 (1-829)

QY 13 ThrilleaenlyrYrAlaTrhPheMetGluSerLeuArgAnginalAlyAspProlyS 32
122 ACACAGAAATCTTAATACACCTTCTGCAAGATACGACGCAACCTAAGATCCAGC 181
QY 33 LeuLyecyBTrGlyIlePrometLeuProAspThrAsenSerThrProlySTrLeuLeu 52
182 TTAGTGATAGAGGAATCCCAATGATCCGACCAACCAACCATATATCTTTTG 241
QY 53 VallyleuGlulnglyAlaAnleuLyThr-----IleThreMetLeuArgArg 69
242 GTTGACCTTAATCTTAAGAAAGATAGAAAGATATATCTTACATTCCTTTAGTACA 301
QY 70 AsnaAnleuTyValMetGlyTySerAspProBheAnglyAnlySvBargTyHls 89
302 AACGACTTGATGAGTGCGCTTGCTGATMAATTT---GAGGCAAAAGTTCCGCGCAT 358
QY 90 IlePheAsnApIleThrSerThrGluArgThrapValGluAnthrLeuCySerSer 109
359 TTCTTTCCAAATCTTAACATT-----GACACCACTTATAGCAAGAAAGTTT 409
QY 110 SerSerSerArgValAlaMetSerIleAsnTyRasSerLeuTyProThrMetGluLyS 129
410 CCAGAACTTCAGGTTTCATTAATATACGTAATGGGAAAGTTACAGTCAATCGAAGC 469
QY 130 LysAlaGluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAsp 149
470 AATGCTGTCACAAAC---CGATTAAAGTTTCCGTTGGGTTGATTAACCTTAACCTTAC 526
QY 150 IleGlyValIleSerGlyValAspSerPhePro-----VallySerThrGluAlaPhe 166
527 ATGAAAGAGCTTATGGATGAGATCAAGCCCAAGATTATAGCAAAAGCTGAAGCTCGG 586
QY 167 PheLeuLeuValAlaIleGlnMetValSerGlyAlaAlaArgPheTyIleGluAsn 186
587 TTCTTACTCATCGCATTCAAATCGTTGCAAGGCCCAAGCTTCAAGTCAATCCAGGA 646
QY 187 Gln-----VallySerThraenPheAsnArgAlaPheTyRProAspProlySValIleAsn 204
647 AGAGCTATCGTACTACAAATCTTAAC-----AATTATAAAATCTCTCG 691
QY 205 LeuGluGluLySerTrpGlyLySIIleSerGluAlaIleHisnAlaIlyAsnGlyAlaLeu 224
692 TTAGAGAAACAACGCGGAGCTATTTCCAAAGGACGATCGTGTTTAAGAAAGCAT 751
QY 225 ProLySerProLeuGluLeuValAspAla---LyeglyThrlySerTrpIleValIleuArgVal 243
752 CAATCTCGCTTAANTTTTACNATACCTTAATGAGGTTCACACATGACAGATTCACAGAGT 811

QY 244 AspGluIleAsnArg 248
Db 812 AGTGATATATAAAAA 826

RESULT 2

BE035039 993 bp mRNA linear EST 07-JUN-2000
NM02A03 MM Mesembryanthemum crystallinum cDNA 5' similar to
antiviral protein, mRNA sequence.
ACCESSION BE035039
VERSION BE035039.1 GI:8330048
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alceaceae; Mesembryanthemum.
1 (bases 1 to 993)
Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
Ferreira, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
CONTACT: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cdm@u.arizona.edu
Insert Length: 1 Std Error: 0.00.
Location/Qualifiers

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Source

1..993
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/clone_lhb="MM"
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XhoI; Plants stressed 6 weeks in 500mM NaCl"

ORIGIN

Alignment Scores:

Pred. No.: 3.38e-22 Length: 993
Score: 266.50 Matches: 67
Percent Similarity: 56.84 Conservative: 25
Best Local Similarity: 41.44 Mismatches: 56
Query Match: 19.64 Indels: 14
DB: 2 Gaps: 3

US-09-978-274A-4 (1-263) x BE035039 (1-993)

QY 103 GluAnThrLeuCySerSerSerSerSerArg-ValAlaMetSerIleAsnTyRAsnSe 122
746 GAAACCTTCTTTAAGGAGCGACCGTTCCAAACATTCATTGGTGTATCACTACATACG 687
QY 122 rLeuTyProThrMetGlyLyBlyValGluValAsnSerArgAsnGlnValGlnLeuG 142
686 TCTG-----GAGAACTCGCGGTCAAGACGAAACAGATTGAGTTGGG 642
QY 142 yIleGlnIleLeuSerSerAspIleGlyLySIIleSerGlyValAspSerPheProVal 162
641 GCTTGTAACCTAGAGTTGGCCATGATCGATTATGTTAAGTAAACATCGATGGAGAA 582
QY 162 gThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluValAlaArgPheLy 182
581 ACTCGAGGCCCAATTCCTTACTGATTCATCCAGATGGTTTCGAAAGCAGCAGGTTCCA 522
QY 182 sTyIleGluAsnGlnVal---LySerThraenPheAsnArgAlaPheTyRProAspProly 201
521 TTATATCGAGACTTAAGGTACCGAAAGTGGGTACATGTTGCTTCAAAACCGATCCGAA 462
QY 201 sValIleAsnLeuGluGluLySerTrpGlyLySIIleSerGluValAlaIleHisnAlaIlySAs 221

Db 461 AGTATTAACTTGAGAACCACTGGGGAAGATTTCGATGATGATTAAGTCACTTAC 402
Qy 221 nglyAlaLeuPro-----LysProLeuGluLeuValAspAlaLeu 234
Db 401 GTCCAAACCACTGTAATTGTAGACAACTTCCCTCCGATTAATCAATCAATGCTGA 342
Qy 234 sglyThrlySTripLeuValLeuArgValAspGluLeuAsnArgAspValAlaLeuLeu 254
Db 341 TGTATACAAATGGAAGGTGATTAAGATTCCCACTTAATAACCTGACTGGGATTACTCA 282
Qy 254 sTyr 255
Db 281 GTTC 278

RESULT 3
BE036639
LOCUS BE036639 1021 bp mRNA linear EST 07-JUN-2000
DEFINITION MP03B03 MP Mesembryanthemum crystallinum cDNA 5' similar to
ribosome-inactivating protein gelonin, mRNA sequence.
ACCESSION BE036639
VERSION BE036639.1 GI:8331648
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alstroceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 1021)
Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Batton, M.,
Ferreira, H., Kawasaki, S., McColough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
CONTACT: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu
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Location/Qualifiers
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/clone_id="MP"
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Alignment Scores:
Pred. No.: 3,53e-22 Length: 1021
Score: 266.50 Matches: 92
Percent Similarity: 52.2% Conservative: 38
Best Local Similarity: 36.9% Mismatches: 95
Query Match: 19.6% Indels: 26
DB: 2 Gaps: 11

US-09-978-274A-4 (1-263) x BE036639 (1-1021)

Qy 3 AsnThrlyleThrPheAspAlaGlyAsnAlaThrlyleAsnlyTyralaThrPheMetGlu 22
Db 219 AACACCGCTGACATCACTC-----GCCCAACCCCAACATATTCACATTCATGACA 272
Qy 23 SerLeuArgAsnGlnAlaValAspProlyLeuLeuCysTyrglylePrometLeuPro 42
Db 273 TCTCTCCGAGCTCAACTCTCTGGC---ACAACCGCATGT-----CAAAATCCC 317
Qy 43 AspThrAsnSerThr-----ProlySTyrlleuLeuVallyLeuGlnGlyAla 58

Db 318 GTGACAGCTCAACCGGACCGGATCTCCAAAGATTGCTGCTGCTGCACTCAAAACAAC 377
Qy 59 AsnLeuLySThrlyleThrLeuMetLeuArgArgAsnLeuTyValMetGlyTyrSer 78
Db 378 TCGCAAAAGACCAACACACCTCGCAATGACGTGACAAAGCGCTATGTCGTGCTTACCGC 437
Qy 79 AspProPheAsnGlyAsnlyCysArgTyrlHislylePheAsnAspLyThrGlu 98
Db 438 GACAAAGCT---GGCGAAAGAACCTGCGCAACTCTCTTACAGATGCTCCACAGCTGCT 494
Qy 99 ArgThrAspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerly 118
Db 495 AGG-----AACCACTCTCTCAAGGCGCGACGTTCCG-----AACAT 533
Qy 119 AsnTyrlAsnSerLeuTyrlProThrMetGluLyValAlaGluValAsnSerArgAsn 138
Db 534 GCGTTCGAGAGGAGCTTCATAGCCTTGAAGAGGCTCAAG---CAAGCCGAAATGCA 590
Qy 139 ValGlnLeuGlylyleGlnleLeuSerSerAspIleGlylyleSerGlyValAspSer 158
Db 591 ATAGAGTTAGGGGTGAATTAACCTAGAGTTGCCATCGAGTCGTTTGGTAG-AACCCG 649
Qy 159 PheProVallySThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAla 178
Db 650 ATTAATGGGAGATGTGAGGCCAAATCTTGCTGATCTATACAGATGTTCTGAGACA 709
Qy 179 AlaArgPheLySTyrlleGluAsnGln---VallySThrAsnPheAsnArgAlaPheTyr 197
Db 710 GCACGTTTAAGTATATTAAGAAAGGTGACCCAAAGTGTATCAATGCTGCTCAAC 769
Qy 198 ProAspProlyValIleAsnLeuGluLySTyrlPdylylyleSer---GluAlaIle 216
Db 770 CCCGACCCGAAAGTCTGAGTTTGGGAAACAAATGGGGAAGATTTCGCAAAATTAATA 829
Qy 217 HisAsnAlaLysAsnGlyAlaLeuProlyS-----ProLeuGluLeuValAspAlaLys 234
Db 830 AGACAGTGCAGCGCAAAACTGTTGTC-AAATATTACCGCGATATTCTTCAATGCTGA 888
Qy 235 GlyThrlySTripLeuValLeuArgVal 243
Db 889 TGTTCATCAATGGAAGGTGATTAAGGTTG 915

RESULT 4
BE036541
LOCUS BE036541 1033 bp mRNA linear EST 07-JUN-2000
DEFINITION MP01B07 MP Mesembryanthemum crystallinum cDNA 5' similar to
antiviral protein, mRNA sequence.
ACCESSION BE036541
VERSION BE036541.1 GI:8331550
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alstroceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 1033)
Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Batton, M.,
Ferreira, H., Kawasaki, S., McColough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
CONTACT: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu
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Location/Qualifiers
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/dev_stage="6 weeks"
/clone_lib="MP"
/note="3 d 500mM NaCl"

Alignment Scores:

Pred. No.:	8,56e-22	Length:	1033
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Percent Similarity:	54.1%	Conservative:	36
Best Local Similarity:	35.6%	Mismatches:	68
Query Match:	19.4%	Indels:	21
DB:	2	Gaps:	7

US-09-978-274a-4 (1-263) x BE036541 (1-1033)

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Qy 71 AsnLeuTyValMetGlyTyrSerAspProPheAsnGlyAsnLysCysArgTyrHisIle 90
Db 47 AGCGTCATGTCGGCTACCGCCGACACCTT--GGCGAAGAACCGTCCCACTTC 103
Qy 91 PheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSerSer 110
Db 104 CTAGAGCATGCTCCACCGTCGCTAGG-----AACAACTCTTCAAGGGCG 151
Qy 111 SerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGluLys 130
Db 152 ACGGTCGG-----AACATTCGCTCGAGGAGTTACATAGCCTTAGAAGAGCT 202
Qy 131 AlAGlValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAspIle 150
Db 203 GCAAG--CAAGCCGAAATGCATAGAGTGGGTGAATAACTAGAGTTGGCAT 259
Qy 151 GlyLysIleSerGlyValAspSerPheProValIleThrGluAlaPhePheLeuVal 170
Db 260 GAGTCGGTTTGTGTGAAGAACCCGATTAATGGGAGGTTAGGCAATTCCTGCTAT 319
Qy 171 AlaIleGlnMetValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnVal---Lys 189
Db 320 GCTATACACATGTTCTGTAAGCAGCAGCTTTAAGATATTTGAAGTAAGTGACCCAA 379
Qy 190 ThrAsnPheAsnArgAlaPheTyrProAspProLysValIleAsnLeuGluGluLysTyr 209
Db 380 AGTGGGTACATGCTGCTTCATACCCGACCCGAAAGTGTGAGTTGGAAACAATTGG 439
Qy 210 GlyLysIleSerGluAlaIleHisAsnAlaLysAsnGlyAlaLeuProLysPro----- 227
Db 440 GGGAAAGTTTCGCAAGAGATTCAATGACA-----CTTGGCGGAAACCTGCTGT 450
Qy 228 -----LeuGluLeuValAspAlaLysGlyThrLysTyrIleValLeu 241
Db 491 ACGAATATTTCACCGCGGATTAAGTTACAAATGCTGATGTTCAACAATGAAGCGAT 550
Qy 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyr 255
Db 551 GATGTTGCCACTTAAACCTGATTGGGATATCAACTTC 592

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RESULT 5
BE035038/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BE035038 816 bp mRNA linear EST 07-JUN-2000
MM02001 MM Mesembryanthemum crystallinum cDNA 5' similar to
antiviral protein, mRNA sequence.
BE035038
BE035038.1 GI:8330047
EST.
Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzooceae; Mesembryanthemum.

REFERENCE
AUTHORS
Bohrer, H.J., Borchert, C., Brazille, S., Brooks, J., Baton, M.,
Perrera, H., Kawasaki, S., McCollough, A., Michaelowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.

TITLE
JOURNAL
COMMENT

Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu.

FEATURES
source
1. 816
Location/Qualifiers

/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/cell_type="epidermal bladder cells"
/dev_stage="12 weeks old"
/clone_lib="WM"
/note="Vector: Bluescript SK+; Site 1: EcoRI; Site 2:
XhoI; Plants stressed 6 weeks in 500mM NaCl"

ORIGIN

Alignment Scores:

Pred. No.:	4,57e-21	Length:	816
Score:	255.50	Matches:	65
Percent Similarity:	54.4%	Conservative:	28
Best Local Similarity:	38.0%	Mismatches:	59
Query Match:	18.9%	Indels:	19
DB:	2	Gaps:	4

US-09-978-274a-4 (1-263) x BE035038 (1-816)

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Qy 103 GluAsnThrLeuCysSerSerSerSerArg----- 113
Db 786 CAAATTCCTTAAGCATGCTTACACAGTCATTAAGAAACCTTCTTAAGGAGCG 727
Qy 114 ---ValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGluLysValGlu 132
Db 726 CCGGTGCAAAACATTCCTCCATTTGGGTGTAATATCATAGCTCTTGAGAAACCTGCGGT 667
Qy 133 ValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLys 152
Db 666 ---CAAGCCGAAACGATATGACGTTGGGCTGTGTAATAGATTGCCATCGATCA 610
Qy 153 IleSerGlyValAspSerPheProValIleThrGluAlaPhePheLeuValAlaIle 172
Db 609 ATTATGATTAATAAAACGATCGATCGAAACCTGAGCCAAATTCATGATTCGCATC 550
Qy 173 GlnMetValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnVal---LysThrAsn 191
Db 549 CAGATGTTTCAGAACACGACGCTTCATTTATATGAACATTAAGGTGCCGAAAGTGG 490
Qy 192 PheAsnArgAlaPheTyrProAspProLysValIleAsnLeuGluGluLysTyrGlyLys 211
Db 489 TCACATGCTTCCTTCAACCCGATCCGAAGATTAATCTTGAGAAACAACGTGGAGAG 430
Qy 212 IleSerGluAlaIleHisAsnAlaLysAsnGlyAlaLeuPro----- 225
Db 429 ATTTCGATGAGATTCATTAAGTCATGATGTCGAAACCACTGCTAATTGTACGAACAT 370
Qy 226 ---LysProLeuGluLeuValAspAlaLysGlyThrLysTyrIleValLeuArgValAsp 244
Db 369 TCCCTCGCATTAATCAATGCTGATGTGACCAATGAAAGGATGAATGATGCC 310
Qy 245 GluIleAsnArgAspValAlaLeuLeuLysTyr 255
Db 309 ACTATTAACCTGACTTGGGATATCAACTTC 277

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RESULT 6
BE037217
LOCUS
DEFINITION
ACCESSION
VERSION

BE037217 639 bp mRNA linear EST 07-JUN-2000
MP1802 MP Mesembryanthemum crystallinum cDNA 5' similar to
ribosome-inactivating protein/antiviral protein, mRNA sequence.
BE037217
BE037217.1 GI:8332233

KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Caryophyllales; Astroceae; Mesembryanthemum.
REFERENCE Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferras, H., Kawasaki, S., McCollough, A., Michalowski, C.B., Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R. Functional Genomics of Plant Stress Tolerance Unpublished (2000)
JOURNAL Contact: Michalowski, C.B.
COMMENT University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cdm@u.arizona.edu.
Location/Qualifiers
1. .639
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/issue_type="apical meristem and leaf primordia"
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Alignment Scores:
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Score: 251.50 Matches: 70
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QY 47 ThrProlyrTyrlLeuValLyeLengInglValaenLeu---LysThrIleThrlleu 65
Db 29 ACAGAACTTCTGTTGGTGTCTCCAAATCAAGTGAATGAGCAAGCAATCATCATTA 88
QY 66 MetLeuArgArAsnLeuTyrlValMetGlyTyrlSerAapProPhaenGlyAsnLys 85
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QY 86 CysArGlyrHisIlePheAsn-----AspIleThrSerThrlGluArg 99
Db 146 TGTGCTACCACTGCTTAAAGAACTAAAGATGTAAGCATCTGTGTGATGATTAATCA 205
QY 100 ThrAspValGluAnthrLeuCySerSerSerSerSerArGValAlaMetSerIleAsn 119
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QY 120 TyrAnSerLeuTyrlProThrMetGluLysValaGluValaAnSerArGAsnGluVal 139
Db 266 TACAGCTTCAATTAATGTAACCTTGAAGAAAGAGTGCCTTGAAGCTAAGGGA----- 319
QY 140 GluLeuGlyIleGlnIleLeuSerSerAspIleGlyLys---IleSerGlyValaAspSer 158
Db 320 AGAAGAGAGTGAATGATTAATTAAGTAAGTAATAGTTCAATTAAGAAAGAGGATTA 379
QY 159 PheTroVallyrThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAla 178
Db 380 ATGAATGAAAGAGTGAAGCTAATCTTCTAGTGGATTCAAATGTTGTGAGAGCT 439
QY 179 AlaArgPheLysTyrlIleGluAsnGluValLysThrAnPheAnArgAlaPhe-TyrPr 198
Db 440 GCAGGTTCTCTTACATACAGAGAGAGTA---GCCAGCATTTGACAAATTTCAAGGCG 496
QY 198 cAspProLysValIleAnLeuGluGluLysTyrlPoliy----- 210

Db 497 TGATGACCTACGATTTGCTTAAAGAAAGAGTGAATGAGCTTCAAAAAATCAAGAC 556
QY 211 ---LysIleSerGluAlaIleHisAsn 218
Db 557 ACMAAGGTACACCTTCAATCAGCAT 584
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LOCUS AM053634
DEFINITION L30-1401r3 Ice plant Lambda Uni-Zap XR expression library, 30 hours
NAcl treatment Mesembryanthemum crystallinum cDNA clone L30-1401
5', mRNA sequence.
ACCESSION AM053634
VERSION AM053634.1 GI:5916827
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Astroceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 837)
Cushman, J.C.
AUTHORS An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
poly(A) tail, 10 nt: 838. .847
PCR Primers
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BACKWARD: T3
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Score: 248.50 Matches: 76
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Query Match: 18.3% Indels: 20
DB: Gaps: 8
US-09-978-274A-4 (1-263) x AM053634 (1-837)
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Db 5 AACACATATTCACATTCATGACATCTCTCCGAGCTCAACTCTGTGC---ACAACGCA 61
QY 35 CysTyrlGlyIleProMetLeuProAapThrAnSerThr-----ProLysTyrl 50
Db 62 TGT-----CAATCCCGGTGACGAGTCAACCGACGAGTCTTCCACGATTC 109
QY 51 LeuLeuValLysLeuGlnGlyAlaAsnLeuTyrlThrIleThrLeuMetLeuArgArgAsn 70

Db 110 GTCTCTCCACCTCCAAAACAACTCCGAAAAGCATCACTCGCATCGACGTACA 169
Qy 71 AsnLeuTyrValMetGlyTyrSerAspProPheAsnGlyAsnLysCysArgTyrHisIle 90
Db 170 AGCCTTATGTCGTCGGCTTACCGGACAGACTT--GACGAAAAGACCGGCCAACCTTC 226
Qy 91 PheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSerSerSer 110
Db 227 CTTAGCATGCTCCACGTCGCTAGG-----AACACCTCTTCAAGGGGCG 274
Qy 111 SerSerArgValAlaMetSerIleAsnTyrAsnSerIleTyrProThrMetGluLys 130
Db 275 ACAGTTTCG-----ACATTGCGTTCGAGAGGAGTTACATAGACCTTAGAAGAGCT 325
Qy 131 AlAGluValAsnSerArgAsnGlnValGlnLeuGlnIleGlnIleLeuSerSerAspIle 150
Db 326 GCAAG--CAAGGCCAAATGCATATAGATTAGGGGTGAATTAACCTAGACTTGCATC 382
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Db 383 GAGTCGGTTTGGTAGAAGACCGATTATGCGCAGGTCAGGCCAATTCTTGCTGATT 442
Qy 171 AlaIleGlnMetValSerGluAlaAlaArgPheLysTyrIleGluAsnGln--ValLys 189
Db 443 GCATATACAGATGTTCTGAAGCAGCAGGTTTAAATATTTGAAGTAAAGGGGACCCAA 502
Qy 190 ThrAsnPheAsnArgAlaPheTyrProAspProLysValIleAsnLeuGlnLysTyr 209
Db 503 AGTGGGTTACATGGGTTGTCMAACCCGACCCGAAAGTG-CTGAGTTTGAGAACATGGG 561
Qy 210 GlyLysIleSerGluAlaIleHisAsnAlaLysAsnGlyAlaLeu 224
Db 562 GGAAGATTCCAGAGATCATAGACAGTTGGCGGCAACCGGTTG 606
RESULT 8
LOCUS CA838757 649 bp mRNA linear EST 12-DEC-2002
DEFINITION MCT020B02.167445 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT020B02.5, mRNA sequence.
ACCESSION CA838757
VERSION CA838757.1 GI:26566522
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 649)
Cushman, J.C.
An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRIMERS
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BACKWARD: T7 21mer
Plate: 020 row: B column: 02
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High quality sequence stop: 649.
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/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

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Pred. No.: 9.1e-20 Length: 649
Score: 245.00 Matches: 62
Percent Similarity: 53.4% Conservative: 24
Best Local Similarity: 38.5% Mismatches: 61
Query Match: 18.1% Indels: 14
DB: 6 Gaps: 4
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Qy 123 LeuTyrProThrMetGluLysValAsnSerArgAsnGlnValGlnLeuGly 142
Db 85 TTA-----GAAATGCTCCAAACCAACGACGAGAACCATAGATTAGGG 129
Qy 143 IleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPheProValLys 162
Db 130 GTGATTAACATAGATTGTCGATCGATCGGTTTATGTTAGTAAACATCGACAGAGAGA 169
Qy 163 ThrGluAlaPhePheLeuValAlaIleGlnMetValSerGluAlaAlaArgPheLys 182
Db 190 AATGAGCCCAAAATCTTCTGATGATCCATACAGATGTTCTGAACACGACGAGTTCAG 249
Qy 183 TyrIleGluAsnGlnValLysThrAsnPhe-----AsnArgAlaPheTyrProAspPro 200
Db 250 TATATTGAGATGATAGGTGAACCAAGTGCCTTAGATTAGATTCGTTTACCCGACCG 309
Qy 201 LysValIleAsnLeuGlnLysTyrPrgLysIleSerGluAlaIleHisAsnAlaLys 220
Db 310 AAATGCTGCTTTTGAAGACCAATTCGGGGAGATTTCCGAGAGATTTCATGAGAGTCT 369
Qy 221 AsnGlyAlaLeuPro-----LysProLeuGlnLeuValAspAlaLys 234
Db 370 --GGGGCAAACTCTGTTATGAATCTTTCACCTCCGATTCGTTAAAGAAACCAAT 426
Qy 235 GlyThrTyrTrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLys 254
Db 427 GGTGATCCATGACGCGTGAATAGTTGACACTTTAGACCTGAATGGGATATCTCAG 486
Qy 255 Tyr 255
Db 487 TTC 489
RESULT 9
LOCUS CA839330 649 bp mRNA linear EST 12-DEC-2002
DEFINITION MCT026C11.171755 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT026C11.5, mRNA sequence.
ACCESSION CA839330
VERSION CA839330.1 GI:26567095
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum
ORGANISM Mesembryanthemum crystallinum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.

REFERENCE 1 (bases 1 to 649)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 026 row: C column: 11
Seq primer: T3 20mer
High quality sequence stop: 649.
Location/Qualifiers

FEATURES
SOURCE 1..649
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT026C11"
/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="rice plant lambda Uni-Zap XR expression
library; 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN
Alignment Scores:
Pred. No.: 9.1e-20 Length: 649
Score: 245.00 Matches: 62
Percent Similarity: 53.4% Conservative: 24
Best Local Similarity: 38.5% Mismatches: 61
Query Match: 18.1% Indels: 14
DB: Gaps: 4

US-09-978-274A-4 (1-263) x CA839330 (1-649)

QY 103 GUAenThrleuCySerSerSerSerSerArgValAlaMetSerIleAsnTYrAsnSer 122
DB 25 GAGAAATCTCTTTCATGAGCAACAGTTGGAACCTTGCTTCAAGGACCTTACACATCC 84
QY 123 LeuTYrProThrMetGluValylValaGluValaAsnSerArgAsnGlnValGlnLeuGly 142
DB 85 TTA-----GAGAAATCTCTTCAAGCAACCAACCAAGCAAGCAAGCAAGCAAGCAAG 129
QY 143 IleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPheProValys 162
DB 130 GTGATTAACATGAGAGTTGCGATGAGTCGGTTATGTATGATGACATGACCAAGTCAGAGA 189
QY 163 ThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluValAlaAlaArgPheLys 182
DB 190 AATAGAGGCAAAATCTTGCTGATGATGCAATGATGATGATGATGATGATGATGATGATG 249
QY 183 TyrIleGluAsnGlnValIleThrAsnPhe-----AsnArgAlaPheTYrProAspPro 200
DB 250 TATATGAGAGTAAGGTACCAACCAAGTCGTTAATGATGATGATGATGATGATGATGATG 309
QY 201 LysValIleAsnLeuGluGluValylTyrGlyLysIleSerGluAlaIleHisAsnAlaLys 220
DB 310 AAATAGCTGCTTTGAGACCAATGCGGGAAGATTGCGAGGAGATTCAAGAGAGTCT 369
QY 221 AsnGlyAlaLeuPro-----LysProLeuGluLeuValAspAlaLys 234
DB 370 ---GGGGGAACCTGCTTGATGAAATCTTCACTCGAATTCGTTAAGAAACCAAT 426

QY 235 GlyThrLysTyrIleValLeuArgValaAspGluIleAsnArgAspValAlaLeuLeuLys 254
DB 427 GGTGATTCATGACGCGGTGATGAGTGTACACTTTAGACCTGAATGGGATCTCAAG 486
QY 255 Tyr 255
DB 487 TTC 489

RESULT 10
CA835532
LOCUS 661 bp mRNA linear EST 12-DEC-2002
DEFINITION MCS038A11 160572 ice plant lambda Uni-Zap XR expression library, 5
days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2
AM). Mesembryanthemum crystallinum cDNA clone MCS038A11 5, mRNA
sequence.

ACCESSION CA835532
VERSION CA835532.1 GI:26563297
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum

REFERENCE 1 (bases 1 to 661)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 038 row: A column: 11
Seq primer: T3 20mer
High quality sequence stop: 661.
Location/Qualifiers

FEATURES
SOURCE 1..661
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCS038A11"
/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="ice plant lambda Uni-Zap XR expression
library; 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase I (2 AM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Library construction was performed
according to Stratagene's recommended protocol for the
lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN
Alignment Scores:
Pred. No.: 9.35e-20 Length: 661
Score: 245.00 Matches: 62
Percent Similarity: 53.4% Conservative: 24
Best Local Similarity: 38.5% Mismatches: 61
Query Match: 18.1% Indels: 14
DB: Gaps: 4

US-09-978-274A-4 (1-263) x CA835532 (1-661)

QY 103 GUAenThrleuCySerSerSerSerSerArgValAlaMetSerIleAsnTYrAsnSer 122
DB 36 GAGAAATCTCTTTCATGAGCAACAGTTGGAACCTTGCTTCAAGGACCTTACACATCC 95
QY 123 LeuTYrProThrMetGluValylValaGluValaAsnSerArgAsnGlnValGlnLeuGly 142

Db 96 TTA-----GAGAAATGCTGCAAAACCAACGACGAAAGCATAGATTAGGG 140
Qy 143 lIleGlnIleuSerSerAepIleGlyLyseRgiYValaPserPheProValys 162
Db 141 GTGATTAACCTAGAGTTTGCATGCAAGTGGTTATGTAAAGACATGCAAGTCAGGA 200
Qy 163 ThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPheLys 182
Db 201 AATGAGGCCAAATCTTGCTGATTCATGACATAGATGTTTGAAGAGCAAGGTTCAAG 260
Qy 183 TyrIleGlnGlnGlnValLysThrAsnPhe-----AsnArgAlaPheTyrProAspPro 200
Db 261 TATATTGAGGTAAAGTGAAACCAAGTCGCTTAGATTATGATGATGCTTACCCGACCCG 320
Qy 201 LysValIleLeuLeuGlnGlnGlnLysTyrPglYLyseRgiYValaIleHisAsnAlaLys 220
Db 321 AAAATGCTGCTTTGGAGACCAATTTGGGGAGAGATTTCGACAGATTCATGAGAGTCT 380
Qy 221 AsnGlyAlaLeuPro-----LysProLeuGlnLeuValaAspAlaLys 234
Db 381 ---GGGGCGAAACCTGCTGTATGAAATCTTCACTCCGATTCGCTTAAAGAAACCAAT 437
Qy 235 GlyThrLysTrpIleValLeuArgValaAspGluIleAsnArgAspValAlaLeuLeuLys 254
Db 438 GGTATTCATGACGCGTGATAGTTGACACTATTAAGACTGAATGGGAGTACTCAAG 497
Qy 255 Tyr 255
Db 498 TTC 500

RESULT 11
LOCUS CA839511 671 bp mRNA linear EST 12-DEC-2002
DEFINITION MCT028D04 172117 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT028D04 5, mRNA sequence.

ACCESSION CA839511 GI:26567276
VERSION CA839511
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alisoaceae; Mesembryanthemum.
1 (bases 1 to 671)
Cushman, J.C.
An expressed sequence tag database for the common ice plant.

REFERENCE
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant.
JOURNAL Mesembryanthemum crystallinum
COMMENT Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 028 row: D column: 04
Seq primer: T3 20mer
High quality sequence stop: 671.

FEATURES
source location/Qualifiers

1..671
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT028D04"
/issue_type="leaf"
/dev_stage="five-week-old"
/clone_id="ice plant Lambda Uni-Zap XR expression

ORIGIN

library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM)."
/note=Vector: Lambda Uni-Zap XR. Bluescript SK-; Site 1: EcoRI, Site 2: XhoI. Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

Alignment Scores:

Pred. No.:	9.56e-20	Length:	671
Score:	245.00	Matches:	62
Percent Similarity:	53.4%	Conservative:	24
Best Local Similarity:	38.5%	Mismatches:	61
Query Match:	18.1%	Indels:	14
DB:	6	Gaps:	4

US-09-978-274a-4 (1-263) x CA839511 (1-671)

Qy 103 GluAsnThrLeuCySerSerSerSerAepIleGlyLyseRgiYValaIleMetSerIleAsnTyrAsnSer 122
Db 25 GAGAAATCTTTCATGAGACAGCTTCGAACTTCGTTCAAGGAGCTTACACATCC 84
Qy 123 LeuTyrTrpThrMetGluLysValaGlnValaAsnSerArgAsnGlnValaGlnLeuGly 142
Db 85 TTA-----GAGAAATGCTGCAAAACCAACGACGAGAGAGCCATAGATTAGGG 129
Qy 143 lIleGlnIleuSerSerAepIleGlyLyseRgiYValaIleHisAsnAlaLys 162
Db 130 GTGATTAACCTAGAGTTTGCATGCAAGTGGGAGAGATTTCGACATGACAGACAGGA 189
Qy 163 ThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPheLys 182
Db 190 AATGAGGCCAAATCTTGCTGATTCATGACATAGATGTTTCTGAAGCAAGGTTCAAG 249
Qy 183 TyrIleGlnGlnGlnValLysThrAsnPhe-----AsnArgAlaPheTyrProAspPro 200
Db 250 TATATTGAGGTAAAGTGAAACCAAGTCGCTTAGATTATGATGATGCTTACCCGACCCG 309
Qy 201 LysValIleLeuLeuGlnGlnGlnLysTyrPglYLyseRgiYValaIleHisAsnAlaLys 220
Db 310 AAAATGCTGCTTTGGAGACCAATTTGGGGAGAGATTTCGACAGATTCATGAGAGTCT 369
Qy 221 AsnGlyAlaLeuPro-----LysProLeuGlnLeuValaAspAlaLys 234
Db 370 ---GGGGCGAAACCTGCTGTATGAAATCTTCACTCCGATTCGCTTAAAGAAACCAAT 426
Qy 235 GlyThrLysTrpIleValLeuArgValaAspGluIleAsnArgAspValAlaLeuLeuLys 254
Db 427 GGTATTCATGACGCGTGATAGTTGACACTATTAAGACTGAATGGGAGTACTCAAG 486
Qy 255 Tyr 255
Db 487 TTC 489

RESULT 12
LOCUS CA833333 689 bp mRNA linear EST 12-DEC-2002
DEFINITION MCS021A09 151944 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS021A09 5, mRNA sequence.

ACCESSION CA833333 GI:26561098
VERSION CA833333
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alisoaceae; Mesembryanthemum.
1 (bases 1 to 689)
Cushman, J.C.
An expressed sequence tag database for the common ice plant.
Mesembryanthemum crystallinum


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Db      141 GTCGATTAACCTAGAGTTTGGATCGACTCGCTTATGTAAGACATGACAGTCAAGACA 200
      163 ThcGluA1aPhePheLeuValAla1leGluMetValSerGluValAlaArgPheLeu 182
      201 AATGAGCCCAATTTCTTGCTGATTCATACAGATGTTCTGAGGACGAGGATTCAG 260
Qy      183 TyrTleGluA1aPheValAlaValSerPhe-----AsnArgAlaPheTyrProAspPro 200
      261 TATATTGAGAGTAGAGGACCAAGTGCCTTAGATTATGATATGATGCTTACACCGACCG 320
Db      201 LysVal1leAsnLeuGluGluValTyrGlyLysTleSerGluValAla1leH1aAsnAlaLys 220
      321 AAAATGCTGCTTTGGAGACCAATTGGGGAGATTTCGACGAGATTCAATGAGAGTCT 380
Qy      221 AsnGlyValaLeuPro-----LysProLeuGluLeuValaAspAlaLys 234
      381 ---GGGGCAAACTGCTGTTGATGATCTTCCACTTCGATTCGTTAAAGAAACCAAT 437
Db      235 GlyThrLysTyrTleVal1leAsnArgValaAspGlu1leAsnArgVala1aLeuLeuLys 254
      438 GGTGATTCATGACGCGGTGATTAAGTTGACACTATTGACCTGAATGGGAGATCTCAG 497
Qy      255 Tyr 255
      498 TTC 500
Db
RESULT 14
LOCUS   CO121195      841 bp      mRNA      linear      EST 16-JUN-2004
DEFINITION GR_Eb02E11.1 GR_Eb Gossypium raimondii cDNA clone GR_Eb02E11 5',
            mRNA sequence.
ACCESSION CO121195
VERSION   CO121195.1 GI:48819882
KEYWORDS  EST.
SOURCE    Gossypium raimondii
ORGANISM  Gossypium raimondii
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
          1 (bases 1 to 841)
REFERENCE Klm,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
          Udang,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
          Wang,R.A.
          Global assembly of Cotton ESTs
          Unpublished (2004)
          Contact: Rod A. Wing
          Arizona Genomics Institute
          The University of Arizona
          Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
          Tel: 520 626 9595
          Fax: 520 621 1259
          Email: rwing@genome.arizona.edu
          Plate: 02 row: E column: 11.
FEATURES
         source
           1..841
             /location="Qualiflere"
             /organism="Gossypium raimondii"
             /mol_type="mRNA"
             /db_xref="taxon:29730"
             /clone="GR_Eb02E11"
             /cissue_type="Floral"
             /dev_stage="3 to +3 DPA"
             /lab_host="DH10B"
             /clone_lib="GR_Eb"
             /note="Vector: pCMV SPORT-6.1; Site_1: NotI; Site_2:
             EcoRV; Library made by Invitrogen with RNA supplied by
             Wendle lab. Directional cloned into NotI-EV. Colonies
             plated/picked by Agt. More glycerol clones held in -80."
ORIGIN
Alignment Scores:
Pred. No.: 7.6e-19 Length: 841
Score: 239.00 Matches: 73

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Percent Similarity: 47.0%
Best Local Similarity: 29.3%
Query Match: 17.6%
DB: 7
Gaps: 9
US-09-978-274a-4 (1-263) x CO121195 (1-841)
Qy      2 1leAsnThrTleThrPheAspAlaGlyAsnAlaThr1leAsnLysTyrAlaThrPheMet 21
      34 ATCTACACAGTAGATTCACACCACTGAAGAGCCACGAGAACTTATCTGAGTTTATG 93
Db      22 GluSerLeuArgGluGluAlaLysAspProLysLeuLysCySerTyrGlyTleProMetLeu 41
      94 AAGGATCTGTACATGATGATGACAGACGCTGACAGATGAAGACCGAGCATGCCGATTTG 153
Qy      42 ProAspThrAsnSerThrPro-----LysTyrLeuLeuValLysLeuGluGly 57
      154 CTTCCCGGATCTCACAGCTTACTGATTCCTGGCAATATGTTCTGTAGAGCTTCMAAT 213
Db      58 AlaAsnLeuLysThrTleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyr 77
      214 ---GTTACCAAACTGTACATTAAGCTTGCATGTCAATGTATATCTTGGGTTAT 270
Qy      78 SerAspProPheAsnGluLysLysCySerGlyHis1lePheAsnAspTleThrSerThr 97
      271 CGTCAAGTGCAGGCTCC-----TATTTCTTAGCATGTCACAGAC--- 312
Db      98 GluArgThrAspValGluAsnThrLeuCySerSerSerSerSerArgValAlaMetSer 117
      313 -----GATTTACGTAATGCTTTGTTCCAGGCACTA-----GGC 348
Qy      118 1leAsnTyrAsnSerLeuTyrProThrMetGluLysLeuAlaGluValAsnSerArgAsn 137
      349 CTACCTTTTACAGGACGATATGCGGACCTTGAAGCGTCTCGGAGATGATGACAGAG 408
Db      138 GluValGluLeuGlyTleGlu1leLysSerSerAspTleGlyLysTleSerGlyVal--- 156
      409 GAATCCCTCTCTGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 468
Qy      157 -----AspSerPheProValLysThrGluAlaPhePheLeuValAla1leGlu 173
      469 CTTAATTAATTAACCATGCCCCCTATC-----GCAAGAGCCCTCATAGTTGCATCCAG 519
Db      174 MetValSerGluValAla1aArgPheLysTyrTleGluAsnGluVal----- 188
      520 ATGCTTTCCGAGCTCGCGGAATGAGAAACATCCACACAAATATCTTGACATTCAGAG 579
Qy      189 -----LysThrAsnPheAsnArgAlaPheTyrProAspProLysVal1leAsnLeuGlu 206
      580 CTTACAGCGGATGGAATCTTATGGAACGTTAATCCAGATGCGCTTAATGATGAGTACGAA 639
Db      207 GluLysTyrGlyLysTleSerGluValAla1leH1aAsnAlaLysAsnGlyAlaLeuProLys 226
      640 ACCAGCTCGGAGGACATTTCTCGGCCATTCAATTCGACACAGATGAAATCTTCGCAAG 699
Qy      227 ProLeuGluLeuVal---AspAlaLys 234
      700 GCAGTTCGTTTATGATGATGCTCAA 726
Db
RESULT 15
LOCUS   CO103587      903 bp      mRNA      linear      EST 16-JUN-2004
DEFINITION GR_Eb0032E01.r GR_Eb Gossypium raimondii cDNA clone GR_Eb0032E01
            3' mRNA sequence.
ACCESSION CO103587
VERSION   CO103587.1 GI:48802273
KEYWORDS  EST.
SOURCE    Gossypium raimondii
ORGANISM  Gossypium raimondii
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
          1 (bases 1 to 903)

```

AUTHORS

Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,
Udall, J. A., Rapp, R. A., Wendel, J. F., Rao, K., Soderlund, C. and
Wing, R. A.

JOURNAL
COMMENT

Global assembly of Cotton ESTs
Unpublished (2004)

Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259

Email: rwing@genome.arizona.edu
Plate: 0032 Row: E Column: 01.
Location/Qualifiers

FEATURES

source

1..903
/organism="Gossypium raimondii"

/mol_type="mRNA"

/db_xref="taxon:29730"

/clone="GR_EB0032E01"

/issue_type="floral"

/dev_stage="3 to +3 DPA"

/lab_host="DH1.0B"

/clone_lib="GR_EB"

/note="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2:
EcoRV; Library made by Invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by AGI. More glycerol clones held in -80."

ORIGIN

Alignment Scores:

Pred. No.:	2.69e-18	Length:	903
Score:	235.00	Matches:	72
Percent Similarity:	46.6%	Conservative:	44
Best Local Similarity:	28.9%	Mismatches:	99
Query Match:	17.3%	Indels:	34
DB:	7	Gaps:	9

US-09-978-274A-4 (1-263) x CO103587 (1-903)

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QY      2  ILeasnthrllethrPhaeAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMet 21
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      172 ATTACACAGTGAAGATTCCACCTGAAGAGCCACGAACTCTTATCTGATGATTATG 231

QY      22  GluSerleuArgAsnGlnAlaLysAspProLysleuLysCysTyrGlyIleProMetIleu 41
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      232 AAGGATCTGTACATGATTGACAGAGCGTGCATAGACGAGACATGCCATATTG 291

QY      42  ProAspThrAsnSerThrPro-----LysTyrIleuValLysLeuGlnGly 57
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      292 CCTCCCGATCTGCACAGCTGATGATCTCGGCAATATGTTGTGTAGAGCTCTCAAT 351

QY      58  AlaAsnleuLysThrIleThrIleuMetLeuArgAsnAsnLysTyrValMetGlyTyr 77
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      352 ---GGTACCAAACTGTCCATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 408

QY      78  SerAspProPheAsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThr 97
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      409 CGTGCAGTGGGGCTCC-----TATTCTTTAGGATGCTCCAGAC--- 450

QY      98  GluArgThrAspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSer 117
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      451 -----GATGTACGTAAATGCTTGTTCACAGGCACTACT-----GGC 486

QY      118 IleAsnTyrAsnSerleuTyrProThrMetGluLysValGluValAsnSerArgAsn 137
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      487 CTACCTTTACAGGACATATGAGGACCTGAGGAGTGTGCGGAGTAGATGACAGAGG 546

QY      138 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyVal--- 156
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      547 GAAATCCTCTGGAATGATGAATGACCAACATATTGATTAACCTGAATTAATCACTAAC 606

QY      157 -----AspSerPheProValLysThrGlnAlaPhePheLeuLeuValAlaIleGln 173
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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Db      607 CCTAATATATACCATGCCCTATC-----GCAAGAGCCCTCATATGATTGATCCAG 657
QY      174 MetValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnVal----- 188
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Db      658 ATGATTTCGAGAGCTGCGGAGATGAGAAACAAATATCTTGCACTTGCAAG 717

QY      189 -----LysThrAsnPheAsnArgAlaPheTyrProAspProLysValIleAsnLeuGlu 206
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      718 CCTACCGCGATGAGAACTTATGAAACGTTTATCATCAGATGCTTATATGATGAGATGAGAA 777

QY      207 GluLysTyrGlyLysIleSerGluAlaIleHisAsnAlaLysAsnGlyAlaLeuProLys 226
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      778 ACCAGCTGGAGAGCAATTCTCTCGGCATTCATCTGACAGATGGAATCTTGCAAG 837

QY      227 ProLeuGluLeuVal---AspAlaLys 234
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Db      838 GCAGTGTGTTAGATATGATGCTCAA 864

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Search completed: April 9, 2006, 06:20:27
Job time : 4781.97 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 8, 2006, 13:04:24 ; Search time 287.08 Seconds
(without alignments)
1628.463 Million cell updates/sec

Title: US-09-978-274A-4
Perfect score: 1357
Sequence: 1 MINTTFDAGNATINKATP.....DEINRVALKKNVNGTCQTT 263

Scoring table: BLOSUM62
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsu62 -TRANS=human40.ccl
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: Issued Patents NA.*
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3: /cgn2_6/ptodata/1/ina/5.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/68.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PCUS.COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PP.COMB.seq.*
8: /cgn2_6/ptodata/1/ina/R.COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1050	77.4	1195	2	US-08-373-858-1	Sequence 1, Appl1
2	1050	77.4	1195	2	US-08-342-7868-1	Sequence 1, Appl1
3	1050	77.4	1379	2	US-08-500-611-1	Sequence 1, Appl1
4	1050	77.4	1379	2	US-08-500-694-1	Sequence 1, Appl1
5	1050	77.4	1379	3	US-07-865-169-1	Sequence 1, Appl1
6	1050	77.4	1379	3	US-09-005-273-1	Sequence 1, Appl1
7	1050	77.4	1379	6	PCT-US96-11546-1	Sequence 1, Appl1
8	1047	77.2	1379	3	US-08-501-253A-1	Sequence 1, Appl1
9	1042	76.8	1379	3	US-07-865-169-2	Sequence 2, Appl1

10	1042	76.8	1379	3	US-09-005-273-3	Sequence 3, Appl1
11	862.5	63.6	918	2	US-08-138-636-1	Sequence 1, Appl1
12	862.5	63.6	918	2	US-08-319-822A-1	Sequence 1, Appl1
13	862.5	63.6	918	2	US-08-471-564-1	Sequence 1, Appl1
14	341	25.1	804	2	US-08-356-161-7	Sequence 7, Appl1
15	341	25.1	804	3	US-08-718-904-23	Sequence 23, Appl1
16	341	25.1	804	3	US-09-449-249-23	Sequence 23, Appl1
17	341	25.1	804	6	PCT-US93-05702-7	Sequence 7, Appl1
18	341	25.1	804	6	PCT-US95-10973A-7	Sequence 7, Appl1
19	340	25.1	765	3	US-08-718-904-79	Sequence 79, Appl1
20	340	25.1	765	3	US-09-449-249-79	Sequence 79, Appl1
21	340	25.1	1167	6	PCT-US95-10973A-57	Sequence 57, Appl1
22	340	25.1	1230	2	US-08-356-161-13	Sequence 13, Appl1
23	340	25.1	1230	2	US-08-718-904-53	Sequence 53, Appl1
24	340	25.1	1230	3	US-09-449-249-53	Sequence 53, Appl1
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26	340	25.1	1230	6	PCT-US93-05702-13	Sequence 13, Appl1
27	340	25.1	1230	6	PCT-US95-10973A-12	Sequence 12, Appl1
28	340	25.1	1230	6	PCT-US95-10973A-13	Sequence 13, Appl1
29	340	25.1	1233	3	US-08-718-904-80	Sequence 80, Appl1
30	340	25.1	1233	3	US-09-449-249-80	Sequence 80, Appl1
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32	340	25.1	1251	3	US-09-449-249-74	Sequence 74, Appl1
33	340	25.1	1251	3	US-08-718-904-74	Sequence 74, Appl1
34	340	25.1	1260	3	US-08-718-904-72	Sequence 72, Appl1
35	340	25.1	1260	3	US-09-449-249-72	Sequence 72, Appl1
36	340	25.1	1266	3	US-08-718-904-75	Sequence 75, Appl1
37	340	25.1	1266	3	US-09-449-249-75	Sequence 75, Appl1
38	340	25.1	1269	3	US-08-718-904-78	Sequence 78, Appl1
39	340	25.1	1269	3	US-09-449-249-78	Sequence 78, Appl1
40	340	25.1	1275	3	US-08-718-904-73	Sequence 73, Appl1
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42	340	25.1	1299	3	US-08-718-904-77	Sequence 77, Appl1
43	340	25.1	1299	3	US-09-449-249-77	Sequence 77, Appl1
44	340	25.1	1299	6	PCT-US95-10973A-58	Sequence 58, Appl1
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ALIGNMENTS

RESULT 1
US-08-373-858-1
; Sequence 1, Application US/08373858
; Patent No. 5631155
; GENERAL INFORMATION:
; APPLICANT: Kim, Man-Keun
; APPLICANT: Lee, Kwan-Ho
; APPLICANT: Na, Byoung-Kook
; APPLICANT: Jeong, Han-Seung
; APPLICANT: Choi, Kyu-Whan
; APPLICANT: Moon, Young-Ho
; APPLICANT: Jeon, Hong-Seob
; TITLE OF INVENTION: Expression Vector for Phytoacta
; TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dardy & Dardy
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/373,858
; FILING DATE: 18-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/17986-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7770
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Phytolacca americana*
TISSUE TYPE: Leaf
US-08-373-858-1

Alignment Scores:

Pred. No.:	2,936-123	Length:	1195
Score:	1050.00	Matches:	200
Percent Similarity:	87.0%	Conservative:	28
Best Local Similarity:	76.3%	Mismatches:	34
Query Match:	77.4%	Indels:	0
DB:	2	Gaps:	0

US-09-978-274a-4 (1-263) x US-08-373-858-1 (1-1195)

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QY 22 GluSerleuarganglnalalyaappProlyleuuleyScyTyrglylePromeleu 41
DB 159 AATGATCTTCGTATGAGGAGAAAGATCCAGTTTAAAGCTATGGAATACCAATGCTG 218
QY 42 ProaPThrAsnSerThrProlyTyrlleuValyleuGlnlyalaanleuLys 61
DB 219 CCAATACAAATCAATCAATCAAGTACGTGTTGAGCTCCAAAGTTCAATTAATAAAA 278
QY 62 ThrlleThrlleuLeuargargasnleuTyrlValmetGlyTyrsEaPProPhe 81
DB 279 ACCATCACTATATGCTGAGACGAAACAAATTTGATGATGAGGTATTCATCCCTT 338
QY 82 AenGlyAsnlyeCyahrgTyrllelePheasnAaplleThrSerThrgluatgThraP 101
DB 339 GAAACCAATMAATGCTGATCAATATCTTAAATGATATCTCAGGTACTGAACCCAAAT 398
QY 102 ValGluAsnThrlleuCyseSerSerSerArgValAlametSerlleaTyraPn 121
DB 399 GTGAGACATCTCTTGGCCAAATGCCAATCTCGTGTGTAATAAACAATTAATCTTGAT 458
QY 122 SerleuTyProThrMetGluTylyValagluValaasnSerlyrganglnValGln 141
DB 459 AGTCGATATCCAACTTGGATCAAAAGCGAGTAAATCAAGAAGTCAAGTCCAACTG 518
QY 142 GlylleGlnlleuSerSerAaplleGlylyleleSerGlyValaPsePheProval 161
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DB 639 AAGTACATAGAGATCAAGTGAAATCTTAATTTTAACGAGCATTCCAACCTTAATCCCAA 698
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DB 759 GAGCTTTACCAACCTCTCGAGCTAGTGAATGCCAGTGTGCCAATGATGATGTTG 818
QY 242 ArgValaPgluileasnargPvalAlaLeuLeuLysTyrlValaanglyThrCyseGln 261
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QY 262 ThThr 263
DB 879 ACAACT 884

RESULT 2

US-08-342-786B-1
Sequence 1, Application US/08342786B

GENERAL INFORMATION:

APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
APPLICANT: Choi, Kyn-Whan
APPLICANT: Lee, Kwan-Ho
APPLICANT: Kim, Man-Keun
TITLE OF INVENTION: A No. 5648234e1 Expression Vector for *Phytolacca*
TITLE OF INVENTION: Antiviral Protein
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby
STREET: 805 Third Ave.
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,786B
FILING DATE: 21-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,024
FILING DATE: 01-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/08862-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
TELEFAX: (212)753-6237

TELEX: 236687

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Phytolacca americana* L.
IMMEDIATE SOURCE:
CLONE: PAP

US-08-342-786B-1

Alignment Scores:
Pred. No.: 2,936-123 Length: 1195
Score: 1050.00 Matches: 200
Percent Similarity: 87.0% Conservative: 28

Best Local Similarity: 76.3%
Query Match: 77.4%
DB: 2
Mismatches: 34
Indels: 0
Gaps: 0

US-09-978-274A-4 (1-263) x US-08-342-786B-1 (1-1195)

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QY 22 GluSerleuArganGlnAlaLysaSPProlyLeuLysCySTyGlyLePrometleu 41
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QY 42 ProAspThraenSerThrProlyTyLeuLeuValLysleuGlnGlyAlaAsnLeuLys 61
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DB 339 GAAACCAATTAATGCTGTTACCATATCTTATGATATCTCAGGTACTGAAGCCAAAGAT 398
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QY 122 SerleuTyProThrmetGluLysLysAlaGluValAsnSerArgaenGlnValGlnLeu 141
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DB 579 AAAACCAAGCGCAATTCCTATGTTGATGACCATCAAAATGATATGAGGCGCAAGATTC 638
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DB 699 GTACTTAATTTGCAAGAGACATGGGTAAGATTTCAACAGCAATTCATGATGCCAAGAT 758
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   ::::::::::::::::::::
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QY 262 ThrThr 263
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DB 879 ACAAAT 884
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RESULT 3

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US-08-500-611-1
; Sequence 1, Application US/08500611
; Patent No. 5756322
; GENERAL INFORMATION:
; APPLICANT: Tumer, Nilgun E.
; TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
; STREET: 600 South Avenue West
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CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,611
FILING DATE: 11-JUL-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCINS 3.0-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
NAME/KEY: mutation
LOCATION: replace(349, "g")
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-611-1
Alignment Scores:
Pred. No.: 3.66e-123 Length: 1379
Score: 1050.00 Matches: 200
Percent Similarity: 87.0% Conservative: 28
Best Local Similarity: 76.3% Mismatches: 34
Query Match: 77.4% Indels: 0
DB: 2 Gaps: 0
US-09-978-274A-4 (1-263) x US-08-500-611-1 (1-1379)
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QY 22 GluSerleuArganGlnAlaLysaSPProlyLeuLysCySTyGlyLePrometleu 41
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DB 351 AATGATCTTCGTATGAAGCAAGATCCAAAGTATGATGATGATGATTCGATCCCTT 410
QY 42 ProAspThraenSerThrProlyTyLeuLeuValLysleuGlnGlyAlaAsnLeuLys 61
   ::::::::::::::::::::
DB 411 CCCAATCAAAATCAATCAATCCAAAGTACGTGTGTGAGCTCAAGTTCAAAATAAAAA 470
QY 62 ThrlleThreumetleuArgaAsnaenLeuTyraLmetGlyTySerAspProPhe 81
   ::::::::::::::::::::
DB 471 ACCATCACTAAATGCTGAGCAAGAACCAATTTGTATGATGATGATTCGATCCCTT 530
QY 82 AsnGlyAsnLysCySaTgTyRHislePheAsnaSPlleThrSerThrgluArgThraSP 101
   ::::::::::::::::::::
DB 531 GAAACCAATTAATGCTGTTACCATATCTTAAATGATATCTCAGGTACTGAAGCCAAAGAT 590
QY 102 ValGluAsnThrlleuCySerSerSerSerSerArgValAlaMetSerlleAsnTyraSP 121
   ::::::::::::::::::::
DB 591 GTAGAGACTACTCTTGGCCCAATGCCAATCTCGTGTATGATAAAAACATTAACCTTGAT 650
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QY 122 SerLeuTyRProThrMetGluValylGluValAsnSerArgAsnGlnValGlnLeu 141
DB 651 AGTCGATATCAATGATGAAATCAAAAGCGAGTAATAATCAAGAACTGAGTCCAACTG 710
QY 142 GlyTlGlnIleLeuSerSerAspIleGlyValIleSerGlyValAspSerPheProVal 161
DB 711 GGAATTCAAATCTCCAGACATGATTAATGAAAGATTTCTGAGATGATGATCACTGAG 770
QY 162 LysThrGluAlaPhePheLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 181
DB 771 AAAACGAGACCGCAATTCCTATTGTGTAGCCATACAAATGATACAGAGCGCAAGATTC 830
QY 182 LysTyrTlIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyrProAspProLys 201
DB 831 AAGTACATGAGATGATCGGTGAAAACATAATTTTAAACAGACATCAACCTTAATCCCAA 890
QY 202 ValIleAsnLeuGluGluValTyrGlyValIleSerGluAlaIleHisAsnAlaLysAsn 221
DB 891 GTACTTAATTTGCAAGAGACATGGGGTGAAGATTTCAACGCAATTCATGATGCCAAGAA 950
QY 222 GlyAlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrLysTyrIleValLeu 241
DB 951 GGAATTTTACCAAACTCTCGAGCTAGTGAATGCCAGTGTGCCAAGTGAATAGTGTG 1010
QY 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsnGlyThrCysGln 261
DB 1011 AGAGTGAATGAATCAAGCTGATGTAGCACTTAAACTAGCTTGAGTGGAGACTGTGAG 1070
QY 262 ThrThr 263
DB 1071 ACAACT 1076
RESULT 4
US-08-500-694-1
Sequence 1, Application US/08500694
Patent No. 5880329
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
TITLE OF INVENTION: DNAs Encoding Fokweed Antiviral Protein
TITLE OF INVENTION: Mutants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,694
FILING DATE: 11-JUL-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS

LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-694-1
Alignment Scores:
Pred. No.: 3,66e-123 Length: 1379
Score: 1050.00 Matches: 200
Percent Similarity: 87.0% Conservative: 28
Best Local Similarity: 76.3% Mismatches: 34
Query Match: 77.4% Indels: 0
DB: 2 Gaps: 0
US-09-978-274A-4 (1-263) x US-08-500-694-1 (1-1379)
QY 2 IleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMet 21
DB 291 GGAATTCACATCTCTACAAATGTTGAGAGTACCAACATTAAGCAATTAACGCACTTTCTG 350
QY 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyTyrIleProMetLeu 41
DB 351 AATGATCTTCGTAAATGAAGCGAAGATCCAAAGTTTAAATGCTATGGAATACCAATGCTG 410
QY 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnIleAlaLeuLys 61
DB 411 CCCAATACAAATACAAATCCAAAGTACGTTGTGTTGAGCTCCAAAGTTCAATTAATAAA 470
QY 62 ThrIleThrLeuMetLeuArgArgAsnLeuTyrValMetGlyTyrSerAspProPhe 81
DB 471 ACCATCACTAATGCTGAGACCAAAATTTGTATGTATGGTTATTCATCTGATCCCTTT 530
QY 82 AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
DB 531 GAAACCAATTAATGCTTACATNTCTTAATGATATCTGAGTCTGAAACCCCAAGAT 590
QY 102 ValGluAsnThrLeuCysSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
DB 591 GTAGAGACTACCTCTTGGCCCAATGCCAATTCGCTGATGTAATAACATAAATTTCAT 650
QY 122 SerLeuTyRProThrMetGluLysValAlaGluValAsnSerArgAsnGlnValGlnLeu 141
DB 651 AGTCGATATCAATGATGAAATCAAAAGCGAGTAATAATCAAGAACTGAGTCCAACTG 710
QY 142 GlyTlGlnIleLeuSerSerAspIleGlyValIleSerGlyValAspSerPheProVal 161
DB 711 GGAATTCAAATCTCCAGACATGATTAATGAAAGATTTCTGAGATGATGATCACTGAG 770
QY 162 LysThrGluAlaPhePheLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 181
DB 771 AAAACGAGACCGCAATTCCTATTGTGTAGCCATACAAATGATACAGAGCGCAAGATTC 830
QY 182 LysTyrTlIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyrProAspProLys 201
DB 831 AAGTACATGAGATGATCGGTGAAAACATAATTTTAAACAGACATCAACCTTAATCCCAA 890
QY 202 ValIleAsnLeuGluGluValTyrGlyValIleSerGluAlaIleHisAsnAlaLysAsn 221
DB 891 GTACTTAATTTGCAAGAGACATGGGGTGAAGATTTCAACGCAATTCATGATGCCAAGAA 950
QY 222 GlyAlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrLysTyrIleValLeu 241
DB 951 GGAATTTTACCAAACTCTCGAGCTAGTGAATGCCAAGTGTGCCAAGTGAATAGTGTG 1010
QY 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsnGlyThrCysGln 261
DB 1011 AGAGTGAATGAATCAAGCTGATGTAGCACTTAAACTAGCTTGAGTGGAGACTGTGAG 1070

Qy	262	ThrThr	263
Db	1071	ACAACT	1076

RESULT 5
US-07-865-169-1

; Sequence 1, Application US/07865169
 ; Patent No. 6015940
 ; GENERAL INFORMATION:

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1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: FLOPPY disk
3 COMPUTER: IBM PC compatible
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: Patent In Release #1.0, Version #1.25
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/07/865,169

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Score:	1050.00
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Best Local Similarity:	76.3%
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DB:	3
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Mismatch:	34
Indels:	0
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US-09-978-274A-4 (1-263) X US-07-865-169-1 (1-1379)

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QY	42	PROASPHTHANSERTHRPROLYSTYIEULEUVALYLSLEUNGINGIYALASNLULYS	61
	
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QY	62	THIIETHLEUWETLEUAHGAHGAANLEULYTRVAMEGILYTSERASPPROHE	81
	
Db	471	ACCATCACTAAATGCTAGAACCAAAACAATTTGTAATGATAGGTTAATTCGATCCCTTT	530

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QY	122	SerIeuYrProThrMetGIuYsValaGIuValaAsnSerArgaAsnGIuAlaGlnIleu	141
Db	651	AGTGAATATCCMAATGGAAATCAAAACGGAGATAAATCMAAGATCAGGTCCAAC	710
QY	142	GIyIleGlnIleIeuSerSerAspIleGIyIysIleSerGIyValaAspSerPheProVal	161
Db	711	GGATTTCAATATCTCGACAGTAATATTGGAAAGATTTCTGGAGTGAATCTCACTGAG	770
QY	162	LYsThrGIuAlaPhePheIeuIeuValaAlleGlnMetValSerGIuAlaAlaArgPhe	181
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QY	182	LYsTYrIleGlnaAsnGIuValLYsThrAsnPheAsnArgAlaPheTYrProAspProLYs	201
Db	831	AAGTACACTAGAGATCGGTGAATAATTTTAAAGAGATTCMAACCTCAATCCCAAA	890
QY	202	ValIleAsnIeuGIuGIuLYsTYrGIyLYsIleSerGIuAlaIleHIsAsnAlaLYsAsn	221
Db	891	GTACTTAATTTGCAAGACATGGGGGTAAAGATTTCCACAGCAATTCATGAAGCCCAAGAT	950
QY	222	GIyAlaIeuProLYsPProIeuGIuIeuValaAspAlaLYsGIYrThLYsTYrIleValIeu	241
Db	951	GGAGTTTACCCAAACCTCTCGAGCTAGTGGATGCCAGTGGTGCACAGTGATAGTGTG	1010
QY	242	ArgValaAspGIuIleAsnArgAspValaIleIeuIeuLYsTYrValaAsnGIYrThCysGln	261
Db	1011	AGAGTGATGAATCAAGCTCGATGTAGCACTTTAAACTACGTTGTGGAGCTGTCAAG	1070
QY	262	ThrThr 263	
Db	1071	ACAAC 1076	

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1  APPLICATION NUMBER: PCT/US96/11546
2  FILING DATE: 11-JUL-1996
3  ATTORNEY/AGENT INFORMATION:
4  NAME: Foley, Shawn P.
5  REGISTRATION NUMBER: 33,071
6  REFERENCE/DOCKET INFORMATION: OClRS 3.3-034
7  TELECOMMUNICATION INFORMATION:
8  TELEPHONE: 908-654-5000
9  TELEFAX: 908-654-7866
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12     LENGTH: 1379 base pairs
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14     STRANDEDNESS: single
15     TOPOLOGY: linear
16     MOLECULE TYPE: cDNA
17     FEATURE:
18     NAME/KEY: CDS
19     LOCATION: 225..1163
20     FEATURE:
21     NAME/KEY: sig_peptide
22     LOCATION: 225..290
23
24 US-09-005-273-1

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 Percent Similarity: 87.0% Conservative: 28
 Best Local Similarity: 76.3% Mismatches: 34
 Query Match: 77.4% Indels: 0
 DB: 6 Gaps: 0

US-09-978-274A-4 (1-263) x PCT-US96-11546-1 (1-1379)

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QY 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeu 41
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DB 351 AATGATCTTCGTAATGAGCGAAGATCCAGTTTAAATGCTAATGCAATCCATGCTG 410
QY 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
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DB 411 CCCAATCAATCAATCAATCCAAAGTACGTTGGTGGCTCCAAAGTTCAATTAATAA 470
QY 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
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DB 471 ACCATCACTAATGCTGAGAGCAAAACATTTGTATGTAGTGGTTATTCGATCCCTTT 530
QY 82 AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
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DB 531 GAAACCAATAAATGCTGTTACCATATCTTTATGATNTCTCAGATCGAAGCCCAAGAT 590
QY 102 ValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
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DB 591 GTAGAGCTACTCTTTGCCAAATGCCAATCTCGTGTAGTAAACATTAACCTTGAT 650
QY 122 SerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAsnGlnValGlnLeu 141
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DB 651 AGTCGATATCCAAATTCGGAATCAAAAGCGGAGTAAATCAAGAACAGAGTCCAACTG 710
QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPheProVal 161
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DB 711 GGAATTCAAATATCTCGACAGTAAATTTGGAAGATTTCTGAGTGAATCTCATTCAG 770
QY 162 LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaIleArgPhe 181
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DB 771 AAAACCAAGCCGAATTCCTATGTGTAGCCATACAAATGTATCAGAGGCGCAAGATTC 830
QY 182 LysTyrIleGlnAsnGlnValLysThrAsnPheAsnArgAlaPheTyrProAspProLys 201
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QY 202 ValIleAsnLeuGlnGluLysTyrGlyLysIleSerGluAlaIleHisAsnAlaLysAsn 221
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QY 222 GlyAlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrLysTyrIleValLeu 241
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DB 951 GGAAGTTTACCCAAACCTCTCGAGCTAGTGATGCCAGTGGTGCMAAGTGAATGTGTG 1010
QY 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsnGlyThrCysGln 261
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DB 1011 AGAGTGAATGAATCAAGCCGTGATGAGCACTTAAACTAAGTGTGGGAGGCTGTGAG 1070
QY 262 ThrThr 263
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DB 1071 ACNACT 1076

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RESULT 8
 US-08-501-253A-1
 ; Sequence 1, Application US/08501253A
 ; Patent No. 6146628
 ; GENERAL INFORMATION:
 ; APPLICANT: Uckun, Fatih
 ; APPLICANT: Tumer, Nilgun
 ; TITLE OF INVENTION: Biotherapeutic Agents Comprising
 ; Recombinant Pap and Pap Mutants

NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merchant & Gould
 STREET: 90 South 7th Street, 3100 No. 6146628west Center
 CITY: Minneapolis
 STATE: MN
 COUNTRY: US
 ZIP: 55402

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/501.253A
 FILING DATE: 11-JUL-1995
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Ketleberger, Denise M.
 REGISTRATION NUMBER: 33,924
 REFERENCE/DOCKET NUMBER: 600.323US01
 TELEPHONE: 612-332-5300
 TELEFAX: 612-332-9081
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1379 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:

NAME/KEY: CDS
 LOCATION: 225..1163
 US-08-501-253A-1

Alignment Scores:
 Pred. No.: 8 81e-123 Length: 1379
 Score: 1047.00 Matches: 199
 Percent Similarity: 87.0% Conservative: 29
 Best Local Similarity: 76.0% Mismatches: 34
 Query Match: 77.2% Indels: 0
 DB: 3 Gaps: 0

US-09-978-274A-4 (1-263) x US-08-501-253A-1 (1-1379)

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QY 2 11easThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMet 21
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DB 291 GTGAATCAATCATCTACATGTTGGAAGTACCACTTCGAATACGCACTTTCTG 350
QY 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeu 41
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DB 351 AATGATCTTCGTAATGAGCGAAGATCCAGTTTAAATGCTAATGCAATCCATGCTG 410
QY 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
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DB 411 CCCAATCAATCAATCAATCCAAAGTACGTTGGTGGCTCCAAAGTTCAATTAATAA 470
QY 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
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DB 471 ACCATCACTAATGCTGAGAGCAAAACATTTGTATGTAGTGGTTATTCGATCCCTTT 530
QY 82 AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
   ::::::::::::::::::::
DB 531 GAAACCAATAAATGCTGTTACCATATCTTTAATGATATCTCAGATCGAAGCCCAAGAT 590
QY 102 ValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
   ::::::::::::::::::::
DB 591 GTAGAGCTACTCTTTGCCAAATGCCAATCTCGTGTAGTAAACATTAACCTTGAT 650
QY 122 SerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAsnGlnValGlnLeu 141
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DB 651 AGTCGATATCCAAATTCGGAATCAAAAGCGGAGTAAATCAAGAACAGAGTCCAACTG 710

```


;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
;; ADDRESSEE: MENTILIK
;; STREET: 600 South, Avenue West
;; CITY: Westfield
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 07090
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/005,273
;; FILING DATE: 09-JAN-1998
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/500,611
;; FILING DATE: 11-JUL-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/500,694
;; FILING DATE: 11-JUL-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/11546
;; FILING DATE: 11-JUL-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Foley, Shawn P.
;; REGISTRATION NUMBER: 33,071
;; REFERENCE/DOCKET NUMBER: OCTRS 3.3-034
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 908-654-5000
;; TELEFAX: 908-654-7866
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1379 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 225..1163
;; FEATURE:
;; NAME/KEY: sig peptide
;; LOCATION: 225..230
;; US-09-005-273-3

Alignment Scores:
Pred. No.: 3.8e-122 Length: 1379
Score: 1042.00 Matches: 199
Percent Similarity: 86.6% Conservative: 28
Best Local Similarity: 76.0% Mismatches: 35
Query Match: 76.8% Indels: 0
DB: 3 Gaps: 0

US-09-978-274A-4 (1-263) x US-09-005-273-3 (1-1379)
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QY 22 GluSerLeuArgAsnGlnAlaValAspProlySerLeuValCysTyrGlyIleProMetLeu 41
DB 351 AATGATCTTCGTATGAGGCAAGAGATCAAGTTTAAATGCTATGGAATACCAATCTG 410
QY 42 ProAspThrAsnSerThrProlySTYrLeuLeuValIlySleuGlnGlyAlaAsnLeuLys 61
DB 411 CCGAATACCAATACCAATTCGAAGCAGCTGTGTTGAGCTCCCAAGTTCAATRAAAAA 470
QY 62 ThrIleuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
DB 471 ACCATCACTTAATGCTGAGACGAACAATTTGTATGATGAGGGGTATTCTGATCCCTTT 530

QY 82 AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
DB 531 GAAACCAATTAATGCTGTACCAATATCTTAATATATCTGAGTACGAAAGCCCAAT 590
QY 102 ValGluAsnThrLeuCysSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
DB 591 GTAGAGACTACTCTTGCCCAATGCCAATCTGTGTAGTAAATAAATTAACCTTTGAT 650
QY 122 SerLeuTyrProThrMetGluLysValGluValAsnSerArgAsnGlnValGlnLeu 141
DB 651 AGTCGATATCCAAATTCGATGAAACCGGAGTAATAATCAAGAAAGTCAGGTCCAAGT 710
QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPheProVal 161
DB 711 GGAATTCAAATTAATCTGACAGATTAATGGAAGATTTCTGAGATGATCTTCACTGAG 770
QY 162 LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 181
DB 771 AAAACCGAAGCCGAATTCCTATTGTTGAGCCATCAATGATTCAGAGGCGAAGATTC 830
QY 182 LysTyrIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyrProAspProLys 201
DB 831 AAGTACATGAGAAATCAGGTGAAAATTAATTTTAAACAGAGCATTCACCTTAATCCCAA 890
QY 202 ValIleAsnLeuGluGluLysTyrGlyLysIleSerGluAlaIleHisAsnAlaLysAsn 221
DB 891 GTACTTAATTTGCAAGAGACATGAGTTAGATTTTCAACAGCAATTCATGAGCCAAAGAT 950
QY 222 GlyAlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrLysTyrIleValLeu 241
DB 951 GGAATTTTACCAAACTCTGAGCTAGTGTGATGCCAGTGTGATGATGTG 1010
QY 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsnGlyThrCysGln 261
DB 1011 AGAGTGTATGAATCAAGCTGATGATGACACTTAAATCACTGATGATGAGGAGTGTGAG 1070
QY 262 ThrThr 263
DB 1071 ACAAAT 1076

RESULT 11
US-08-138-636-1
Sequence 1, Application US/08138636
Patent No. 5348865
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seoh
APPLICANT: Choi, Kyu-Whan
APPLICANT: Lee, Kwan Ho
APPLICANT: Kim, Man Keun
TITLE OF INVENTION: No. 5348865e1 Genome Coding Phytoleuca Antiviral
TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 THIRD AVE.
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,636
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351

US-09-978-274A-4 (1-263) X US-08-319-622A-1 (1-918)

[illegible]

RESULT 13
US-08-471-564-1
; Sequence 1, Application US/08471564

? APPLICANT: Moon, Young-Ho
 ? APPLICANT: Jeon, Hong-Seoh
 ? APPLICANT: Choi, Kyu-Whan
 ? APPLICANT: Lee, Kwan Ho
 ? APPLICANT: Kim, Man Keun
 ? TITLE OF INVENTION: No. 573326e1 Genome Coding Phytoelcra Antiviral
 ? TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
 ? NUMBER OF SEQUENCES: 2
 ? CORRESPONDENCE ADDRESS:

```

1 ADDRESSER: DARBY & DARBY
2 STREET: 805 THIRD AVE.
3 CITY: NEW YORK
4 STATE: NY
5 COUNTRY: USA
6 ZIP: 10022
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: Patentin Release #1.0, Version #1.25
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/08/471,564
14 FILING DATE:
15 CLASSIFICATION: 435
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: 08/210,396
18 FILING DATE:
19 APPLICATION NUMBER: US 08/138,636
20 FILING DATE: 15-OCT-1993
21 CLASSIFICATION: 435
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Ludwig, S. Peter
24 REGISTRATION NUMBER: 25,351
25 REFERENCE/DOCKET NUMBER: 0136/18818US
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (212) 527-7700
28 TELEFAX: (212) 753-6237
29 TELEX: 236687
30 INFORMATION FOR SEQ ID NO: 1:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 918 base pairs
33 TYPE: nucleic acid
34 STRANDEDNESS: single
35 TOPOLOGY: linear
36 MOLECULE TYPE: cDNA to mRNA
37 HYPOTHEetical: NO
38 ANTI-SENSE: NO
39 ORIGINAL SOURCE:
40 ORGANISM: Phytolacca insularis
41 IMMEDIATE SOURCE:
42 CLONE: antiviral protein (PIP)
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44 US-08-471-564-1
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50 Best Local Similarity: 66.4% Mismatches: 52
51 Query Match: 63.6% Indels: 4
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Qy 195 AlapherYrProAspProLyValIleAsnLeuGluGluYrTpGlyLysIleSerGlu 214
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Db 745 AAA-----GTAGGCAAGTGAAGACTTG-----CAATGGGACTCCTT 783
Qy 254 LysTYrVal 256
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Db 784 ATGTATTG 792
RESULT 15
US-08-718-904-23
Sequence 23, Application US/08718904
Patent No. 6037329
GENERAL INFORMATION:
APPLICANT: Baird, J. Andrew
APPLICANT: Chandler, Lois Ann
APPLICANT: Soshnowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6037329tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.415C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..804
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..804
OTHER INFORMATION: /note= "Nucleotide sequence
OTHER INFORMATION: corresponding to the clone M13 mp18-G9 in Example I.B.2."
NAME/KEY: mat_peptide
LOCATION: 46..804
OTHER INFORMATION: /product= "Saporin"
US-08-718-904-23
Alignment Scores:
Pred. No.: 1,84e-33 Length: 804
Score: 341.00 Matches: 94

Percent Similarity: 55.5% Conservative: 52
Best Local Similarity: 35.7% Mismatches: 95
Query Match: 25.1% Indels: 22
DB: 3 Gaps: 10
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Qy 2 IleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnYrTYrAlaThrPheMet 21
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Qy 22 GluSerLeuArgAnGlnAlaLysAspProLySLeuYrCyTYrGlyIleProMet--- 40
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Db 106 GATAAATCCGAAACACAGCTAAAGATCCAACTGAAATACGCTGACCAATACCC 165
Qy 41 LeuProAspThrAsnSerThrProLySyrLeuLeuVallyLeuGlnGlyAlaAsnLeu 60
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Db 166 GTGATAGGCCCACTTAAAGAAAAATTCCTTGAATTAATTCNAAGTTCCCGA--- 222
Qy 61 LysThrIleThrLeuMetLeuArgArgAsnLeuYrValMetGlyTYr-----Ser 78
|||
Db 223 GGAACGGTCTCACTTGGCTTAAACGCGATTAATCTGTATGTGTCGCGATCTTGCAATG 282
Qy 79 AspProPheAnGlyAsnLysCyArgTYrHisIlePheAsnApIleThrSerThrGlu 98
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Db 283 GATAACAGATGTTAATCCGCA---TATTACTTCAGATCAAGAAATTAATTCGCCGAG 339
Qy 99 ArgThrAspValGluAsnThrLeuCySerSerSerSerSerArgValaIleMetSerIle 118
|||
Db 340 TTAACC-----GCCCTTTCACAGAGCCACACACTGCAAAATCAGAAAGCTTTA 387
Qy 119 AsnTYrAsnSerLeuYrProThrMetGluLysAlaGluVal-----Asn 134
|||
Db 388 GAATACACAGAAATTTATCACTGATTAAGAAAGATCCCGATTAACACAGAGATCAA 447
Qy 135 SerArgAnGlnValGlnLeuGlyIleGlnIleLeuSerSerArgPileGlyLysIleSer 154
|||
Db 448 AGTAAAAAGAACTCCGGTGGGATGATGACTTCTTCAACGTCAAGAAAGCAAGTAAAC 507
Qy 155 GlyValAspSerPheProVallyrThrGluAlaPhePheLeuLeuValaIleGlnMet 174
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Db 508 ---AAGAAGGCACTGTGTGTTAAAGACGAGCTGATTCCTTATCGCTATTCAGATG 564
Qy 175 ValSerGluAlaAlaArgPheLysTYrIleGluAsnGlnVallyrThrAsnPheAsnArg 194
|||
Db 565 ACGGCTAGAGGAGGCGATTAAGGTACATCAAAACTTGTATCAAGAACCTTCCCAAC 624
Qy 195 AlapherYrProAspProLyValIleAsnLeuGluGluYrTpGlyLysIleSerGlu 214
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Db 625 AAGTTCAACTCGGAAACAAAGTATTCAGTTTGAGGTTAACTGAAAAAATTTCTACG 684
Qy 215 AlAlIleHs--AenAlaLysAnGlyAlaLeuProLySProLeuGluLeuValaSpAla 233
|||
Db 685 GCAATATACGGGAGTCCAAAAACGCGCTTTAATAAAGATTATGATTCGGGTTTGA 744
Qy 234 LysGlyThrYrTpIleValIleuArgValaAspGluIleAsnArgAspValaAlaLeuLeu 253
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Qy 254 LysTYrVal 256
|||
Db 784 ATGTATTG 792
Search completed: April 8, 2006, 14:02:09
Job time : 294.08 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 9, 2006, 01:45:16 ; Search time 941.609 Seconds
(without alignments)
2309.713 Million cell updates/sec

Title: US-09-978-274A-4
Perfect score: 1357
Sequence: 1 MINTTFDAGNATINKYATF.....DEINRDVALLKYVNGTCQTT 263

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/abse/ABSSWB.spool/US09978274/rnat 07042006_173040_28552/app_query.faeta.1
-DB=Published.Applications.NA.Main -QWTS=fastcap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -UNITS=bites -START=1 -END=-1
-MARRK=blousum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEP8SIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abes03h
-USRR=US09978274 @CCN 1.1 2039 @runat 07042006_173040_28552 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1357	100.0	792	3	US-09-978-274A-3
2	1352	99.6	945	3	US-09-978-274A-1
3	1312	96.7	1092	3	US-09-978-274A-19
4	1050	77.4	1379	3	US-09-978-274A-30
5	1050	77.4	1379	10	US-11-106-187-1
6	1042	76.8	1368	3	US-09-978-274A-31
7	1038.5	76.5	1376	8	US-10-467-009-1

8	793	58.4	465	3	US-09-978-274A-5	Sequence 5, Appl1
9	564	41.6	333	3	US-09-978-274A-7	Sequence 7, Appl1
10	453	33.4	934	3	US-09-978-274A-32	Sequence 32, Appl1
11	453	33.4	934	10	US-11-106-187-3	Sequence 3, Appl1
12	452	33.3	855	10	US-11-106-187-20	Sequence 20, Appl1
13	349	25.7	765	3	US-09-792-793A-66	Sequence 66, Appl1
14	349	25.7	765	6	US-10-375-209A-66	Sequence 66, Appl1
15	349	25.7	984	3	US-09-792-793A-60	Sequence 60, Appl1
16	349	25.7	984	6	US-10-375-209A-60	Sequence 60, Appl1
17	349	25.7	993	3	US-09-792-793A-63	Sequence 63, Appl1
18	349	25.7	993	6	US-10-375-209A-63	Sequence 63, Appl1
19	349	25.7	999	3	US-09-792-793A-54	Sequence 54, Appl1
20	349	25.7	999	3	US-09-792-793A-57	Sequence 57, Appl1
21	349	25.7	999	6	US-10-375-209A-54	Sequence 54, Appl1
22	349	25.7	999	6	US-10-375-209A-57	Sequence 57, Appl1
23	342	25.2	935	9	US-10-919-750-4	Sequence 4, Appl1
24	341	25.1	804	3	US-09-861-257-38	Sequence 38, Appl1
25	341	25.1	804	6	US-10-189-360-23	Sequence 23, Appl1
26	340	25.1	765	3	US-09-861-257-23	Sequence 23, Appl1
27	340	25.1	765	6	US-10-189-360-79	Sequence 79, Appl1
28	340	25.1	1230	6	US-10-189-360-53	Sequence 53, Appl1
29	340	25.1	1233	3	US-09-861-257-24	Sequence 24, Appl1
30	340	25.1	1233	6	US-10-189-360-80	Sequence 80, Appl1
31	340	25.1	1251	3	US-09-861-257-77	Sequence 77, Appl1
32	340	25.1	1251	6	US-10-189-360-74	Sequence 74, Appl1
33	340	25.1	1260	3	US-09-861-257-75	Sequence 75, Appl1
34	340	25.1	1260	6	US-10-189-360-72	Sequence 72, Appl1
35	340	25.1	1266	3	US-09-861-257-78	Sequence 78, Appl1
36	340	25.1	1266	6	US-10-189-360-75	Sequence 75, Appl1
37	340	25.1	1269	3	US-09-861-257-81	Sequence 81, Appl1
38	340	25.1	1269	6	US-10-189-360-78	Sequence 78, Appl1
39	340	25.1	1275	3	US-09-861-257-76	Sequence 76, Appl1
40	340	25.1	1275	6	US-10-189-360-73	Sequence 73, Appl1
41	340	25.1	1299	3	US-09-861-257-80	Sequence 80, Appl1
42	340	25.1	1299	6	US-10-189-360-77	Sequence 77, Appl1
43	340	25.1	1320	3	US-09-861-257-77	Sequence 76, Appl1
44	340	25.1	1320	6	US-10-189-360-76	Sequence 76, Appl1
45	337	24.8	804	3	US-09-861-257-35	Sequence 35, Appl1

ALIGNMENTS

RESULT 1
US-09-978-274A-3
; Sequence 3, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Ackinson, Howard
; APPLICANT: Neelan, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 792
; TYPE: DNA
; ORGANISM: *Phytolacca americana*
US-09-978-274A-3

Alignment Scores:
Pred. No.: 4.23e-163
Score: 1357.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 3
Length: 792
Matches: 792
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-978-274A-4 (1-263) x US-09-978-274A-3 (1-792)

QY	1	MetIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysThrPhe	20
Db	1	ATGTAATAATGACATCACCTTGTAGTGGAAATAGCCACATTAAACAAATATGCACTTT	60
QY	21	MetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysErgIleProMet	40
Db	61	ATGGAATCTCTTGCTATCAAGCGAAGATCCAAACTAAATGCTATAGGATCCAAATG	120
QY	41	LeuProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeu	60
Db	121	CTACCTGATATCTAATTCGACCCCTTAAGTACTTAATGGTTTAACTCCAAAGGCGAACTTA	180
QY	61	LysThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspPro	80
Db	181	AAAACATTACATTAATCGCGAGACCAAAATTAATTACGTATGGCTATTCGATCCC	240
QY	81	PheAsnGlyAsnLysCysArgTyrHsIlePheAsnAspIleThrSerThrGluArgThr	100
Db	241	TTCAAATGGCAATAGTGTGCTTACCTAATATTAATTAATGATTAACAAGCAGCAAGCACT	300
QY	101	AspValGluAsnThrLeuCysSerSerSerSerSerSerArgValAlaMetSerIleAsnTyr	120
Db	301	GATGTGGAGATACCTCTTGCTCAAGATTCAGTCTCGGTGCAATGTCCATTAACTAC	360
QY	121	AsnSerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAsnGlnValGln	140
Db	361	AATAGCTTATATCCGACCAATGAGAAAGAAAGCAAGTAATCTCAAGAAATCAAGTCCAA	420
QY	141	LeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPhePro	160
Db	421	TTCGGAATTCAAATTAATCTCAGCAAGATGACATTTGGAAATCTCGAGGTGATTCAATCCCT	480
QY	161	ValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArg	180
Db	481	GTTAAAATCAGAGGCTTTTTTTCTACTGTGATGCCATCCAAATGTTTCAGAGGACGGCA	540
QY	181	PheLysTyrIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyrProAspPro	200
Db	541	TTCAGATCATATAGAACCAAGTCAAGATTAATTTTAATAGACATCTCACTCGATCCC	600
QY	201	LysValIleAsnLeuGlnGluLysTyrGlyLysIleSerGluAlaIleHisAsnAlaLys	220
Db	601	AAAGTAATTAATCTTGGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACAAATGCCAAG	660
QY	221	AsnGlyValLeuProLysPheLeuGluLeuValAspAlaLysGlyThrLysTyrIleVal	240
Db	661	AATGGGGCTTTTACCBAACCACTTAGCTATGATGCCAAAGATCCAAATGATGATGTT	720
QY	241	LeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsnGlyThrCys	260
Db	721	CTTAGAGTGAATCAATCAATCGTATGTGGCACTCTTAAGTACGTAAATGGAACCTGT	780
QY	261	GlnThrThr	263
Db	781	CAGACAACT	789
RESULT 2			
US-09-978-274A-1			
Sequence 1, Application US/09978274A			
Patent No. US20020116737A1			
GENERAL INFORMATION:			
APPLICANT: Thomas, Christopher			
APPLICANT: McPherson, Michael			
APPLICANT: Atkinson, Howard			
APPLICANT: Neelam, Anil			
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM			
FILE REFERENCE: 9341-028			
CURRENT APPLICATION NUMBER: US/09/978,274A			
CURRENT FILING DATE: 2001-10-15			
PRIOR APPLICATION NUMBER: 0025225.4			
PRIOR FILING DATE: 2000-10-14			

RESULT 3

US-09-978-274A-19
; Sequence 19, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PAP-S/Cystatin fusion
US-09-978-274A-19

Alignment Scores:

Pred. No.: 4,19e-157 Length: 1092
Score: 1312.00 Matches: 255
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 96.7% Indels: 0
DB: 3 Gaps: 0

US-09-978-274A-4 (1-263) x US-09-978-274A-19 (1-1092)

QY 1 MetIleasnthrllethrPheaspAlaGlyAsnAlaThrIleAsnlyeTyraIaThrPhe 20
DB 1 ATGATTAATAATACGATCACTTTGATGCTGGAAATGCGACATTAACAATAATGCGACCTTT 60
QY 21 MetGluSerLeuAArgAsnGlnAlaLysAspProLysLeuLysCySyrGlyIlePromet 40
DB 61 ATGCAATCTCTTCCTTAATCAAGCAAGATCCAAATCAAAATGCTATGCGATCAATG 120
QY 41 LeuProAspThrAsnSerThrProLysTyrlleuLeuValLysleuGlnGlyAlaAsnLeu 60
DB 121 CTACCTGAATCAATATTCGACCCCTTAAGTACTTATTTGTTAAGCTCCCAAGTGCAAACCTA 180
QY 61 LysThrIleThrLeuMetLeuAArgAsnAsnLeuTyraIleMetGlyTyrsSerAspPro 80
DB 181 AAAACCATTAACATTAATGCTGAAGCAAAATTAATTAATGATGAGTGGCTATTCGATCC 240
QY 81 PheAsnGlyAsnLysCySArgTyrllePheAsnAspIleThrSerThrGluArgThr 100
DB 241 TTCAATGCAATATAGTGTGCTTACCATATATTATTAATGATTATTAACAGCACCGAAGCACT 300
QY 101 AspAlaGluAsnThrLeuCySerserSerSerSerArgValAlaMetSerIleAsnTy 120
DB 301 GATGTGAAGATTAATCTTGTCTCAAGTCTCAAGTCTCGTGTGCAATGTCATTAACTAC 360
QY 121 AsnSerLeuTyrrProThrMetGluLysLysAlaGluValaAsnSerArgAsnGlnValGln 140
DB 361 AATAGCTTATATCCGACCATGAGAAAGAAAGCAAGAACTCAAGAAATCAAGTCCAA 420
QY 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValaAspSerPhePro 160
DB 421 TTGGAAATTCAAATAATCTCAGCAGTGCACATTGAAAATCTCTGAGGTGATTCAATCCCT 480
QY 161 ValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArg 180
DB 481 GTAAATACTAGGCTTTTCTTCTAGTGTACCAATCCAAATGAGTTTCAAGAGCGCGGA 540
QY 181 PheLysTyrlleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyrrProAspPro 200

DB 541 TTCAAGTCAATAGAGAACCAAGTCAAGCTAATTTTAAATAGCATTTTACCTGATCC 600
QY 201 LysValIleAsnLeuGluGlyLysTyrlleSerGluAlaIleHisAsnAlaLys 220
DB 601 AAAGTAATTAATCTTGAGAGAGAAAGTGGGCAAAATCTCTGAGCAATTCACAAATGCCAAG 660
QY 221 AsnGlyAlaLeuProLysProLeuGlnLeuValaAspAlaLysGlyThrIleTyrrIleVal 240
DB 661 AATGGGCTTAACTCCAAACCACTTGAGCTAGTGAATGCCAAAGTACCAAGTGAATAGTT 720
QY 241 LeuArgValaAspGluIleAsnArgAspValAlaLeuLeuLysTyrr 255
DB 721 CTTAGAGTGAATGAATCAATCGTGAATGTCATCTTCAATGATAC 765

RESULT 4

US-09-978-274A-30
; Sequence 30, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Phytiolacca americana
US-09-978-274A-30

Alignment Scores:

Pred. No.: 2,35e-123 Length: 1379
Score: 1050.00 Matches: 200
Percent Similarity: 87.0% Conservative: 28
Best Local Similarity: 76.3% Mismatches: 34
Query Match: 77.4% Indels: 0
DB: 3 Gaps: 0

US-09-978-274A-4 (1-263) x US-09-978-274A-30 (1-1379)

QY 2 IleAsnthrllethrPheaspAlaGlyAsnAlaThrIleAsnlyeTyraIaThrPheMet 21
DB 291 GTGAATCAATCAATCTCAATGTTGAAAGTACCAATTAAGCAATAGCGCACTTTCTG 350
QY 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCySyrGlyIlePrometLeu 41
DB 351 AATGATCTTGTATGAAGGAAGATCCAAAGTTAAATGCTATGGAATTCAGATGCTG 410
QY 42 ProAspThrAsnSerThrProLysTyrlleuLeuValLysleuGlnGlyAlaAsnLeuLys 61
DB 411 CCCAATCAAAATTAATTCAAAGTACGTGTGTGAGCTCCCAAGGTTCCAAAATMAAAA 470
QY 62 ThrIleThrLeuMetLeuAArgAsnAsnLeuTyraIleMetGlyTyrsSerAspProPhe 81
DB 471 ACCATCACTTAATGCTGAAGCAAAACAATTTGATGATGAGTTATTCGATCCCTTT 530
QY 82 AsnGlyAsnLysCySArgTyrllePheAsnAspIleThrSerThrGluArgThrAsp 101
DB 531 GAAACCAATAAATGCTTACCAATATCTTAATGATATTCAGGTAATGCAAGCAAGAT 590
QY 102 ValGluAsnThrLeuCySerserSerSerSerArgValAlaMetSerIleAsnTyrrAsn 121
DB 591 GTAGAGCTACTCTTGTCCCAATGTCGATGTTGTAATAACATTAATCTTGTAT 650
QY 122 SerLeuTyrrProThrMetGluLysLysAlaGluValaAsnSerArgAsnGlnValGlnLeu 141

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Db 651 AGTCGATATCCAACTGGATGATCAAAAGCGGAGCTAAATCAAGAGATCAAGTCAAGTCAACTG 710
Qy 142 GYIILEGIIIELEUSERSERAPILEGILYVRIIESERGIYVALASPSEPHEPROVAL 161
Db 711 GGAATTCBAATCTCGACAGATTAATTTGGAAGATTTCTGGAGTGAATGTCATTACTGAG 770
Qy 162 LysThrGluAlaPhePheLeuValAlaILEGImetValSerGluAlaAargPhe 181
Db 771 AAAACCGAAGCCGAAATCTATTGTGTAGCCATCAATGGTATCAGAGGCGAAGATTC 830
Qy 182 LysThrILEGIIIELEUSERSERAPILEGILYVRIIESERGIYVALASPSEPHEPROVAL 201
Db 831 AAGTACCTAGAGATCGGTGAAGAACTTAATTTAAGAGAGATTCAAACCTTAACCCAAA 890
Qy 202 ValILEUSERSERAPILEGILYVRIIESERGIYVALASPSEPHEPROVAL 221
Db 891 GTACTTAATTTGCAAGAGACATGGGGTAAATTTCAACAGCATTCATGATGCCAAGAT 950
Qy 222 GYIYALALEUPROLYSPROLEUGIULAUVALASPALALYSGIYTHRYSTPILEVALILEU 241
Db 951 GGAATTTTACCCAAACCTCTCGAGCTAGTGATGCCAGTGGCCAAAGTGAATGTGTG 1010
Qy 242 ArgValASPGLIULILEUSERSERAPILEGILYVRIIESERGIYVALASPSEPHEPROVAL 261
Db 1011 AGAGTGTATAAATCAAGCTGATGAGCACTTTAAACTACGTGTGGAGCTGTCTG 1070
Qy 262 ThrThr 263
Db 1071 ACAAAT 1076
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RESULT 5

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US-11-106-187-1
; Sequence 1, Application US/1106187
; Publication No. US20050183162A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NIGUN E.
; APPLICANT: WANG, PINGER
; TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
; FILE REFERENCE: OCIRS 3.9-060 CONT
; CURRENT APPLICATION NUMBER: US/11/106,187
; PRIOR FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US/09/721,047
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: PCT/US99/11301
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/086,374
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Phytolacca americana
; NAME/KEY: CDS
; LOCATION: (225)..(1163)
US-11-106-187-1
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Alignment Scores:

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pred. No.: 2,35e-123 length: 1379
Score: 1050.00 matches: 200
Percent Similarity: 87.0% conservative: 28
Best Local Similarity: 76.3% mismatches: 34
Query Match: 77.4% indels: 0
DB: 10 gaps: 0
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US-09-978-274A-4 (1-263) x US-11-106-187-1 (1-1379)

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Qy 2 ILEASNTHTRIETHPHEAPALAGLYASNAIATHRIIEASNTYRYRALATHPHEMET 21
Db 291 GTGAATACATATCATCAATATGTTGGAAGTACCAACCTTAGCAAAATACGCCATTTTCTG 350
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Qy 22 GluSerLeuArgAsnGluAlaLysASPProLyLeuLysCysTyrGIYILEPROMETLEU 41
Db 351 AATGATCTTCGTATGAAGCGAAGAAATCCAAAGTTTAAATGCTATGGAATATCCAAATGCTG 410
Qy 42 ProASPThrAnsSerThrProLySTYrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
Db 411 CCCAATACAAATCAATCAATCAAGATAGCTGTGTGATGAGCTCCAAAGGTTCAAAATTAATA 470
Qy 62 ThrILEUSERSERAPILEGILYVRIIESERGIYVALASPSEPHEPROVAL 81
Db 471 ACCATCACTAATTCCTGAGACCAACAAATTTGTATGTATGAGGTTATTTCTGATCCCTTT 530
Qy 82 AsnGlyAsnLysCysArgTyrHIEIIEPheAsnAPILEThSerThrGluArgThrASP 101
Db 531 GAAACCAATTAATGTGTTCATCTTAATCTTAATGATATCTCAAGTACTGAACCCCAAGAT 590
Qy 102 ValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerILEASNTYRYASN 121
Db 591 GTAGAGACTACTCTTTGGCCCAATGCCAATTCCTGTGTATGTAATAAACAATMAACTTTGAT 650
Qy 122 SerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAsnGluValGlnLeu 141
Db 651 AGTCGATATCCAACTGGATGATCAAAAGCGGAGTAAATCAAGAGATTCAGTCCAACTG 710
Qy 142 GYIILEGIIIELEUSERSERAPILEGILYVRIIESERGIYVALASPSEPHEPROVAL 161
Db 711 GGAATTCBAATCTCGACAGATTAATTTGGAAGATTTCTGGAGTGAATGTCATTACTGAG 770
Qy 162 LysThrGluAlaPhePheLeuValAlaILEGImetValSerGluAlaAargPhe 181
Db 771 AAAACCGAAGCCGAAATCTATTGTGTAGCCATCAATGGTATCAGAGGCGAAGATTC 830
Qy 182 LysThrILEGIIIELEUSERSERAPILEGILYVRIIESERGIYVALASPSEPHEPROVAL 201
Db 831 AAGTACCTAGAGATCGGTGAAGAACTTAATTTAAGAGAGATTCAAACCTTAATCCAAA 890
Qy 202 ValILEUSERSERAPILEGILYVRIIESERGIYVALASPSEPHEPROVAL 221
Db 891 GTACTTAATTTGCAAGAGACATGGGGTAAATTTCAACAGCATTCATGATGCCAAGAT 950
Qy 222 GYIYALALEUPROLYSPROLEUGIULAUVALASPALALYSGIYTHRYSTPILEVALILEU 241
Db 951 GGAATTTTACCCAAACCTCTCGAGCTAGTGATGCCAGTGGGCCAAGTGAATGTGTG 1010
Qy 242 ArgValASPGLIULILEUSERSERAPILEGILYVRIIESERGIYVALASPSEPHEPROVAL 261
Db 1011 AGAGTGTATAAATCAAGCTGATGAGCACTTTAAACTACGTGTGGAGCTGTCTG 1070
Qy 262 ThrThr 263
Db 1071 ACAAAT 1076
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RESULT 6

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US-09-978-274A-31
; Sequence 31, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neilson, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Phytolacca americana
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US-09-978-274A-31

Alignment Scores:

Pred. No.:	2,46e-122	Length:	1368
Score:	1042.00	Matches:	199
Percent Similarity:	86.6%	Conservative:	28
Best Local Similarity:	76.0%	Mismatches:	35
Query Match:	76.8%	Indels:	0
DB:	3	Gaps:	0

US-09-978-274A-4 (1-263) x US-09-978-274A-31 (1-1368)

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QY 2 ILeaanthrillethrpheaspalaglYasnaIathrilleasnlysyYrAlathrPheMet 21
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Db 291 GTGAATCAATCATCTCAATGTTGAAGTACCACTTAGCAATAGCCACTTTTGG 350
QY 22 GluserleuAArgaenglnAlalyeAspProlyleuLyScyYrGlyIleProMetleu 41
   ::::::::::::::::::::
Db 351 AATGATCTTGTAAATGAAGCGAAGATCCAAAGTTAAATGCTATGGAATACCAATGCTG 410
QY 42 ProAspThrAnsSerThrProlysyYrleuLeuValIysleuGlnGlyAlaAsnleuLyS 61
   ::::::::::::::::::::
Db 411 CCCAATCAATATCAATCCAAATCCAAAGCAGTGTGGTCCCAAGTTCAAAATMAAAA 470
QY 62 ThrIleThrleuMetleuAArgaAsnleuYrValMetGlyYrSerAspProPhe 81
   ::::::::::::::::::::
Db 471 ACCATCAACATAAGCTGAGAGCAAACTTGTATGTGATGGTTATTCGATCCCTTT 530
QY 82 AsnGlyAsnLyScyYrGlyYrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
   ::::::::::::::::::::
Db 531 GAAACCAATMAATGCTGTACCAATATCTTAAATGATCTCAAGTACGAAAGCCAAAGAT 590
QY 102 ValGluAsnThrleuCySerSerSerSerSerArgValAlaMetSerIleAsnTyraSn 121
   ::::::::::::::::::::
Db 591 GTAGAGACTACTCTTTGCCAAATGCCAATTCCTGTGTAGTAAACATMAACTTTGAT 650
QY 122 SerleuYrProthMetGluLylyeAlaGluValaAsnSerArgaenglnValGlnleu 141
   ::::::::::::::::::::
Db 651 AGTGATATCCAAATCAATCGGAATCAAAAGCGGAGTAAATCAAGAGTCAGTCCAACTG 710
QY 142 GlyIleGlnIleleuSerSerAspIleGlylyeIleSerGlyValaAspSerPheProVal 161
   ::::::::::::::::::::
Db 711 GGAATTCMAATATCTCGACAGTAAATGTGAAAGATTTCTGAGAGTCAATTCATTCAGT 770
QY 162 LysThrGluAlaPhePheleuLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 181
   ::::::::::::::::::::
Db 771 AAAACCGAAGCCGAATTCCTAATGTGTAGCCATACAAATGATGATCGAGGCAAGATTC 830
QY 182 LysYrIleGluAenglnValIysThrAsnPheAsnArgAlaPheYrProAspProLyS 201
   ::::::::::::::::::::
Db 831 AAGTACATAGAGATCGGTGAAAACCTAATTTTAAACAGACATTCACACCTAATCCCAA 890
QY 202 ValIleAsnleuGlnGluLySTrGlylyeIleSerGluAlaIleHisAsnAlalyeAsn 221
   ::::::::::::::::::::
Db 891 GTACTTAAATTTGCAAGAGACATGCGGTAAATTTTCAACAGCAATTCATGATGCAAGAT 950
QY 222 GlYAlaLeuProLySProleuGluLeuValaAspAlaIysGlyThrIysTrpIleValleu 241
   ::::::::::::::::::::
Db 951 GGAATTTTAAACCAATTCCTAATGTGTAGCCATACAAATGATGATCGCAAGTATGTGTG 1010
QY 242 ArgValaAspGluIleAsnArgaAspValaIleleuLeuLySTrValaAsnGlyThrCyGln 261
   ::::::::::::::::::::
Db 1011 AGAGTGTATGAATCAAGCCGATGTAGCACTTTAAACTACGTTGGTGGAGAGCTGTGAG 1070
QY 262 ThrThr 263
   ::::::::::::::::::::
Db 1071 ACAACT 1076
```

RESULT 7

US-10-467-009-1

; Sequence 1, Application US/10467009

; Publication No. US20040241673A1

; GENERAL INFORMATION:

; APPLICANT: RUTGERS, THE STATE UNIVERSITY

; TITLE OF INVENTION: NON-CYOTOXIC PAP MUTANTS

; FILE REFERENCE: OCTRS 3.4-076

; CURRENT APPLICATION NUMBER: US/10/467,009

; PRIORITY FILING DATE: 2003-08-01

; PRIOR APPLICATION NUMBER: 60/266,396

; PRIORITY FILING DATE: 2001-02-02

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1376

; TYPE: DNA

; ORGANISM: Phytolacca americana

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (225)..(1160)

US-10-467-009-1

Alignment Scores:

Pred. No.:	6,97e-122	Length:	1376
Score:	1038.50	Matches:	200
Percent Similarity:	86.6%	Conservative:	27
Best Local Similarity:	76.3%	Mismatches:	34
Query Match:	76.5%	Indels:	1
DB:	8	Gaps:	1

US-09-978-274A-4 (1-263) x US-10-467-009-1 (1-1376)

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QY 2 ILeaanthrillethrpheaspalaglYasnaIathrilleasnlysyYrAlathrPheMet 21
   ::::::::::::::::::::
Db 291 GTGAATCAATCATCTCAATGTTGAAGTACCACTTAGCAATAGCCACTTTTCTG 350
QY 22 GluserleuAArgaenglnAlalyeAspProlyleuLyScyYrGlyIleProMetleu 41
   ::::::::::::::::::::
Db 351 AATGATCTTGTAAATGAAGCGAAGATCCAAAGTTAAATGCTATGGAATACCAATGCTG 410
QY 42 ProAspThrAnsSerThrProlysyYrleuLeuValIysleuGlnGlyAlaAsnleuLyS 61
   ::::::::::::::::::::
Db 411 CCCAATCAATATCAATCCAAATCCAAAGCAGTGTGGTCCCAAGTTCAAAATMAAAA 470
QY 62 ThrIleThrleuMetleuAArgaAsnleuYrValMetGlyYrSerAspProPhe 81
   ::::::::::::::::::::
Db 471 ACCATCAACATAAGCTGAGAGCAAACTTGTATGTGATGGTTATTCGATCCCTTT 530
QY 82 AsnGlyAsnLyScyYrGlyYrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
   ::::::::::::::::::::
Db 531 GAAACCAATMAATGCTGTACCAATATCTTAAATGATCTCAAGTACGAAAGCCAAAGAT 590
QY 102 ValGluAsnThrleuCySerSerSerSerSerArgValAlaMetSerIleAsnTyraSn 121
   ::::::::::::::::::::
Db 591 GTAGAGACTACTCTTTGCC---CCAGCCAATTCCTGTGTAGTAAACATMAACTTTGAT 647
QY 122 SerleuYrProthMetGluLylyeAlaGluValaAsnSerArgaenglnValGlnleu 141
   ::::::::::::::::::::
Db 648 AGTGATATCCAAATCAATCGGAATCAAAAGCGGAGTAAATCAAGAGTCAGTCCAACTG 707
QY 142 GlyIleGlnIleleuSerSerAspIleGlylyeIleSerGlyValaAspSerPheProVal 161
   ::::::::::::::::::::
Db 708 GGAATTCMAATATCTCGACAGTAAATGTGAAAGATTTCTGAGAGTCAATTCATTCAGT 767
QY 162 LysThrGluAlaPhePheleuLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 181
   ::::::::::::::::::::
Db 768 AAAACCGAAGCCGAATTCCTAATGTGTAGCCATACAAATGATGATCGCAAGATTC 827
QY 182 LysYrIleGluAenglnValIysThrAsnPheAsnArgAlaPheYrProAspProLyS 201
   ::::::::::::::::::::
Db 828 AAGTACATAGAGATCGGTGAAAACCTAATTTTAAACAGACATTCACACCTAATCCCAA 887
QY 202 ValIleAsnleuGlnGluLySTrGlylyeIleSerGluAlaIleHisAsnAlalyeAsn 221
   ::::::::::::::::::::
Db 888 GTACTTAAATTTGCAAGAGACATGCGGTAAATTTTCAACAGCAATTCATGATGCAAGAT 947
QY 222 GlYAlaLeuProLySProleuGluLeuValaAspAlaIysGlyThrIysTrpIleValleu 241
```

Db 948 GAGTTTACCAACCTCTGACCTGATGATCCAGTGCTGCCAAGTGATAGTGTG 1007
Qy 242 ArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyrValAsnGlyThrCysGln 261
Db 1008 AGAGTGGATGAAATCAAGCCGATGATGACCTTTAACTACGTTGGTGGAGCTGTGAG 1067
Qy 262 ThrThr 263
Db 1068 ACAACT 1073
RESULT 8
US-09-978-274A-5
; Sequence 5, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Neelam, Anil
; APPLICANT: Atkinson, Howard
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 465
; TYPE: DNA
; ORGANISM: *Phytolacca americana*
US-09-978-274A-5
Alignment Scores:
Pred. No.: 3,47e-91 Length: 465
Score: 793.00 Matches: 154
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 58.4% Indels: 0
Gaps: 0
US-09-978-274A-4 (1-263) x US-09-978-274A-5 (1-465)
Qy 1 MetIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPhe 20
Db 1 ATGATTAATAGCATCACTTGTGATGCTGGAATGCCACATTAACAATATGCCACCTTT 60
Qy 21 MetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMet 40
Db 61 ATGGAATCTCTGCTGATCAAGCGAAGATCCAAATGCTAATGCTATGGCATTCCAATG 120
Qy 41 LeuProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeu 60
Db 121 CTACCTGATCACTAATTCAGCCCTTAAGTACTTATGTTAAGCTCCCAAGTGCAAACTTA 180
Qy 61 LysThrIleThrIleuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspPro 80
Db 181 AAAACCATTCACATTAAGCTGAGCGAAGATTAACGTAACTGAGTGGCTATTCGATCCC 240
Qy 81 PheAsnGlyAsnLysCysValGlyTyrHisIlePheAsnAspIleThrSerThrGluArgThr 100
Db 241 TTCAATGGCAATAGTGTCTTACCATATATTTATGATATTTCAAGCACCGAAGCACT 300
Qy 101 AspValGluAsnThrLeuCysSerSerSerSerSerSerSerSerSerSerSerSerSerSer 120
Db 301 GATGTGGAGAACTCTTGTCTCAAGTCTCAAGTCTCTGTGTGCAATGTCATTAACTAC 360
Qy 121 AsnSerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAsnGlnValGln 140
Db 361 AATAGCTTATATCGACCAATGAGAAAGAAAGCAAGAAATTAATCAAGAAATCAAGTCCA 420
Qy 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154

Db 421 TTGGGAATTCAAATACCTACAGCATGACATTCGAAAAATCTCT 462
RESULT 9
US-09-978-274A-7
; Sequence 32, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Neelam, Anil
; APPLICANT: Atkinson, Howard
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 333
; TYPE: DNA
; ORGANISM: *Phytolacca americana*
US-09-978-274A-7
Alignment Scores:
Pred. No.: 4,54e-62 Length: 333
Score: 564.00 Matches: 109
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 41.6% Indels: 0
Gaps: 0
US-09-978-274A-4 (1-263) x US-09-978-274A-7 (1-333)
Qy 155 GlyValAspSerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMet 174
Db 4 GAGTGGATTCATTCCTGTAAATCTGAGGCTTTTCTTACTAGTGGATCCCAATG 63
Qy 175 ValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPheAsnArg 194
Db 64 GTTCAGAGGACGGGATTCAGATCAGAGAACCAAGTCAAGCTAATTTAATAG 123
Qy 195 AlaPheTyrProAspProLysValIleAsnLeuGluLysTyrGlyLysIleSerGln 214
Db 124 GCATTCACCTCTGATCCCAAGATTAATTTGAGAGAGATGGGCAAAATCTCTGAG 183
Qy 215 AlaIleHisAsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLys 234
Db 184 GCATTCACAAATCCAAAGATGGGCTTTAACCAAACTTGAAGCTAAGTGGATGCCAA 243
Qy 235 GlyThrLysThrIleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 254
Db 244 GTTACCAAGGTGATATTTCTTACAGTGAATGAATCAATCGTATGGCATCTTAAG 303
Qy 255 TyrValAsnGlyThrCysGlnThrThr 263
Db 304 TACGTTAATGAACTGTGCAGACAACT 330
RESULT 10
US-09-978-274A-32
; Sequence 32, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Neelam, Anil
; APPLICANT: Atkinson, Howard
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A

PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 32
LENGTH: 934
TYPE: DNA
ORGANISM: *Phytolacca americana*
US-09-978-274A-32

Alignment Scores:
Pred. No.: 4.14e-47 Length: 934
Score: 453.00 Matches: 112
Percent Similarity: 56.0% Conservative: 41
Best Local Similarity: 41.0% Mismatches: 94
Query Match: 33.4% Indels: 26
DB: Gaps: 11

US-09-978-274A-4 (1-263) x US-09-978-274A-32 (1-934)

QY 3 AsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGlu 22
DB 73 TCMAACATAGCTTTGACGTGAGATGCCACACCAAACTTACTTAATTTCTGACT 132

QY 23 SerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuPro 42
DB 133 AGTTTGGAGAGAGCTGTAAGAACAGAAATTGACATGCCATGGATGATATATGCCACA 192

QY 43 AspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLysThr 62
DB 193 ACCCTCACTGAACAACCAAGTATGTGTGGTGCCTCAAAATTCGATCT---GGAACA 249

QY 63 IleThrLeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPheAsn 82
DB 250 TTCACATTTAGCAATCAAGAGGGGAACTTATATTTGAGGCTATTTGACATTTACAT 309

QY 83 GlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAspVal 102
DB 310 GGA---AAATGTCGTATTCGATCTTCAAGAT-----TCGAATCCGATGCC 354

QY 103 GluAsnThrLeuCysSerSerSerSerArg-----ValAlaMetSerIleAsnTyr 120
DB 355 CAAAGACCCGTTTCCCGGGGACAAAGCAAGCTGCACTCAAAATATATCCCTAT 414

QY 121 AsnSerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAsnGlnValGln 140
DB 415 GAAAGAGTTTCAAAAGGATGAATCAAAAGGT-----GGGGCTAGAACTAAATTTAGG 468

QY 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPhePro 160
DB 469 TTAGGAAAGATTAACATCAAGATCGAATGGTAAATCTACGGCAGAGATGCCAGAT 528

QY 161 -----ValLysThrGluAlaPhePheLeuValAlaIleGlnMetValSer 176
DB 529 CAGAGACGATTCAAAATAAGAGCTGAATTTCTTTATAGCCGTTCAATGCTTACT 588

QY 177 GluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPheAsnArgAla--- 195
DB 589 GAGGCATCAAGGTTCAATATACATTGAGAACAAAGAGGCTAAATTTGATGATGCCAAT 648

QY 196 ---PheTyrProAspProLysValIleAsnLeuGlnGlyLysTyrGlyLysIleSerGlu 214
DB 649 GGGATATGACGCAATCTTAAGCTATTTCCCTAGAGAAAATTTGGACAGCTTTTCAAG 708

QY 215 AlaIleHisAsnAlaLysAsnGly-----AlaLeuProLysProLeuGln 229
DB 709 GTCAAT-----GCAAAAGTTGGCACTCCGGTATAGTACTTACTTACTCGAGAC 762

QY 230 LeuValAspAlaLysGlyThrLysTyrIleValLeuArgValAspGlnIleAsnArgAsp 249
DB 763 CTAAAGATGAGATTAATAAATCTTGACTAGCGCCACCAATTAATATCCCTAT 414

QY 250 Val---AlaLeuLeuLysTyrValAsnGlyThrCysGln 261

DB 823 ATTATGGACTCTTACCCACGTT-----ACTTGCAAG 855

RESULT 11
US-11-106-187-3
Sequence 3, Application US/11106187
Publication No. US20050183162A1
GENERAL INFORMATION:
APPLICANT: TUMER, NILGUN E.
APPLICANT: MANG, PINGER
TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
FILE REFERENCE: OCIRS 3.9-060 CONT
CURRENT APPLICATION NUMBER: US/11/106.187
CURRENT FILING DATE: 2005-04-14
PRIOR APPLICATION NUMBER: US/09/721.047
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: PCT/US99/11301
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/066,374
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 3
LENGTH: 934
TYPE: DNA
ORGANISM: *Phytolacca americana*
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (1)..(75)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (76)..(930)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(930)
US-11-106-187-3

Alignment Scores:
Pred. No.: 4.14e-47 Length: 934
Score: 453.00 Matches: 112
Percent Similarity: 56.0% Conservative: 41
Best Local Similarity: 41.0% Mismatches: 94
Query Match: 33.4% Indels: 26
DB: Gaps: 11

US-09-978-274A-4 (1-263) x US-11-106-187-3 (1-934)

QY 3 AsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGlu 22
DB 73 TCMAACATAGCTTTGACGTGAGATGCCACACCAAACTTACTTAATTTCTGACT 132

QY 23 SerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuPro 42
DB 133 AGTTTGGAGAGAGCTGTAAGAACAGAAATTGACATGCCATGGATGATATATGCCACA 192

QY 43 AspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLysThr 62
DB 193 ACCCTCACTGAACAACCAAGTATGTGTGGTGCCTCAAAATTCGATCT---GGAACA 249

QY 63 IleThrLeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPheAsn 82
DB 250 TTCACATTTAGCAATCAAGAGGGGAACTTATATTTGAGGCTATTTGACATTTACAT 309

QY 83 GlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAspVal 102
DB 310 GGA---AAATGTCGTATTCGATCTTCAAGAT-----TCGAATCCGATGCC 354

QY 103 GluAsnThrLeuCysSerSerSerSerArg-----ValAlaMetSerIleAsnTyr 120
DB 355 CAAAGACCCGTTTCCCGGGGACAAAGCAAGCTGCACTCAAAATATATCCCTAT 414

QY 121 AsnSerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAsnGlnValGln 140

Db 415 GAAAGAGTACCAAGGATGATCAAGGGT-----GGGGCTAGAACTAAATTAGG 468
Qy 141 LeuGlyIleGlnIleuSerSerApIleGlyIleSerGlyValAspSerPhePro 160
Db 469 TTACGAAAGATACACTCAAGAGTCGAATGGTTAAATCTACGCAAGATGCAAGGAT 528
Qy 161 -----ValIleThrGlnIlePhePheLeuValAlaIleGlnMetValSer 176
Db 529 CAGACAGATATCAAAAAATGAGGCTGAATTTCTCTTATAGCGGTTCAATGTTACT 588
Qy 177 GluAlaIleAlaPhePheSerIleGlnIleValIleThrAsnPheAsnArgAla--- 195
Db 589 GAGGATCAAGGTTCAATCATTTGAGAACCAAGTGAAGGCTAAATTTGATGATGCAAT 648
Qy 196 ---PheIleProAspProIleValIleAsnLeuGlnIleIleIleGlyIleSerGlu 214
Db 649 GGGATATAGCCAGATCTTAAGCTATTTCCCTTAGAGAAAAATGGGACAGTGTTCAG 708
Qy 215 AlaIleHisAsnAlaIleAsnGly-----AlaLeuProIlePheGln 229
Db 709 GTCATT-----GCAAAAGTTGGCACTCCGGTATAGTACTTACTTACCTTACCTGAGAC 762
Qy 230 LeuValAspAlaIleIleGlyIleIleValIleValIleAspGluIleAsnArgAsp 249
Db 763 CTAAAGATAGATATATAAACCCTTGACCTAGCGCCACCATGACGACTTAAGAACGAC 822
Qy 250 Val---AlaLeuLeuIleIleValIleAsnGlyIleThrCysGln 261
Db 823 ATTAGGCACTCTTAACCAACGTT-----ACTTGCAAG 855

RESULT 12

US-11-106-187-20
/ Sequence 20, Application US/11106187
/ Publication No. US20050183162A1
/ GENERAL INFORMATION:
/ APPLICANT: TOWER, NINGUN E.
/ APPLICANT: WANG, PINGER
/ TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
/ FILE REFERENCE: OCIRS 3.9-060 CONT
/ CURRENT APPLICATION NUMBER: US/11/106,187
/ CURRENT FILING DATE: 2005-04-14
/ PRIOR APPLICATION NUMBER: US/09/721,047
/ PRIOR FILING DATE: 2000-11-22
/ PRIOR APPLICATION NUMBER: PCT/US99/11301
/ PRIOR FILING DATE: 1999-05-21
/ PRIOR APPLICATION NUMBER: 60/086,374
/ PRIOR FILING DATE: 1998-05-22
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 20
/ LENGTH: 855
/ TYPE: DNA
/ ORGANISM: Phytolacca americana
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(855)
US-11-106-187-20

Alignment Scores:

Pred. No.: 4.81e-47 Length: 855
Score: 452.00 Matches: 112
Percent Similarity: 56.1% Conservative: 90
Best Local Similarity: 41.3% Mismatches: 43
Query Match: 33.3% Indels: 26
DB: 10 Gaps: 11

US-09-978-274a-4 (1-263) x US-11-106-187-20 (1-855)

Qy 5 ILeThPheAspAlaGlyAsnAlaThrIleAsnIleThrAlaThrPheMetGluSerIleu 24
Db 4 ATTAGTGTTCACCTTGAGATGCCACACCAAGAAACCTACTTAATTTTCGACTAGTTTG 63
Qy 25 ArgAsnGlnAlaIleAspProIleValIleAsnGlyIleThrCysGlnIlePheMetLeuProAspThr 44

Db 64 CGAAGAGCTGTGAAGCAAGAAATGACATGCGCATGATGATTAATGGCACACCTTC 123
Qy 45 AsnSerThrProIleIleValIleValIleGlnIleValIleAsnLeuIleThrIleThr 64
Db 124 ACTGAACMACCCAAAGATATGTTGGTTCACCTCAATTCGAACT---GGAACTTCACA 180
Qy 65 LeuMetLeuArgArgAsnAsnLeuIleValIleMetGlyIleThrSerAspProPheAsnGlyAsn 84
Db 181 TTACATCATCAAGGAGAACTTATTTTGAGAGGCTATTTCTGACATTTCAATGCA--- 237
Qy 85 ILeCysArgGlyIleIlePheAsnAspIleThrSerThrGlnIleValIleValIleGluAsn 104
Db 238 AAATGTCTTATCGATCTTCAAGAT-----TCGAATCCGATGCCCAAGAG 265
Qy 105 ThrLeuCysSerSerSerSerArg-----ValAlaMetSerIleAsnIleThrAsnSer 122
Db 286 ACCGTTGCCCCGGGACCAAGCAAGCCTGCACTCAGAAATATATCCCTATGAAAG 345
Qy 123 LeuIleProThrMetGluIleValIleValIleAsnSerArgAsnGlnIleGlnIle 142
Db 346 AGTTACAAAGGATGCAATCAAGGGT-----GGGGCTTAGACTTAATTTAGGTTTAGCA 399
Qy 143 ILeGlnIleLeuSerSerApIleGlyIleIleSerGlyValIleAspSerPhePro----- 160
Db 400 AAGATTAACACTCAAGATGCAATGGTTAAATCTTACGGCAAGATGCAACGATCAGAG 459
Qy 161 -----ValIleThrGlnIleAlaPhePheLeuValAlaIleGlnMetValSerGluAla 178
Db 460 CAGTATCAAAAAATAGAGGTGAATTTCTTATAGCGGTTCAATTTGTTACTAGGCA 519
Qy 179 AlaArgPheIleIleGlnIleValIleValIleThrAsnPheAsnArgAla-----Phe 196
Db 520 TCAAGGTTCAATCAATTCATGAGCAAGTGAAGGCTTAATTTGATGATGCAATGGGAT 579
Qy 197 TyrProAspProIleValIleAsnLeuGlnIleIleIleIleIleIleIleIleIleIle 216
Db 580 CAGCCAGATCTTAACCTATTTCCCTAGAGAAAAATGGACAGTGTTCCTAAGTCAT 639
Qy 217 HisAsnAlaIleAsnGly-----AlaLeuProIlePheGlnIleVal 231
Db 640 -----GCAAAAGTTGGCACTCCGGTATAGTACTTACTTACCTGAGACCTTAAGA 693
Qy 232 AspAlaIleGlyIleThrIlePheIleValIleValIleAspGluIleAsnArgAspVal--- 250
Db 694 GATGAGATATATAACCTTGATGACGCGCACCATAGACGACTTAAGAACGACTTAG 753
Qy 251 AlaLeuLeuIleIleValIleAsnGlyIleThrCysGln 261
Db 754 GCACTCTTAACCAACGTT-----ACTTGCAAG 780

RESULT 13

US-09-792-793a-66
/ Sequence 66, Application US/09792793A
/ Patent No. US20020168370A1
/ GENERAL INFORMATION:
/ APPLICANT: McDonald, John R.
/ APPLICANT: Cogline, Philip
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
/ FILE REFERENCE: 25020-601D
/ CURRENT APPLICATION NUMBER: US/09/792,793A
/ CURRENT FILING DATE: 2001-02-22
/ NUMBER OF SEQ ID NOS: 93
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 66
/ LENGTH: 765
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Construct encoding
/ OTHER INFORMATION: Methionine-Saporin fusion protein
/ NAME/KEY: CDS

Db 640 ACCGCCATTATGATGACGCGAAGACCTGTTTCATATAAAGATTAGATTGGTTTC 699
 QY 232 pAla-----LysGlyThrIleTPile 239
 Db 700 GGTAAAGTACGTACGATGAAAGACCTGCATAATGGGTC 736

RESULT 15
 US-09-792-793A-60
 ; Sequence 60, Application US/09792793A
 ; Patent No. US20020168370A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McDonald, John R.
 ; APPLICANT: Cogging, Philip
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
 ; FILE REFERENCE: 25020-601D
 ; CURRENT APPLICATION NUMBER: US/09/792,793A
 ; NUMBER OF FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 93
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 60
 ; LENGTH: 984
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine-
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(984)
 US-09-792-793A-60

Alignment Scores:
 Pred. No.: 9.64e-34 Length: 984
 Score: 349.00 Matches: 94
 Percent Similarity: 56.1% Conservative: 48
 Best Local Similarity: 37.2% Mismatches: 90
 Query Match: 25.7% Indels: 21
 DB: 3 Gaps: 9

US-09-978-274A-4 (1-263) x US-09-792-793A-60 (1-984)

QY 1 MetIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPhe 20
 Db 220 ATGCTACTAGTATGATACCTCGACCTGTCATCCGACCCGCGCAATATAGCAGCTTC 279
 QY 21 MetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrArgIleProMet 40
 Db 280 GTGATTAAGATTGCTAACAAGATCCGAATCTGAATAACGGTGGTACTGATATT 339
 QY 41 --LeuProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsn 59
 Db 340 GCGGTATCGGTCCGCGCAAGAAAGATTCTCGGCATTAACCTTCAAGCTCCCGT 399
 QY 60 LeuLysThrIleThrLeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyr----- 77
 Db 400 ---GCACTGTTCTCTGGGCTGAAGCGGATTAACCTGTATGTTGTTCCTATCTGGCG 456
 QY 78 SerAspProPheAsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThr 97
 Db 457 ATGATTAATACGAACCGTGAACCGGCC--TACTACTTTCGTAGCGAGATTACGAGCGCG 513
 QY 98 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerArgValAlaMetSer 117
 Db 514 GAATCACT-----GCTCTGTTCCCGAGCGCACTGCATAACCAAAAGCA 561
 QY 118 IleAsnTyrAsnSerLeuTyrProIleMetGluLysIleValGluVal----- 133
 Db 562 CTGGAATATACGGAAGATTACCATCATCAGAGAAGAACGCGCATCACCCAGGCGCAT 621
 QY 134 AsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIle 153
 Db 622 CAATCCGCAAGAAAGATGGGTCTGGGTATGATCTGCTGAGCAAGACATGGAAGCGGTC 681

QY 154 SerGlyValAspSerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGln 173
 Db 682 AAC---AAAAAGCTCCGCGTGTAAAGACAAAGCCGCTTCTGCTGATCGCCATTACG 738
 QY 174 MetValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPheAsn 193
 Db 739 ATGACGCGACAGAACCGCCGCTTCCGCTACATTCAAGAACTGGTCAATCAAAAATTCCG 798
 QY 194 ArgAlaPheTyrProAspProLysValIleAsnLeuGluGluLysTyrGlyLysIleSer 213
 Db 799 AACAGTTCAATTCGAGATTAAGTCATTCACTCGAGGTTAATTGAAAAAAATTTCC 858
 QY 214 GluAlaIleHis--AsnAlaLysAsnGlyAlaLeuProLysProLeuGlu--LeuValAs 232
 Db 859 ACCGCCATTATGATGACGCGAAGAACGGTGTTCATATAAAGATTATGATTTGGTTTC 918
 QY 232 pAla-----LysGlyThrIleTPile 239
 Db 919 GGTAAAGTACGTACGATGAAAGACCTGCATAATGGGTC 955

Search completed: April 9, 2006, 03:12:46
 Job time : 945.609 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_p2n model

Run on: April 9, 2006, 01:48:26 ; Search time 689.867 Seconds
(without alignments)
1525.144 Million cell updates/sec

Title: US-09-978-274A-4

Perfect score: 1357
Sequence: 1 MINTTFDAGNATINKYATF.....DEINRDVALKLVNGTCQTT 263

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9267905 segs, 2000278028 residues

Total number of hits satisfying chosen parameters: 18535810

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOP=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blomsum62
-TRANS=human40.cdd -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MATHEN=2000000000 -HOST=abses03p
-USER=US0978274 @CGN_1_1_2451 @runat_07042006_173042_28604 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEBO TIMEOUT=120
-MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA.New:*
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2: /SIDS5/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /SIDS5/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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15: /SIDS5/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1050	77.4	1360	US-11-010-795-19	Sequence 19, Appl 1
2	453	33.4	934	US-11-010-795-21	Sequence 21, Appl 1

3	296.5	21.8	1855	8	US-10-893-584-35	Sequence 35, Appl 1
4	294.5	21.7	1813	8	US-10-893-584-245	Sequence 245, App
5	293	21.6	1810	8	US-10-893-584-168	Sequence 168, App
6	292.5	21.6	1807	8	US-10-893-584-196	Sequence 196, App
7	292	21.5	1855	8	US-10-893-584-3	Sequence 3, Appl 1
8	292	21.5	1855	8	US-10-893-584-5	Sequence 5, Appl 1
9	292	21.5	1855	8	US-10-893-584-7	Sequence 7, Appl 1
10	292	21.5	1855	8	US-10-893-584-9	Sequence 9, Appl 1
11	292	21.5	1855	8	US-10-893-584-13	Sequence 13, Appl 1
12	292	21.5	1855	8	US-10-893-584-17	Sequence 17, Appl 1
13	292	21.5	1855	8	US-10-893-584-15	Sequence 15, Appl 1
14	292	21.5	1855	8	US-10-893-584-19	Sequence 19, Appl 1
15	292	21.5	1855	8	US-10-893-584-21	Sequence 21, Appl 1
16	292	21.5	1855	8	US-10-893-584-23	Sequence 23, Appl 1
17	292	21.5	1855	8	US-10-893-584-25	Sequence 25, Appl 1
18	292	21.5	1855	8	US-10-893-584-27	Sequence 27, Appl 1
19	292	21.5	1855	8	US-10-893-584-29	Sequence 29, Appl 1
20	292	21.5	1855	8	US-10-893-584-31	Sequence 31, Appl 1
21	292	21.5	1855	8	US-10-893-584-33	Sequence 33, Appl 1
22	292	21.5	1855	8	US-10-893-584-37	Sequence 37, Appl 1
23	292	21.5	1855	8	US-10-893-584-39	Sequence 39, Appl 1
24	292	21.5	1855	8	US-10-893-584-48	Sequence 48, Appl 1
25	292	21.5	1855	8	US-10-893-584-50	Sequence 50, Appl 1
26	292	21.5	1855	8	US-10-893-584-52	Sequence 52, Appl 1
27	292	21.5	1855	8	US-10-893-584-54	Sequence 54, Appl 1
28	292	21.5	1855	8	US-10-893-584-74	Sequence 74, Appl 1
29	292	21.5	1855	8	US-10-893-584-77	Sequence 77, Appl 1
30	292	21.5	1855	8	US-10-893-584-80	Sequence 80, Appl 1
31	292	21.5	1855	8	US-10-893-584-83	Sequence 83, Appl 1
32	292	21.5	1855	8	US-10-893-584-86	Sequence 86, Appl 1
33	292	21.5	1855	8	US-10-893-584-89	Sequence 89, Appl 1
34	292	21.5	1855	8	US-10-893-584-92	Sequence 92, Appl 1
35	292	21.5	1855	8	US-10-893-584-95	Sequence 95, Appl 1
36	292	21.5	1855	8	US-10-893-584-98	Sequence 98, Appl 1
37	292	21.5	1855	8	US-10-893-584-101	Sequence 101, App
38	292	21.5	1855	8	US-10-893-584-104	Sequence 104, App
39	292	21.5	1855	8	US-10-893-584-110	Sequence 110, App
40	292	21.5	1855	8	US-10-893-584-113	Sequence 113, App
41	292	21.5	1855	8	US-10-893-584-116	Sequence 116, App
42	292	21.5	1855	8	US-10-893-584-119	Sequence 119, App
43	292	21.5	1855	8	US-10-893-584-122	Sequence 122, App
44	292	21.5	1855	8	US-10-893-584-125	Sequence 125, App
45	292	21.5	1861	8	US-10-893-584-11	Sequence 11, Appl 1

ALIGNMENTS

RESULT 1
US-11-010-795-19
: Publication 19, Application US/11010795
: GENERAL INFORMATION:
: APPLICANT: TUMER, NIIIGUN E.
: APPLICANT: DI, RONG
: TITLE OR INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
: FILE REFERENCE: OCTRS 3.0-085
: CURRENT APPLICATION NUMBER: US/11/010.795
: PRIOR FILING DATE: 2004-12-13
: PRIOR FILING DATE: 2003-12-12
: NUMBER OF SEQ ID NOS: 44
: SOFTWARE: Patentin Ver. 3.3
: SEQ ID NO 19
: LENGTH: 1360
: TYPE: DNA
: ORGANISM: Phytolacca americana
: FEATURS:
: NAME/KEY: CDS
: LOCATION: (207)..(1145)
US-11-010-795-19
Alignment Scores:


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Db      709  GTCATT-----GCAGAGTGGACCTCGGATGATGACTGTACTTACTTACTGAGAC 762
Qy      230  LeuValAspAlaValysGlyThrIleValLeuArgValAspGluIleAsnArg 249
Db      763  CTAAAGATGGAATATATAACCTTGACCTACGGCCACACATGACGACTTAAGAAGAC 822
Qy      250  Val---AlaLeuLeuValysValAsnGlyThrCysGln 261
Db      823  ATTATGGCACTCCTAACCCACGTT-----ACTGTCAGAG 855

RESULT 3
US-10-893-584-35
; Sequence 35, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Putac, Admit
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893, 584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PAP-246 insert
US-10-893-584-35

Alignment Scores:
Pred. No.:      3,24e-24      Length:      1855
Score:          296.50      Matches:      86
Percent Similarity: 45.2%      Conservative: 46
Best Local Similarity: 29.5%      Mismatches: 101
Query Match:    21.8%      Indels:      59
Db:             8          Gaps:      11

US-09-978-274A-4 (1-263) x US-10-893-584-35 (1-1855)
Qy      5  IllethrpheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGluSerIleu 24
Db      136  ATAAACTTACCAACGCGGCTGCACTGTGCAAGTACACAACTTTATCATGAGCTGTT 195
Qy      25  ArgAsnGlnAlaValysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 44
Db      196  CGGGGTGTTTAAACAACGAGCGATGATGAGACATATATACCAAGTTCCTCCAAACGA 255
Qy      45  AsnSerThrPro-----LysTyrIleuLeuValysLeuGlnGlyAlaAsnLeuLys 61
Db      256  GTTGTTGCTTATTAACCAACGCTTTATTTAGTTGAACCTCAAAATCATGACAGAGCTT 315
Qy      62  ThrIleThrLeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
Db      316  TCTGTTCATTTAGCGCTGAGATGATCAACCATGATATATGTGGCTACCGT----- 366
Qy      82  AsnGlyAsnLysCysArgTyr----- 88
Db      367  GCTGGAATATGCGCATATTTCTTCATCTGACATCAGAAAGATGACGAAGCATGACT 426
Qy      89  HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSer 108
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Qy      109  SerSerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGlu 128
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Qy      129  LysLysAlaGluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSer 148
Db      493  CAACCTGCTGT---AATCTGAGAGAAATATCATGAGTTGGGAATGTCCACTGAGAG 549
Qy      149  AspIleGlyLysIle-----SerGlyValAspSerPheProValLysThrGlu 164
Db      550  GCTATCTCAGCGCTTATTTATTTACAGTATGCTGTCAGCTTCCAACCTGCTGCT 609
Qy      165  AlaPhePheLeuLeuValAlaIleGlnMetValSerGlnAlaIleHisAsnAlaLysAsnGly 184
Db      610  TCTCTT-----ATATATTGCATCCAAATGATTTTCAGAGGACGACAAATATAT 663
Qy      185  GluAsnGlnValLysThr-----AsnPheAsnArgAlaPheTyrProAspProLysVal 202
Db      664  GAGGAGAAATGCGCAGAGAAATTAAGTATACACCGGAGATCTGCACGATCTTACGCTA 723
Qy      203  IleAsnLeuGluGlyLysTyrGlyLysIleSerGlnAlaIleHisAsnAlaLysAsnGly 222
Db      724  ATTACACTTGGAGATATGTTGGGGGAGCTTCCACTCAATTCAAGAGCTTAACCAAGA 783
Qy      223  AlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrLysTyrIleValLeuArg 242
Db      784  GCCCTTCTAGTCCAAATTCACCTGCAAGACGTAATGTTCAAATTCAGTGTATAGAT 843
Qy      243  ValAspGluIleAsnArgAspValAlaLeuLeuLysTyr----- 255
Db      844  GTGAGTATATTAATCCCTATCATGATGCTCTGATGATGATGATGATGATGATGATGAT 903
Qy      256  -----ValAsnGlyThrCysGln 261
Db      904  TCACAGTTTCTGGGGTGTGAATGATCGTGTGA 939

RESULT 4
US-10-893-584-245
; Sequence 245, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Putac, Admit
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893, 584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 245
; LENGTH: 1813
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-245

Alignment Scores:
Pred. No.:      5.41e-24      Length:      1813
Score:          294.50      Matches:      86
Percent Similarity: 45.6%      Conservative: 44
Best Local Similarity: 30.2%      Mismatches: 102
Query Match:    21.7%      Indels:      53
Db:             8          Gaps:      11

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Qy 223 AAlauepProlyspProleugluLeuValaspAlalySGlyThrylThrypIleValleuarg 242
Db 784 GCCTTTCCTAGTCAATTCAGTCAAGAGAGCTAAATGTTCCAAATTCAGTGTACAGT 843
Qy 243 ValaspGluileasnaArgaspValAlaleuLeuLyTyT-----Val 256
Db 844 GTGAGTATATTAAATCCCTATCATCTCTCAATGAGTATAGATGCTCCGCAAGAAATT 903
Qy 257 AsnGlyThrCys 260
Db 904 GCAGGGCAGTGT 915
RESULT 6
US-10-893-584-196
; Sequence 196, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 196
; LENGTH: 1807
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-196
Alignment Scores:
Pred. No.: 9,266-24 Length: 1807
Score: 292.50 Matches: 86
Percent Similarity: 45.98 Conservative: 44
Best Local Similarity: 30.44 Mismatches: 102
Query Match: 21.64 Indels: 51
Gaps: 11
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Qy 25 ArgasnGlnAlaIalysaspProlyspLeuLyScyTyGlyIlePomeLeuProaspHr 44
Db 196 CGCGGTGCTTAAACAACCTGAGCTGANTGACACATGAATAACCAAGTGTCCAAACGA 255
Qy 45 AsnserThrPro-----LyTyrlLeuLeuVallybLeuGlnGlyAlaAsnLeuLy 61
Db 256 GTTGCTTTCCTTAATTAACCAACGCTTATTTAGTGAACCTCAATCATACGACAGCTT 315
Qy 62 ThrIleThrleuMetLeuArgaspAsnLeuTyValMetGlyTySeraspProPhe 81
Db 316 TCTGTTCATTAAGCGCTGAGATGACCAATCATATGTCGGCTACCGT----- 366
Qy 82 AsnGlyAsnLyScyArgTyT----- 88
Db 367 GCTGAATAATGCGCATATTCTTTCATCTCTGACATACGAAAGATGCAGAAACATCACT 426
Qy 89 HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrleuCySer 108

Db 427 CATCTTTC-----ACTGATGTTCAAAAT----- 450
Qy 109 SerSerSerArgValAlaMetSerIleAsnTyraSerLeuTyProThrMetGlu 128
Db 451 -----CATATACATTCGCTTGTGGTAAAT-----TATGATACACTTGA 492
Qy 129 LysIysAlaGluValAsnSerArgAsnGlnAlaGlnLeuGlyIleGlnIleuSerSer 148
Db 493 CACTTGCTGTG---ATCTGAGAGAAATATCGAGTTGGGAAATGTCTCCAGAGAGAG 549
Qy 149 AspIleGlyIle-----SerGlyValAspSerPheProVallyThrGlu 164
Db 550 GCTATCTCAGCGCTTATATTATACAGTCTGTGGCACTGACCTTCCAACTGTGCTGT 609
Qy 165 AlaPhePheLeuValAlaIleGlnMetValSerGluAlaIalargPheLyTyIle 184
Db 610 TCCCTT-----ATTAATTCATCCAAATGATTTCCAGAAAGCAAGATTCCAATATATT 663
Qy 185 GluAsnGlnVallySerThr-----AsnPheAsnArgAlaPheTyrrProaspProlyspVal 202
Db 664 GAGGAGAAATGCGCACAGAAATTAAGTACACCGAGATCTGCACCGATCTTACGCTA 723
Qy 203 ILeasneugGluGlyTyrglyLyseIleSerGluAlaIleHisAsnAlaIysAsnGly 222
Db 724 ATTAACCTTGAGAAATAGTGGGGAGACTTTCAGTCAATTCAGAGCTTAACCAAGGA 783
Qy 223 AAlauepProlyspProleugluLeuValaspAlalySGlyThrylThrypIleValleuarg 242
Db 784 GCCTTTCCTAGTCAATTCAGTCAAGAGAGCTAAATGTTCCAAATTCAGTGTACAGT 843
Qy 243 ValaspGluileasnaArgaspValAlaleuLeuLyTyT-----Valasn 257
Db 844 GTGAGTATATTAAATCCCTATCATCTCTCATGTTGATATGATCCCAAGACAGATGTC 903
Qy 258 GlyThrCys 260
Db 904 GCAGGGCAGTGT 912
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US-10-893-584-3
; Sequence 3, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cathepsin B linker regions of PAP-214
US-10-893-584-3
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Pred. No.: 1,1e-23 Length: 1855
Score: 292.00 Matches: 83
Percent Similarity: 46.5% Conservative: 44

Best Local Similarity: 30.4% Mismatches: 100
Query Match: 21.5% Indels: 46
DB: 8 Gaps: 10

US-09-978-274A-4 (1-263) x US-10-893-584-3 (1-1855)

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136 ATAAACTTACCAACAGCGGGGCGACCTGCAAGCTACCAAACTTTATCATGAGCTGT 195
DB 25 ArgAsnGlnAlaIalysaProlYleuIleuYcyTyGlyIlePromeIeuProAspThr 44
196 CGCGCTGCTTAAACAACGTGAGCTGATGAGACATATATACCAAGTGGCTCAACAGA 255
QY 45 AsnSerThrPro-----LyTyrlleuIeuValIylsleuGlnGlyAlaAsnIleuLys 61
256 GTTGTTGGCTTAAACCAACGCTTATTTACTTGAACCTCAAAATCATGACGACTT 315
DB 62 ThrIleThrlleuMetIeuIargAsnaIleuTyValMetGlyTyIleSerAspProPhe 81
316 TCTGTATCATTTAGCGCTGATGTCACCAATGCATATATGTCGCGCTACCGT----- 366
QY 82 AsnGlyAsnlyscYsaArgTy----- 88
367 GCTGGAATAGCCGATATTTCTTTCATCTGACATACGAGAGATGCAAGACATCACT 426
DB 89 HleIlePheAsnaPleThrSerThrgIuArgThrasPValGluAsnThrlleuCySer 108
427 CATCTTTTC-----ACTGATGTTCAAAAT----- 450
QY 109 SerSerSerSerArgValAlaMetSerIleAsnTyIleAsnSerIeuTyIleProThrMetGlu 128
451 -----CGATATACATTCGCTTGGTGGTAAAT-----TATGATAGACTTGA 492
QY 129 LysIleValIaGluValaIleAsnSerArgAsnGlnValGlnleuGlyIleGlnIleuSerSer 148
493 CAACCTGCTGCT--AATCTGAGAGAAATATGAGATGGGAATGGTCCACTAGAGAG 549
DB 149 AspIleGlyIleYsIle-----SerGlyValAspSerPheProValIleThrgIu 164
550 GCTATCTCAGCGCTTATTTATTAACGATACGCTGCTGACCTCAACTCGCTCGCT 609
QY 165 AlaPhePheIleuValAlaIleGlnMetValSerGluAlaIalargPheIleYsIle 184
610 TCTCTT-----ATAATTCATCCAAATGATTTCAAGACAGCAAGATTCATATAT 663
QY 185 GluAsnGlnValIleYsThr-----AsnPheAsnArgAlaPheTyIleProAspProlYsVal 202
664 GAGGAGAAATGCGCAGAGAAATTTAGGTACACCGAGATCTGCACCAAGATCTGAGCT 723
DB 203 IleAsnIleuGlnIleuYsIleSerGlnAlaIleIleAsnAlaIalysaAsnGly 222
724 ATTAACCTTGAAGATGTTGGGGGAGACTTTCACCTGCAATTCAGAGCTTAACAGGA 783
QY 223 AlaIleuProlYsProlleuGlnIleuValaIalysGlyIleThrlleuIleValleuArg 242
784 GCTTTGCTAGTCAATTCAAATTCGCAAGACGTAATGTTCCAAATTCAGTGTGTACAT 843
QY 243 ValAspGluIleAsnArgAspValAlaIleuIleuYsTyIle 255
844 GTGAGTATATTAATCCCTATCATAGCTCTCATGTGTAT 882
DB

RESULT 8
US-10-893-584-5
; Sequence 5, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Adam
; APPLICANT: Steoli, Dominik
; TITLE OF INVENTION: Richn-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections

FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 1855
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PAP-216 insert
US-10-893-584-5

Alignment Scores:

Pred. No.:	1,1e-23	Length:	1855
Score:	292.00	Matches:	83
Percent Similarity:	46.5%	Conservative:	44
Best Local Similarity:	30.4%	Mismatches:	100
Query Match:	21.5%	Indels:	46
DB:	8	Gaps:	10

US-09-978-274A-4 (1-263) x US-10-893-584-5 (1-1855)

QY 5 IleThrpheAaplaaglYasnaIaThrIleasnlyrYrAlaThrpheMetGluSerIeu 24
136 ATAAACTTACCAACAGCGGGGCGACCTGCAAGCTACCAAACTTTATCATGAGCTGT 195
DB 25 ArgAsnGlnAlaIalysaProlYleuIleuYcyTyGlyIlePromeIeuProAspThr 44
196 CGCGCTGCTTAAACAACGTGAGCTGATGAGACATATATACCAAGTGGCTCAACAGA 255
QY 45 AsnSerThrPro-----LyTyrlleuIeuValIylsleuGlnGlyAlaAsnIleuLys 61
256 GTTGTTGGCTTAAACCAACGCTTATTTACTTGAACCTCAAAATCATGACGACTT 315
DB 62 ThrIleThrlleuMetIeuIargAsnaIleuTyValMetGlyTyIleSerAspProPhe 81
316 TCTGTATCATTTAGCGCTGATGTCACCAATGCATATATGTCGCGCTACCGT----- 366
QY 82 AsnGlyAsnlyscYsaArgTy----- 88
367 GCTGGAATAGCCGATATTTCTTTCATCTGACATACGAGAGATGCAAGACATCACT 426
DB 89 HleIlePheAsnaPleThrSerThrgIuArgThrasPValGluAsnThrlleuCySer 108
427 CATCTTTTC-----ACTGATGTTCAAAAT----- 450
QY 109 SerSerSerSerArgValAlaMetSerIleAsnTyIleAsnSerIeuTyIleProThrMetGlu 128
451 -----CGATATACATTCGCTTGGTGGTAAAT-----TATGATAGACTTGA 492
QY 129 LysIleValIaGluValaIleAsnSerArgAsnGlnValGlnleuGlyIleGlnIleuSerSer 148
493 CAACCTGCTGCT--AATCTGAGAGAAATATGAGATGGGAATGGTCCACTAGAGAG 549
DB 149 AspIleGlyIleYsIle-----SerGlyValAspSerPheProValIleThrgIu 164
550 GCTATCTCAGCGCTTATTTATTAACGATACGCTGCTGACCTCAACTCGCTCGCT 609
QY 165 AlaPhePheIleuValAlaIleGlnMetValSerGluAlaIalargPheIleYsIle 184
610 TCTCTT-----ATAATTCATCCAAATGATTTCAAGACAGCAAGATTCATATAT 663
QY 185 GluAsnGlnValIleYsThr-----AsnPheAsnArgAlaPheTyIleProAspProlYsVal 202
664 GAGGAGAAATGCGCAGAGAAATTTAGGTACACCGAGATCTGCACCAAGATCTGAGCT 723
DB

QY 203 ILeaenLeugluJlylYrPglYlyslIeserGlualIleHIsAenAlalyAaNgly 222
DB 724 ATTACCTTGAGATAGTTGGGGAGACTTTCACATTCAGAGCTCAACAGCA 783
QY 223 ALaenuprolyspProleugluLeuValaenAlalySglYthYrTlPleValleuArg 242
DB 784 GCGTTTGCTAGTCCAAATTCACATTCGCAAGAGCTAATGTTCCAAATTCAGTGTACGAT 843
QY 243 ValaenpGluIleAenArgAenValAlaleuLeuYr 255
DB 844 GTGAGTATATTATATCCCTATCATAGCTCTCATGCTGAT 882
RESULT 9
US-10-893-584-7
Sequence 7, Application US/10893584
Publication No. US20050272048A1
GENERAL INFORMATION:
APPLICANT: Borgford, Thor
APPLICANT: Braun, Curtis
APPLICANT: Purac, Admit
APPLICANT: Stoll, Dominik
TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
TITLE OF INVENTION: Viral or Parasitic Infections
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 1855
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pAP-218 insert
US-10-893-584-7
Alignment Scores:
Pred. No.: 1,1e-23 Length: 1855
Score: 292.00 Matches: 83
Percent Similarity: 46.5% Conservative: 44
Best Local Similarity: 30.4% Mismatches: 100
Query Match: 21.5% Indels: 46
Gaps: 10
US-09-978-274A-4 (1-263) x US-10-893-584-7 (1-1855)
QY 5 ILeHrheAenAlaGlyAenAlaThrlaenlyTyraIarhrPheMetGlusleu 24
DB 136 ATAAACTTTCACACAGCGGGTGTGCACTGTGCAAGACTACACAACTTATACAGAGCTTT 195
QY 25 ArgAenGluAlalyAenpProlyLeuLeuYrGlyIlePrometLeuProAspThr 44
DB 196 CGCGGTGTTTAAACAATCGAGCTGATGTAGACATGATATACAGGTGTGCCAAACAGA 255
QY 45 AenSerThrPro-----LyTyrlLeuLeuVallyleuGlnGlyAlaAenLeuYs 61
DB 256 GTTGCTTGCTTAAACCAACGCGTTTATTAGTGAACCTCAATCATGACGAGCTT 315
QY 62 ThrlaenleuMetLeuAArgAenAenLeuYrValMetGlyTyrsenAspProPhe 81
DB 316 TCTGTTCATTAGGCTGATGTACCAATCATATGTGTGCTACCGT----- 366
QY 82 AenGlyAenlyCyAArgTy----- 88
DB 367 GCTGAAATAGCGCATATTCTTTCATCTCAGCATCAGGAAGATGCAAGACATCACT 426
QY 89 HIsleIleAenAenpIleThrSerThrluArgThraSpValGluAenThrluCyser 108

DB 427 CATCTTT-----ACTGATGTTCAAAAT----- 450
QY 109 SerSerSerAArgValAlaMetSerIleAenTyraenSerLeuYrProThMetGlu 128
DB 451 -----CATATACATTCGCTTGTGTGATAT-----TATGATACACTGAA 492
QY 129 LyAlyAgluValAenSerAArgAenGlnValGlnleuGlyIleGlnIleLeuSerSer 148
DB 493 CACTGTGCTGT-----ATCTGAGAGAAATATTCAGATGGGAAATGTCTCACTAGAGAG 549
QY 149 AenIleGlylyIle-----SerGlyValAenSerPheProVallyThrGlu 164
DB 550 GCTATCTCAGCGCTTATTATTATACAGATCTGTGCACTGACCTTCAACTGTGCTGT 609
QY 165 AlAphenleuLeuValAlaIleGlnMetValSerGluAlaIaArgPheLeuYrIle 184
DB 610 TCCCTT-----ATAAATTTGCATCCAAATGATTTACAGAGCAGCAGATTCCAATATAT 663
QY 185 GluAenGlnVallyThr-----AenPheAenArgAlaPheTyrrProAspProlyVal 202
DB 664 GAGGAGAAATGCGCAGAGAAATTAAGTACACCGAGATCTGACCAAGATCTTACGCTA 723
QY 203 ILeaenLeugluJlylYrPglYlyslIeserGlualIleHIsAenAlalyAaNgly 222
DB 724 ATTACCTTGAGATAGTTGGGGAGACTTTCACATTCAGAGCTCAACAGCTCAACAGCA 783
QY 223 ALaenuprolyspProleugluLeuValaenAlalySglYthYrTlPleValleuArg 242
DB 784 GCGTTTGCTAGTCCAAATTCACATTCGCAAGAGCTAATGTTCCAAATTCAGTGTACGAT 843
QY 243 ValaenpGluIleAenArgAenValAlaleuLeuYr 255
DB 844 GTGAGTATATTATATCCCTATCATAGCTCTCATGCTGAT 882
RESULT 10
US-10-893-584-9
Sequence 9, Application US/10893584
Publication No. US20050272048A1
GENERAL INFORMATION:
APPLICANT: Borgford, Thor
APPLICANT: Braun, Curtis
APPLICANT: Purac, Admit
APPLICANT: Stoll, Dominik
TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
TITLE OF INVENTION: Viral or Parasitic Infections
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 1855
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pAP-220 insert
US-10-893-584-9
Alignment Scores:
Pred. No.: 1,1e-23 Length: 1855
Score: 292.00 Matches: 83
Percent Similarity: 46.5% Conservative: 44
Best Local Similarity: 30.4% Mismatches: 100
Query Match: 21.5% Indels: 46
Gaps: 10

Db 136 ATAACTTTACCAAGGGGTGCCACTGTGCAAGCTTACCAAACTTTATCAGACTGTT 195
Qy ArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 44
Db 196 CGCGGTGCTTTAACTGAGCTGATGTGAGACATGATATACAGGTGGCCAAACAGA 255
Qy AsnSerThrPro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
Db GTTGCTTTGCCCTTAAACCAACGGTTATTTATTTAGTTAACTCTCAAAATCATGACAGCTT 315
Qy 62 ThrIlePheMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
Db 316 TCTGTATCATTTAGCGCTGATGTCCACCAATGATATGTGTGGCTACCGT----- 366
Qy 82 AsnGlyAsnLysCysArgTyr----- 88
Db 367 GCTGAAATATGCGCATTTTCTTTTCATCTGCACATCAGGAAGATGCAAGCAATCACT 426
Qy 89 HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSer 108
Db 427 CATCTTTTC-----ACTGATGTTCAAAAT----- 450
Qy 109 SerSerSerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGlu 128
Db 451 -----CGATATACATTTCGCTTTGGTGGTAAAT-----TATGATAGACTTGAA 492
Qy 129 LysLysAlaGluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSer 148
Db 493 CAACCTTGCTGCT---AATCTGAGAGAAATATGCAAGTTGGGAATGCTCCACTAGAGAG 549
Qy 149 AspIleGlyLysIle-----SerGlyValAspSerPheProValLysThrGlu 164
Db 550 GCTATCTCAGCGCTTTATTTATTTACAGTACGTGGCTGCACTGCTTCCAACTGCGCTGCT 609
Qy 165 AlaPhePheLeuLeuValAlaIleGlnMetValSerGlnAlaAlaArgPheLysTyrIle 184
Db 610 TCCCTT-----ATAATTGCATTCCAATATATTTCAAGACCAAAATTCCAATATATTT 663
Qy 185 GluAsnGlnValLysThr-----AsnPheAsnArgAlaPheTyrProAspProLysVal 202
Db 664 GAGGAGAAATGCGCAGCAAGAAATTTAGTACACCGAGATCTGCACCAAGATCTCTAGCTGA 723
Qy 203 IleAsnLeuGlnLysTyrPglyLysIleSerGlnAlaIleHisAsnAlaLysAsnGly 222
Db 724 ATTAACCTTGAGATATGTTGGGGAGACTTCCCACTGCAATTCAAGAGTCTAACCAAGGA 783
Qy 223 AlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLysTrpIleValLeuArg 242
Db 784 GCCTTTGCTAGTCCAAATTCACGCAAAAGACGTAAATGTTCCAAATTCAGTGTGTACGAT 843
Qy 243 ValAspGluIleAsnArgAspValAlaLeuLeuLysTyr 255
Db 844 GTGAGTATATTAAATCCCTATCATAGCTCTCATGTGTAT 882

RESULT 14
US-10-893-584-19
Sequence 19, Application US/10893584
Publication No. US20050272048A1
GENERAL INFORMATION:
APPLICANT: Borgford, Thor
APPLICANT: Braun, Curtis
APPLICANT: Purac, Admir
APPLICANT: Stoll, Dominik
TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
PRIOR FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058

US-09-978-274a-4 (1-263) x US-10-893-584-19 (1-1855)
Qy 5 IleThrPheAspAlaGluValAsnAlaThrIleAsnLysTyrAlaThrPheMetGluSerLeu 24
Db 136 ATAACTTTACCAAGGGGTGCCACTGTGCAAGCTTACCAAACTTTATCAGACTGTT 195
Qy 25 ArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 44
Db 196 CGCGGTGCTTTAACTGAGCTGATGTGAGACATGATATACAGGTGGCCAAACAGA 255
Qy 45 AsnSerThrPro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
Db 256 GTTGCTTTGCCCTTAAACCAACGGTTATTTATTTAGTTAACTCTCAAAATCATGACAGCTT 315
Qy 62 ThrIlePheMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
Db 316 TCTGTATCATTTAGCGCTGATGTCCACCAATGATATGTGTGGCTACCGT----- 366
Qy 82 AsnGlyAsnLysCysArgTyr----- 88
Db 367 GCTGAAATATGCGCATTTTCTTTTCATCTGCACATCAGGAAGATGCAAGCAATCACT 426
Qy 89 HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSer 108
Db 427 CATCTTTTC-----ACTGATGTTCAAAAT----- 450
Qy 109 SerSerSerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGlu 128
Db 451 -----CGATATACATTTCGCTTTGGTGGTAAAT-----TATGATAGACTTGAA 492
Qy 129 LysLysAlaGluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSer 148
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Qy 149 AspIleGlyLysIle-----SerGlyValAspSerPheProValLysThrGlu 164
Db 550 GCTATCTCAGCGCTTTATTTATTTACAGTACGTGGCTGCACTGCTTCCAACTGCGCTGCT 609
Qy 165 AlaPhePheLeuLeuValAlaIleGlnMetValSerGlnAlaAlaArgPheLysTyrIle 184
Db 610 TCCCTT-----ATAATTGCATTCCAATATATTTCAAGACCAAAATTCCAATATATTT 663
Qy 185 GluAsnGlnValLysThr-----AsnPheAsnArgAlaPheTyrProAspProLysVal 202
Db 664 GAGGAGAAATGCGCAGCAAGAAATTTAGTACACCGAGATCTGCACCAAGATCTCTAGCTGA 723
Qy 203 IleAsnLeuGlnLysTyrPglyLysIleSerGlnAlaIleHisAsnAlaLysAsnGly 222
Db 724 ATTAACCTTGAGATATGTTGGGGAGACTTCCCACTGCAATTCAAGAGTCTAACCAAGGA 783
Qy 223 AlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLysTrpIleValLeuArg 242
Db 784 GCCTTTGCTAGTCCAAATTCACGCAAAAGACGTAAATGTTCCAAATTCAGTGTGTACGAT 843

PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 195
LENGTH: 1855
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PAP-230 insert
US-10-893-584-19

Alignment Scores:
Pred. No.: 1,1e-23 Length: 1855
Score: 292.00 Matches: 83
Percent Similarity: 46.5% Conservative: 44
Best Local Similarity: 30.4% Mismatches: 100
Query Match: 21.5% Indels: 46
DB: Gaps: 10

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121 CTACCTGATACTAATTCGACCCCTAAGTACTTATTGGTTAAGCTCCAAGGTGCAACCTA 18

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Db 121 CTACCTGATCTAATTCAGACCCCTTAAGTACTTATGTTAAGCTCAAGGTGCAAACTTA 180
Qy 181 AAAACGATTCACCTAATAGTGGAGCGAAATTAACCTTATACGATGGGCTATTCTGATCCC 240
Db 181 AAAACGATTCACCTAATAGTGGAGCGAAATTAACCTTATACGATGGGCTATTCTGATCCC 240
Qy 241 TTCAATGGCAATAGTGTCTGTTACCATATATTTAATGATATTAACAAGCAGGAGCT 300
Db 241 TTCAATGGCAATAGTGTCTGTTACCATATATTTAATGATATTAACAAGCAGGAGCT 300
Qy 301 GATGTGAGAAATCTCTTTGCTCAAGTTCTAGTTCTGTTGCAATGTCATTAACTAC 360
Db 301 GATGTGAGAAATCTCTTTGCTCAAGTTCTAGTTCTGTTGCAATGTCATTAACTAC 360
Qy 361 AATAGCTTATATCCGACCATGAGAAAGAGAGAGAAAGTAACTCAAGAAATCAAGTCCA 420
Db 361 AATAGCTTATATCCGACCATGAGAAAGAGAGAGAAAGTAACTCAAGAAATCAAGTCCA 420
Qy 421 TTGGGAATTCAAATTAATCTCAGACAGTGAATTGGAATAATCTCTTAA 465
Db 421 TTGGGAATTCAAATTAATCTCAGACAGTGAATTGGAATAATCTCTTAA 465

RESULT 2
AX427704 792 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 3 from Patent WO0233107.
DEFINITION AX427704
ACCESSION AX427704
VERSION AX427704.1 GI:21537816

SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Bakayotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS
TITL
JOURNAL
1 Neelam, A., Atkinson, H.J., Mcpherson, M.J. and Thomas, C.J.R.
Plant cell death system
Patent: WO 0233107-A.3 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
Location/Qualifiers

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/organism="Phytolacca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"
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1..3
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463..492
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612
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681..686
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complement(765..792)
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790..792
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ORIGIN

Query Match 99.4%; Score 462; DB 6; Length 792;
Best Local Similarity 100.0%; Pred.No.1.7e-94;

Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATTAATACGATCACTTTGATGCTGGAATGCCACATTAACAATATGCACTTT 60
Db 1 ATGATTAATACGATCACTTTGATGCTGGAATGCCACATTAACAATATGCACTTT 60
Qy 61 ATGGAATCTCTTGTATATCAAGGAAAGATCCAAACTAAATGCTATGGCATACCAATG 120

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Db 61 ATGGAATCTCTTGTATATCAAGGAAAGATCCAAACTAAATGCTATGGCATACCAATG 120
Qy 121 CTACCTGATCTAATTCAGACCCCTTAAGTACTTATGTTAAGCTCAAGGTGCAAACTTA 180
Db 121 CTACCTGATCTAATTCAGACCCCTTAAGTACTTATGTTAAGCTCAAGGTGCAAACTTA 180
Qy 181 AAAACGATTCACCTAATAGTGGAGCGAAATTAACCTTATACGATGGGCTATTCTGATCCC 240
Db 181 AAAACGATTCACCTAATAGTGGAGCGAAATTAACCTTATACGATGGGCTATTCTGATCCC 240
Qy 241 TTCAATGGCAATAGTGTCTGTTACCATATATTTAATGATATTAACAAGCAGGAGCT 300
Db 241 TTCAATGGCAATAGTGTCTGTTACCATATATTTAATGATATTAACAAGCAGGAGCT 300
Qy 301 GATGTGAGAAATCTCTTTGCTCAAGTTCTAGTTCTGTTGCAATGTCATTAACTAC 360
Db 301 GATGTGAGAAATCTCTTTGCTCAAGTTCTAGTTCTGTTGCAATGTCATTAACTAC 360
Qy 361 AATAGCTTATATCCGACCATGAGAAAGAGAGAGAAAGTAACTCAAGAAATCAAGTCCA 420
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Qy 421 TTGGGAATTCAAATTAATCTCAGACAGTGAATTGGAATAATCTCTTAA 462
Db 421 TTGGGAATTCAAATTAATCTCAGACAGTGAATTGGAATAATCTCTTAA 462

RESULT 3
AX427720 1092 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 19 from Patent WO0233107.
DEFINITION AX427720
ACCESSION AX427720
VERSION AX427720.1 GI:21537829

SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS
TITL
JOURNAL
1 Neelam, A., Atkinson, H.J., Mcpherson, M.J. and Thomas, C.J.R.
Plant cell death system
Patent: WO 0233107-A.19 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
Location/Qualifiers

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/db_xref="taxon:32630"
/note="PAP-S/Cystatin fusion"
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/note="Binding site for primer P81BP"
681..686
/note="Modified XbaI site"
variation
complement(742..786)
misc_feature
/note="Binding site for primer PCS-PAPSR"
766..806
/note="Binding site for primer PCS-Delta86P"
766..786
/note="REV NIA protease cleavage site"
complement(1066..1092)
/note="Binding site for primer SYNPOTdelta86SR"

ORIGIN

Query Match 99.4%; Score 462; DB 6; Length 1092;
Best Local Similarity 100.0%; Pred.No.1.5e-94;

Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATTAATACGATCACTTTGATGCTGGAATGCCACATTAACAATATGCACTTT 60
Db 1 ATGATTAATACGATCACTTTGATGCTGGAATGCCACATTAACAATATGCACTTT 60
Qy 61 ATGGAATCTCTTGTATATCAAGGAAAGATCCAAACTAAATGCTATGGCATACCAATG 120

Db 61 ATGAAATCTCTTGGTATCAAGCGAAGATCCAAATCAAAATAGCTATGCAATACCAATG 120
Qy 121 CTACCTGATACCTAATTCGACCCCTTAAGTACTTAATGTTAGCTCCAGGTGCAAACTTA 180
Db 121 CTACCTGATACCTAATTCGACCCCTTAAGTACTTAATGTTAGCTCCAGGTGCAAACTTA 180
Qy 181 AAAACCATTAACATTAAGCTGAGAGCAAAATTAATTACGTAGGGCTAATTCGATCC 240
Db 181 AAAACCATTAACATTAAGCTGAGAGCAAAATTAATTACGTAGGGCTAATTCGATCC 240
Qy 241 TTCAATGCAATTAAGTGTCTGCTTACCATATTTATTAATGATTTACAGACCGAAGCACT 300
Db 241 TTCAATGCAATTAAGTGTCTGCTTACCATATTTATTAATGATTTACAGACCGAAGCACT 300
Qy 301 GATGTGAGAAATACCTTTGCTCAAGTCTTAAGTCTGCTGTTGCAATGCAATTAACATAC 360
Db 301 GATGTGAGAAATACCTTTGCTCAAGTCTTAAGTCTGCTGTTGCAATGCAATTAACATAC 360
Qy 361 AATAGCTTAATTCGACAGCAGTGAAGAAAGACAGAAAGTAACTCAAGAAATCAAGTCCA 420
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Qy 421 TTGGGAATTCGAAATTAATCTCAAGCAGTGAATTTGGAATTAATCTCT 462
Db 421 TTGGGAATTCGAAATTAATCTCAAGCAGTGAATTTGGAATTAATCTCT 462

RESULT 4
AX427702 945 bp DNA linear PAT 20-JUN-2002
LOCUS AX427702
DEFINITION Sequence 1 from Patent WO0233107.
ACCESSION AX427702
VERSION AX427702.1 GI:21537815
KEYWORDS

SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS
TITLE
JOURNAL
1 Noelam, A., Atkinson, H.J., Mcpherson, M.J. and Thomas, C.J.R.
Plant cell death system
Patent: WO 0233107-A 1 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)

FEATURES
source
1. .945
/organism="Phytolacca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"
misc_feature
1. .24
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misc_feature
complement(735..776)
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misc_feature
736..777
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variation
750..759
/note="Sequence replacing removed XbaI site"
misc_feature
complement(922..945)
/note="Binding site for primer pPS2SR"

ORIGIN
Query Match 98.7%; Score 459; DB 6; Length 945;
Best Local Similarity 100.0%; Pred. No. 7.7e-94;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ATAAATGATGATCACTTTGATGCTGAAGATGCCAATTAACAATATGCACTTTATG 63
Db 73 ATAAATGATGATCACTTTGATGCTGAAGATGCCAATTAACAATATGCACTTTATG 132
Qy 64 GAATCTCTTGTATCAAGGAAAGATCCAAATTAATGCTATGCTATCCAAATGCTA 123
Db 133 GAATCTCTTGTATCAAGGAAAGATCCAAATTAATGCTATGCTATCCAAATGCTA 192

Qy 124 CCTGATACCTAATTCGACCCCTTAAGTACTTAATGTTAGCTCCAGGTGCAAACTTA 183
Db 193 CCTGATACCTAATTCGACCCCTTAAGTACTTAATGTTAGCTCCAGGTGCAAACTTA 252
Qy 184 ACCATTAACATTAAGCTGAGAGCAAAATTAATTACGTAGGGCTAATTCGATCCCTC 243
Db 253 ACCATTAACATTAAGCTGAGAGCAAAATTAATTACGTAGGGCTAATTCGATCCCTC 312
Qy 244 AATGCAATTAAGTGTCTGCTTACCATATTTATTAATGATTTACAGACCGAAGCACTGAT 303
Db 313 AATGCAATTAAGTGTCTGCTTACCATATTTATTAATGATTTACAGACCGAAGCACTGAT 372
Qy 304 GTGAGAAATACCTTTGCTCAAGTCTTAAGTCTGCTGTTGCAATGCAATTAACATAC 363
Db 373 GTGAGAAATACCTTTGCTCAAGTCTTAAGTCTGCTGTTGCAATGCAATTAACATAC 432
Qy 364 AGCTTAATTCGACAGCAGTGAAGAAAGACAGAAAGTAACTCAAGAAATCAAGTCCA 423
Db 433 AGCTTAATTCGACAGCAGTGAAGAAAGACAGAAAGTAACTCAAGAAATCAAGTCCA 492
Qy 424 GGAATTCGAAATTAATCTCAAGCAGTGAATTTGGAATTAATCTCT 462
Db 493 GGAATTCGAAATTAATCTCAAGCAGTGAATTTGGAATTAATCTCT 531

RESULT 5
PAPASRIP 1249 bp mRNA linear PLN 18-APR-2005
LOCUS PAPASRIP
DEFINITION P.americana mRNA for pokeweed antiviral protein.
ACCESSION X98079
VERSION X98079.1 GI:1707648
KEYWORDS
PAP-S gene; pokeweed antiviral protein (PAP); ribosome-inactivating protein.

SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS
TITLE
JOURNAL
1 Poyet, J.L. and Hoeveler, A.
cDNA cloning and expression of pokeweed antiviral protein from
seeds in *Bescherichia coli* and its inhibition of protein synthesis
in vitro
FRBS Lett. 406 (1-2), 97-100 (1997)
9109394

REFERENCE
AUTHORS
TITLE
JOURNAL
2 (bases 1 to 1249)
Poyet, J.L.
Direct Submission
Submitted (22-MAY-1996) J.L. Poyet, Laboratoire de
Biochimie-Biologie Molculaire, UFR Sciences et Techniques, 16
route de Gray, 25030 Besancon Cedex, FRANCE
Revised by author 20-SEP-1996

REMARK
FEATURES
source

1. .1249
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1. .1249
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106..1050
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/db_xref="InterPro:IPR01574"
/db_xref="UniProt/TREMBL:P93444"
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106..177
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178..1047
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ORIGIN

Query Match 98.7%; Score 459; DB 15; Length 1249;
Best Local Similarity 100.0%; Pred. No. 7.1e-94;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 ATAAATGCAATCCTTTGATGCTGGAATGCCCAATTAACAATATGCCACTTTATG 63
DB 178 ATAAATGCAATCCTTTGATGCTGGAATGCCCAATTAACAATATGCCACTTTATG 237
QY 64 GAATCTCTTGATCAAGGAAAGATCCAAACTAATAGCTATGGCATACCAATGCTA 123
DB 238 GAATCTCTTGATCAAGGAAAGATCCAAACTAATAGCTATGGCATACCAATGCTA 297
QY 124 CCGATATCAATTCGACCCCTTAAGTACTTATTTAGCTCCAAAGGTGCAACTTAA 183
DB 298 CCGATATCAATTCGACCCCTTAAGTACTTATTTAGCTCCAAAGGTGCAACTTAA 357
QY 184 ACCATTACATTAATGCTGGAAGCAAAATTAATTAAGTATGAGCTATTTCTGATCCTTC 243
DB 358 ACCATTACATTAATGCTGGAAGCAAAATTAATTAAGTATGAGCTATTTCTGATCCTTC 417
QY 244 AATGCAATAAGTGTGCTCAATATTTAATGATTTAACAAGCACCGAAGCATGAT 303
DB 418 AATGCAATAAGTGTGCTCAATATTTAATGATTTAACAAGCACCGAAGCATGAT 477
QY 304 GTGAGAAATACCTTTGCTCAAGTTCATGTTCTGCTGTCGCAATGTCATTAATCAAT 363
DB 478 GTGAGAAATACCTTTGCTCAAGTTCATGTTCTGCTGTCGCAATGTCATTAATCAAT 537
QY 364 AGCTTATATCCGACCATGGAAGAAAGCAAGTAACTCGAAGTCAAGTCAATG 423
DB 538 AGCTTATATCCGACCATGGAAGAAAGCAAGTAACTCGAAGTCAAGTCAATG 597
QY 424 GGAATTCAAATACCTCAGCAGTGACATGGAATAATCTCT 462
DB 598 GGAATTCAAATACCTCAGCAGTGACATGGAATAATCTCT 636

RESULT 6
AB071855 786 bp DNA linear PLN 19-MAR-2002
LOCUS
DEFINITION Phytolacca americana pap2 gene for PAP-S2, partial cds.
AB071855
AB071855.1 GI:19570839
VERSION
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Honjo, E. and Watanabe, K.
Cloning of genomic DNA encoding two types of pokeweed antiviral
protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
their recombinant proteins with other PAP isoforms
Unpublished
2 (bases 1 to 786)
Watanabe, K. and Honjo, E.
Direct Submission
Submitted (19-SEP-2001) Keiichi Watanabe, Saga University,

Department of Applied Biological Sciences, Honjo-machi, Saga city,
Saga 840-8502, Japan (E-mail: watanakei@cc.saga-u.ac.jp,
Tel: 81-952-28-8774, Fax: 81-952-28-8774)

FEATURES
source
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/organism="Phytolacca americana"
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/db_xref="GI:19570840"

ORIGIN

Query Match 96.3%; Score 447.8; DB 15; Length 786;
Best Local Similarity 98.5%; Pred. No. 2.8e-91;
Matches 452; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 4 ATAAATGCAATCCTTTGATGCTGGAAGCCCAATTAACAATATGCCACTTTATG 63
DB 1 ATCAATACCTTCACTTTGATGCTGGAAGTCCCAATTAACAATATGCCACTTTATG 60
QY 64 GAATCTCTTGATCAAGGAAAGATCCAAACTAATAGCTATGGCATACCAATGCTA 123
DB 61 GAATCTCTTGATCAAGGAAAGATCCAAACTAATAGCTATGGCATACCAATGCTA 120
QY 124 CCGATATCAATTCGACCCCTTAAGTACTTATTTAGCTCCAAAGGTGCAACTTAA 183
DB 121 CCGATATCAATTCGACCCCTTAAGTACTTATTTAGCTCCAAAGGTGCAACTTAA 180
QY 184 ACCATTACATTAATGCTGGAAGCAAAATTAATTAAGTATGAGCTATTTCTGATCCTTC 243
DB 181 ACCATTACATTAATGCTGGAAGCAAAATTAATTAAGTATGAGCTATTTCTGATCCTTC 240
QY 244 AATGCAATAAGTGTGCTCAATATTTAATGATTTAACAAGCACCGAAGCATGAT 303
DB 241 AATGCAATAAGTGTGCTCAATATTTAATGATTTAACAAGCACCGAAGCATGAT 300
QY 304 GTGAGAAATACCTTTGCTCAAGTTCATGTTCTGCTGTCGCAATGTCATTAATCAAT 363
DB 301 GTGAGAAATACCTTTGCTCAAGTTCATGTTCTGCTGTCGCAATGTCATTAATCAAT 360
QY 364 AGCTTATATCCGACCATGGAAGAAAGCAAGTAACTCGAAGTCAAGTCAATG 423
DB 361 AGCTTATATCCGACCATGGAAGAAAGCAAGTAACTCGAAGTCAAGTCAATG 420
QY 424 GGAATTCAAATACCTCAGCAGTGACATGGAATAATCTCT 462
DB 421 GGAATTCAAATACCTCAGCAGTGACATGGAATAATCTCT 459

RESULT 7
AB071854 783 bp DNA linear PLN 19-MAR-2002
LOCUS
DEFINITION Phytolacca americana pap1 gene for PAP-S1, partial cds.
AB071854
AB071854.1 GI:19570837
VERSION
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE
gene
CDS

1
Honjo, E. and Watanabe, K.
Cloning of genomic DNA encoding two types of pokeweed antiviral
protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
their recombinant proteins with other PAP isoforms
Unpublished
2 (bases 1 to 783)
Watanabe, K. and Honjo, E.
Direct Submission
Submitted (19-SEP-2001) Keiichi Watanabe, Saga University,
Department of Applied Biological Sciences, Honjo-machi, Saga city,
Saga 840-8502, Japan (E-mail: watakei@scc.saga-u.ac.jp,
Tel:81-952-28-8774, Fax:81-952-28-8774)
Location/Qualifiers
1. .783
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ORIGIN
Query Match 76.0%; Score 353.4; DB 15; Length 783;
Best Local Similarity 87.1%; Pred. No. 7.2e-70;
Matches 400; Conservative 0; Mismatches 56; Indels 3; Gaps 1;

4 ATAAATACGATCACCCTTGTGATGCTGGAATGCCACCTTAACTATGCACTTATG 63
1 ATCAATACGATACGCTTGCAGCTGGAATGCCACCTTAACTATGCTTATGCTTATG 60
64 GAATCTCTTGTGATCAAGCGAAGATCCAAATTAATGCTATGCTATGCAATGCTA 123
61 GAATCTCTTGTGATCAAGCGAAGATCCAAATTAATGCTATGCTATGCAATGCTA 120
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121 CCCAATATCAATGATGACCCCTAAGTACTTATGCTTAAAGCTCAAGGTGCAACTAA 180
184 ACCATTACATTAAGCTGAGCGAAGTAACTTAACGATGAGGCTATTCGATCCCTTC 243
181 ACCATTACATTAAGCTGAGCGAAGTAACTTAACGATGAGGCTATTCGATCCCTTC 238
244 AATGCAATTAAGTGTGCTTACCATATATTAATGATATTAACAACGACGACGATGAT 303
239 -AGACAAATTAAGTGTGCTTACCATATATTAATGATATTAACAACGACGATGAT 297
304 GTGGAATTAAGTGTGCTTACCATATATTAATGATATTAACAACGACGATGAT 363
298 GTGGAATTAAGTGTGCTTACCATATATTAATGATATTAACAACGACGATGAT 357
364 AGCTTATTAAGTGTGCTTACCATATATTAATGATATTAACAACGACGATGAT 423
358 GGCTTATTAAGTGTGCTTACCATATATTAATGATATTAACAACGACGATGAT 417
424 GGAATTAAGTGTGCTTACCATATATTAATGATATTAACAACGACGATGAT 462
418 GGAATTAAGTGTGCTTACCATATATTAATGATATTAACAACGACGATGAT 456

RESULT 8
AY327475

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE
gene
CDS

AY327475 939 bp mRNA linear PLAN 01-JUL-2004
Phytolacca heterotepala anti-viral protein PAP (RIP1) mRNA,
complete cds.
AY327475
AY327475.1 GI:37625511
Phytolacca heterotepala
Phytolacca heterotepala
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
1 (bases 1 to 939)
Delli Bovi, P. and Corrado, G.
Direct Submission
Submitted (23-JUN-2003) Department of Soil, Plants and
Environmental Sciences, University of Naples 'Federico II', via
Universita' 100, Portici, Naples 80055, Italy
Location/Qualifiers
1. .939
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1. .939
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1. .939
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QLSILQIDSDIGKISGVSSEKTEAFLLVALQISAAAFKTIENQKTFNRDPS
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ORIGIN
Query Match 67.5%; Score 314; DB 15; Length 939;
Best Local Similarity 80.3%; Pred. No. 5.9e-61;
Matches 368; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

5 TAAATACGATCACCCTTGTGATGCTGGAATGCCACCTTAACTATGCACTTATG 64
68 TGAATACATCAATCAATGATGAGTGAAGTACACCATTAAGCAATTAAGGCACTTTCG 127
65 AATCTCTTGTGATCAAGCGAAGATCCAAATTAATGCTATGCTATGCAATGCTAC 124
128 ATGATCTCTGATTAAGCGAAGATCCAAATTAATGCTATGCTATGCAATGCTAC 187
125 CTGATTAATTAAGCGAAGATCCAAATTAATGCTATGCTATGCTATGCAATGCTAC 184
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305 TGAATTAAGTGTGCTTACCATATATTAATGATATTAACAACGACGACGATGAT 364
368 TAGGATTAAGTGTGCTTACCATATATTAATGATATTAACAACGACGACGATGAT 427
365 GCTTATTAAGTGTGCTTACCATATATTAATGATATTAACAACGACGACGATGAT 424
428 GTGATTAAGTGTGCTTACCATATATTAATGATATTAACAACGACGACGATGAT 487
425 GAAATTAAGTGTGCTTACCATATATTAATGATATTAACAACGACGACGATGAT 462

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LOCUS	Sequence 1 from Patent EP08089302.			PAT 05-MAY-1999
DEFINITION	A67183			
ACCESSION	A67183.1	GI:4756167		
VERSION				
KEYWORDS				
SOURCE				
ORGANISM	Phytolacca insularis			
	Phytolacca insularis			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;			
	Caryophyllales; Phytolaccaceae; Phytolacca.			
REFERENCE	1 (bases 1 to 882)			
AUTHORS	Moon, Y., Choi, J., Yun, Y., Jin, J., Hong, E., Lee, J., Choi, K., Lee, J.,			
	Song, S., Choi, Y., Kim, C. and Kim, M.			
TITLE	Novel genes encoding antiviral proteins of Phytolacca insularis			
	Naked and recombinant microorganisms expressing the same proteins			
JOURNAL	Patent: EP 0808930-A 1 26-NOV-1997;			
	JINRO LTD (KR)			
COMMENT	Other publication JP 9308489 19971202			
	Other publication CA 2186303 19971123			
	Other publication AU 6570596 19971127.			
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QY	121 CTACCTGATTAATTCGACCCCTTAAGTATTAATGTTAAGTCCAAAGTCAAACTTA	180		
DB	121 TTGCCAATCAAAATCCAAATCCAAAGTACGTGTGGTAAAGTCCAAAGTTCAAATGAA	180		
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DB	181 AAAACCATTAACCTAATGCTGAGAGAAATTAATTAACTTAATGCTATGCTATGCTCC	240		
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QY	301 GATGTAAGATTAATCTTTGCTCAAGTCTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCT	360		
DB	301 GATGTAAGATTAATCTTTGCTCAAGTCTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCT	360		
QY	361 AATAGCTTAATTCGACCATGGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	420		
DB	361 GATAGCTTAATTCGACCATGGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	420		
QY	421 TTGGGAATTCAAATTAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	482		
DB	421 CTGGGAATTCAAATTAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	482		
RESULT 10				
LOCUS	AY603354	714 bp	DNA	linear
				PLN 17-MAY-2004

DEFINITION	Phytolactase acinosa antiviral protein PAPA2 (papa2) gene, papa2-s allele, partial cds.
ACCESSION	AJ603354
VERSION	AJ603354.1
KEYWORDS	GI:47175558
SOURCE	
ORGANISM	Phytolacta acinosa (food pokeweed)
REFERENCE	Phytolactase acinosa
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.
JOURNAL	1 (bases 1 to 714)
REFERENCE	Chen,G., Lei,J., Zeng,G. and Cao,B. Phytolactase acinosa anti-viral protein PAP (PAPA2) DNA Unpublished 2 (bases 1 to 714)
AUTHORS	Chen,G., Lei,J., Zeng,G. and Cao,B.
TITLE	Direct Submission
JOURNAL	Submitted (20-APR-2004) Horticultural College, South China Agricultural University, Wushan, Guangzhou, Guangdong 510642, PR China
FEATURES	
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mRNA	
gene	
CDS	
ORIGIN	
Query Match	67.2%; Score 312.4; DB 15; Length 714;
Best Local Similarity	80.1%; Pred. No. 1,5e-60;
Matches 367;	Conservative 0; Mismatches 91; Indels 0; Gaps 0;
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Dd	62 ATAATCTTCGTAATGAAAGCAAAGATCCAAGTTMAAATGCTATGGAATACCAATGTTC 121
Oy	125 CTGATACTAAATGCACCCCTTAAGTACTATTTGGTTAAGTCCAAAGTCAAACTTAATA 184
Dd	122 CCAATACAAATCCAAATCCAAAGTAGTGTGGTTAAGTCCAAAGTTCAAAATGAATAAAA 181
Oy	185 CCATTAACCTAATGCTGAGACGAATTAATTAACGTATGATGGGCTATTCTGATCCCTTCA 244
Dd	182 CCATCAACATTAATGCTGAGACGAATTAATTAATGATGATGATGATGATGATGATGATG 241
Oy	245 ATGGCAATTAATGCTGATCAATATATTTATGATATTAACAAGCAGCAAGCACTGATG 304
Dd	242 ATTACCAATTAATGCTGATCAATATCTTTATGATATCTGAGATGATGATGATGATGATG 301
Oy	305 TGAGAAATCTCTTGTCTCAAGTTCTAGATTCGTGTTGCAATGTCCATTAATCAATA 364

Db 302 TAGAGACTACTCTTGGCCCAATCCCAATCTCGTGTAGTAAACAAATTAATATGATA 361

Qy 365 GCTATATCCGACCATGGAAGAAAGAAAGTAACTCAAGAAATCAAGTCCAAATGG 424

Db 362 GTCATATCCAACTTGGATCAAAAGCGGAGTAAATCAAGAGTCAAGTTCAACTGG 421

Qy 425 GAATTCAAATATCTGACGATGACATTTGAAAAATCTCT 462

Db 422 GAATTCAAATATCTGACGATGACATTTGAAAAATTTCT 459

RESULT 11

AF533515 1114 bp mRNA linear PLN 01-AUG-2005

LOCUS PhytoIaccia octandra anti-viral protein (pap) mRNA, partial cds.

DEFINITION AF533515

ACCESSION AF533515.1 GI:33329822

VERSION

KEYWORDS

SOURCE PhytoIaccia octandra

ORGANISM

Phytolacca octandra

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE 1 (bases 1 to 1114)

AUTHORS Lin, J.S. and McNately, K.P.

TITLE Direct Submission

JOURNAL Submitted (29-JUL-2002) Reproductive Technologies, AgResearch Wallaceville, Ward Street, Upper Hut, Wellington, New Zealand

FEATURES

Source

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/translation="ISVWLIAPSTWAVNTIIYVGSITTSKYTSLDRLNKAOP NLKCYIPMLPTNPDPRKYLVEIQSNKTTITMLRRNLYVWGSDPRPKCRPH IRLDISGTERODVETTLCPNPNSVIRKINIDSRPTLESKAKVKSQVQIGIITD SDIGKISGVTSFKETAEFLVAIQVSEARKEYLENQKINFNRAFNPNPVLNL ERTWGIKISTAIHDAKNGVLPPELVDASGAKWIVSRVDIKPVDALLNYSQCTT YNOMAMSOLIMSTYYNMANIGDLFEGP"

ORIGIN

Query Match 66.5%; Score 309.2; DB 15; Length 1114;

Best Local Similarity 79.7%; Pred. No. 6.9e-60;

Matches 365; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

Qy 5 TAAATACGATCACTTTGATGCTGAAATGCGACCATTAACAATATGCGACTTTATGG 64

Db 46 TGAATACATCATCTTACATGTTGGAAGTACACCATTAAGAAATACACCACTTCTGG 105

Qy 65 AATCTCTTGTATCAAGCGAAAGATCCAAATCAAAATGCTATGCGATACCAATGCTAC 124

Db 106 ATGATCTTGTATCAAGCGAAAGATCCAAATCAAAATGCTATGGAATACCAATGCTGC 165

Qy 125 CTGATCTAATTCGACCCCTTAAGTACTTATGTTAAGCTCCAGGTCGCAAACTAATAAA 184

Db 166 CCAATTAACAATTCGACGATCCAAAGTACGTGTGAGCTCCAAAGTTCAAAATAAAAA 225

Qy 185 CCATTACACTAATGCTGAGCGAAATTAATTAATGATGAGGCTAATTCGATCCCTTCA 244

Db 226 CCAATCACTAATGCTGAGCGAAATTAATTAATGATGAGGCTAATTCGATCCCTTGG 285

Qy 245 ATGGCAATTAAGTGTGTTACCAATATTTAATTAATTAATTAATTAATTAATTAATTA 304

Db 286 ATACCAATTAAGTGTGTTACCAATATTTAATTAATTAATTAATTAATTAATTAATTA 345

Qy 305 TGAATATCTCTTGGCTCAAGTCTTAGTCTCGTGTGCAATGTCATTATACATACATA 364

Db 346 TAGAGACTACTCTTGGCCCAATCCCAATCTCGTGTATTAATAAACAATTAATATGATA 405

Qy 365 GCTATATCCGACCATGGAAGAAAGAAAGTAACTCAAGAAATCAAGTCCAAATGG 424

Db 406 GTCATATCCAACTTGGATCAAAAGCGGAGTAAATCAAGAGTCAAGTCCAACTGG 465

Qy 425 GAATTCAAATATCTGACGATGACATTTGAAAAATCTCT 462

Db 466 GAATTCAAATATCTGACGATGACATTTGAAAAATTTCT 503

RESULT 12

AY049785 1164 bp mRNA linear PLN 23-OCT-2001

LOCUS PhytoIaccia acinosa anti-viral protein PAP (PAP) mRNA, complete cds.

DEFINITION AY049785

ACCESSION AY049785.1 GI:16356654

VERSION

KEYWORDS

SOURCE PhytoIaccia acinosa (food pokeweed)

ORGANISM

Phytolacca acinosa

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE 1 (bases 1 to 1164)

AUTHORS Peng, X., Yuan, Y. and Qiang, B.

TITLE Direct Submission

JOURNAL Submitted (27-JUL-2001) Department of Biochemistry, Institute of Basic Medical Science, Chinese Academy of Medical Sciences, 5 Dong Dan San Tiao, Beijing 100005, P.R. China

FEATURES

Source

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/gene="PAP"

2..943

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/protein_id="AAL15442.1"

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ORIGIN

Query Match 65.8%; Score 306; DB 15; Length 1164;

Best Local Similarity 79.3%; Pred. No. 3.6e-59;

Matches 363; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

Qy 5 TAAATACGATCACTTTGATGCTGAAATGCGACCATTAACAATATGCGACTTTATGG 64

Db 69 TGAATACATCATCTTACATGTTGGAAGTACACCATTAAGAAATACGCACTTCTGG 128

Qy 65 AATCTCTTGTATCAAGCGAAAGATCCAAATCAAAATGCTATGCGATACCAATGCTAC 124

Db 129 ATATCTTGTATCAAGCGAAAGATCCAAATCAAAATGCTATGGAATACCAATGCTGC 188

Qy 125 CTGATCTAATTCGACCCCTTAAGTACTTATGTTAAGCTCCAGGTCGCAAACTAATAAA 184

Db 189 CCAATTAACAATTCGACGATCCAAAGTACGTGTGAGCTCCAAAGTTCAAAATAAAAA 248

Qy 185 CCATTACACTAATGCTGAGCGAAATTAATTAATGATGAGGCTAATTCGATCCCTTCA 244

Db 249 CCAATCACTAATGCTGAGCGAAATTAATTAATGATGAGGCTAATTCGATCCCTTGG 308

OY		245	ATGGCAATTAAGTGTGTTACCATATATTAAAGAATTACAAGCACCGAAGCACTGATG	304
Db		309	ATACCAATTAAGTGTCGTTACCAATACCTTTTAGATGATATCTCAGATCTGACGCCCAAGTG	368
OY		305	TGAGAAATACTCTTTTGCTCAAGTTCTAGTCTCGTGTGCATATGTCATTACTAATAA	364
Db		369	TAGAACACTACTCTTTGGCCCAATGCCAATTCGATGTAGTAAAAACAATAACTATGAT	428
OY		365	GCTTATATCCGACCATGGAAGAAAAGAAAGAAAGTAACTCAAGAAATCAAGTCCAATTG	424
Db		429	GTCGATATCCCAACATTGGAAATCAAAGCGGGATAAATCAAGAAAGTCAGATTCAACTGG	488
OY		425	GAATTCAATACTCAGACGTGACATTGGAAAAATCTCT	462
Db		489	GAATTCANATCTCCAGACGATATATTGGAAAAATTTCT	526
RESULT 13				
LOCUS	AY603353	714 bp	DNA	linear
DEFINITION	Phyolacca acinosa antiviral protein PAPA1 (papal) gene, papal-s allele, partial cds.			PLN 17-MAY-2004
ACCESSION	AY603353			
VERSION	AY603353.1	GI:47175556		
KEYWORDS				
SOURCE				
ORGANISM	Phyolacca acinosa (food pokeweed)			
REFERENCE	Phyolacca acinosa			
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phyloclaccaceae; Phyolacca.			
JOURNAL	1 (bases 1 to 714) Chen, G., Lei, J., Cao, B. and Zeng, G. Phyolacca acinosa anti-viral protein PAP (PAPA1) DNA Unpublished 2 (bases 1 to 714) Chen, G., Lei, J., Cao, B. and Zeng, G. Direct Submission Submitted (20-Apr-2004) Horticultural College, South China Agricultural University, Wushan, Guangzhou, Guangdong 510642, PR China			
FEATURES				
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CDS				
mRNA				
gene				
ORIGIN				
Query Match	65.3%;	Score 303.8;	DB 15;	Length 714;
Best Local Similarity	78.9%;	Pred. No. 1.3e-58;		
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Db 61 AATGATCTCTGGTAATGAAGCAGGAAGATCCAAAGTTTAAATAGTCTATGGAATACCAATGCTG 120

QY 124 CCTGATCTAATATGGAACCCCTTAGTACTTAATGGTTAGCTCCAGGAGGCAAACTTAATA 183

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Db 241 GAACCAATTAATGTGCTTACCATTATTTAATGATATTTACAGGATACGAAACGCCMAAT 300

QY 304 GTGGAGATTAATCTTTGCTCAAGTTCTTGTTCTCGATGTGCAATGTCATTAACTACAAT 363

Db 301 GTAGAGATTAATCTTTGCTCCCAATGCCAATTCGTGTGTTAGTAGAAAATTAATCTTTGAT 360

QY 364 AGCTTATATCCGACCATGAGAAAGAAAGACAGAACTAATCTAAGAAATCAAGTCCAATTG 423

Db 361 AGTCGATATCCAACTTGAATCAAAAAGCGGAGATTAATCAAGAAATCAAGTCCAATG 420

QY 424 GGAATTCAAATATCTCAGCAGTGAATTCGAAAAATTCCT 462

Db 421 GGAATTCAAATATCTCAGCAGTGAATTCGAAAAATTCCT 459

FEATURES	source
LOCUS	AF338910
DEFINITION	Phytolacca americana antiviral protein (mpap) mRNA, partial cds.
ACCESSION	AF338910
VERSION	AF338910.1 GI:13398616
KEYWORDS	
SOURCE	Phytolacca americana (American pokeweed)
ORGANISM	Phytolacca americana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE	1 (bases 1 to 711) Chen, D., Wang, X. and Zhou, G. Pokeweed antiviral protein gene, partial cds Unpublished
AUTHORS	2 (bases 1 to 711) Wang, X., Chen, D. and Zhou, G. Direct Submission Submitted (20-JAN-2001) Plant Pathology, Institute of Plant Protection, Chinese Academy of Agriculture Sciences, Yuanmingyuanxilin No.2, Beijing 100094, China
JOURNAL	Location/Qualifiers
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REFERENCE	/organism="Phytolacca americana"
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Query Match 65.1%; Score 302.8; DB 15; Length 711;
Best Local Similarity 78.8%; Pred. No. 2.2e-58;
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QY 65 AATCTCTGTAATGAGGAAAGATCCAAACTAAATGCTATGAGCAATACCAATGCTAC 124
DB 62 ATGATCTTGTATGATGAGGAAAGATCCAAAGTTTAAATGCTATGAGCAATGCTAC 121
QY 125 CTGATCTAATTTGCAACCCCTTAAGTACTTATGTTAGCTCCAAAGTCCAACTTAA 184
DB 122 CCAATACAAATACAAATGCAAGTACGTTGTTAGCTCCAAAGTCCAACTTAA 181
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QY 425 GAATTCAAATCTGAGGAGTCAATGGAAGAAATCTCT 462
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RESULT 15
AY572976 942 bp mRNA linear PLN 05-APR-2004
LOCUS Phytolacca americana antiviral protein (PAP) mRNA, complete cds.
DEFINITION
ACCESSION AY572976
VERSION AY572976.1 GI:45826466
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolacaceae; Phytolacca.
REFERENCE
AUTHORS Xiao, Z.A. and Jiang, Y.
TITLE A gene encoding the pokeweed antiviral protein in the leaf of
Phytolacca americana
JOURNAL
REFERENCE
AUTHORS
JOURNAL
TITLE
Xiao, Z.A.
Submitted (13-MAR-2004) College of Life Sciences, Beijing Normal
University, No. 19 Xinjiekouwai Street, Haidian District, Beijing
100875, China

FEATURES
source
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QUGIYIDSNIGKISGWSFTEKTEFLVAICMWSAARFKIENOVKTNFAFN
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ORIGIN
Query Match 65.1%; Score 302.8; DB 15; Length 942;
Best Local Similarity 78.8%; Pred. No. 2e-58;
Matches 361; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

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DB 128 ATGATCTTGTATGATGAGGAAAGATCCAAAGTTTAAATGCTATGAGCAATGCTAC 187
QY 125 CTGATCTAATTTGCAACCCCTTAAGTACTTATGTTAGCTCCAAAGTCCAACTTAA 184
DB 188 CCAATACAAATACAAATGCAAGTACGTTGTTAGCTCCAAAGTCCAACTTAA 247
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DB 368 TAGAGACTACTTTGCTCAAGTTCTGATGCTGATGCTGATGCTGATGCTGATGCTG 427
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DB 428 GTCAATATCCAAATGGAATCAAGGAGGAGTAAATCAAGAGTCAAGTCCAAATGG 487
QY 425 GAATTCAAATCTGAGGAGTCAATGGAAGAAATCTCT 462
DB 488 GAATTCAAATCTGAGGAGTCAATGGAAGAAATCTCT 525

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Job time : 2736.97 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 8, 2006, 23:57:17 ; Search time 280.284 Seconds
(without alignments)
11056.934 Million cell updates/sec

Title: US-09-978-274A-5

Perfect score: 465
Sequence: 1 atgataatacagtcacactt.....acattggaataatctctctaa 465

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%
Listing first 45 summaries

Database :

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- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
- 6: Geneseq2002as:*
- 7: Geneseq2002bs:*
- 8: Geneseq2003as:*
- 9: Geneseq2003bs:*
- 10: Geneseq2003cs:*
- 11: Geneseq2003ds:*
- 12: Geneseq2004as:*
- 13: Geneseq2004bs:*
- 14: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	465	100.0	465	6	AAD42717 Pokeweed
2	462	99.4	792	6	AAD42716 Pokeweed
3	462	99.4	1092	6	AAD42729 Pokeweed
4	459	98.7	945	6	AAD42715 Pokeweed
5	313.2	67.4	882	2	AAT99556 Pokeweed
6	306	65.8	1164	11	ADMT74765 Pokeweed
7	304.4	65.5	1164	11	ADMT74751 Pokeweed
8	301.2	64.8	1378	12	ADG76061 Pokeweed
9	301.2	64.8	1379	3	AAT45197 Pokeweed
10	301.2	64.8	1379	3	AAT59220 Pokeweed
11	301.2	64.8	1379	4	AAC87929 P. american
12	301.2	64.8	1379	6	AAD42738 Pokeweed
13	301.2	64.8	1379	10	AD105787 Pokeweed
14	299.6	64.4	1195	2	AAT056672 Pokeweed
15	298	64.1	1195	2	AAT081457 Pokeweed
16	298	64.1	1378	6	AAD42739 Pokeweed
17	298	64.1	1379	3	AAT59221 Pokeweed
18	282.8	60.8	2472	2	AAT043967 Pokeweed
19	266.4	57.3	2369	2	AAT99557 Pokeweed

20	266.4	57.3	2369	2	ABA96543 PhytoIacc
21	238.8	51.4	918	2	AAT064893 Antiviral
22	238.8	51.4	918	2	AAT04782 DNA pWMC2
23	97.8	21.0	608	2	ABA96547 Cloning v
24	97.8	21.0	603	2	ABA96547 Cloning v
25	54.6	11.7	934	3	AAT45198 Wild-type
26	54.6	11.7	934	6	AAD42740 Pokeweed
27	46.6	10.0	765	3	AAT61131 DNA encod
28	46.6	10.0	984	3	AAT61125 DNA encod
29	46.6	10.0	993	3	AAT61128 DNA encod
30	46.6	10.0	999	3	AAT61122 DNA encod
31	46.6	10.0	999	3	AAT61119 DNA encod
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37	43.2	9.3	1233	10	ADH92070 Fibroblas
38	41.6	8.9	2000	11	ACL35363 Rice stre
39	41.6	8.9	9723	6	ABL34380 Human imm
40	39.8	8.6	2000	11	ACL37108 Rice stre
41	39.6	8.5	783	2	AAT18231 Amplified
42	39.6	8.5	1002	2	AAT17959 HBGR Val
43	39.6	8.5	1002	2	AAT18219 Linker am
44	39.6	8.5	1004	2	AAT18232 Sapotin-H
45	39.6	8.5	1154	2	AAT35743 SAP-Alame

ALIGNMENTS

RESULT 1	
AAD42717	
ID	AAD42717 standard; DNA; 465 BP.
XX	
AC	AAD42717;
XX	
DT	15-NOV-2002 (first entry)
XX	
DE	Pokeweed PAP-Salpa protein encoding DNA.
XX	
KW	Necrotic effect; transgenic plant; antiviral protein; pokeweed; gene;
KW	PAP-Salpa; ds.
XX	
OS	Phytolacca americana.
XX	
FH	Key
FT	Location/Qualifiers
CDS	1..465
FT	/tag= a
FT	/product= "PAP-Salpa protein"
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PN	WO200233107-A2.
XX	
PD	25-APR-2002.
XX	
PF	15-OCT-2001; 2001WO-GB004593.
XX	
PR	14-OCT-2000; 2000GB-00025217.
XX	
PA	(ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX	
PI	Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX	
DR	WPI; 2002-489891/52.
XX	
DR	P-PSDB; AAE25920.
PT	
PT	Inducing necrotic effect in specific cells of plant by transforming plant
PT	with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT	which acts in response to application of specific stimulus to plant.
XX	
PS	Claim 3; Page 77; 87pp; English.
XX	
XX	The invention relates to a method of inducing a necrotic effect in

CC	specific cells of a plant. The method involves transforming the plant
CC	with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC	PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
CC	in response to the application of a specific stimulus to the plant so as
CC	to facilitate expression of the pokeweed antiviral protein in specific
CC	cells of the plant. The method is useful for inducing a necrotic effect
CC	in specific cells of a plant. The present sequence is pokeweed PAP-Salpa
CC	protein encoding DNA
XX	
XX	Sequence 465 BP; 165 A; 97 C; 76 G; 127 T; 0 U; 0 Other;
Query Match	100.0%; Score 465; DB 6; Length 465;
Best Local Similarity	100.0%; Pred. No. 4,76-114;
Matches 465; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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DB	1 ATGATTAATACGATCACCTTTGATGCTGGAAATGCCACATTAACTAATATGCCACCTTT 60
QY	61 ATGGAATCTCTTCGTATATCAAGCGAAAGATCCAAACTTAAATGCTATGGCATACCAATG 120
DB	61 ATGGAATCTCTTCGTATATCAAGCGAAAGATCCAAACTTAAATGCTATGGCATACCAATG 120
QY	121 CTACCTGATCTAATTTGCAACCCCTTAAGTACTTATGTTAAGTCCCAAGTGCACCAACTA 180
DB	121 CTACCTGATCTAATTTGCAACCCCTTAAGTACTTATGTTAAGTCCCAAGTGCACCAACTA 180
QY	181 AAAACCATTAACCTAATGCTGAGCGAAATTAATTATACGATGGCTATTTGATGCC 240
DB	181 AAAACCATTAACCTAATGCTGAGCGAAATTAATTATACGATGGCTATTTGATGCC 240
QY	241 TTCAATGGCATTAAGTGTGCTTACCAATATTTAATGATATTTACAGACCGAAGCGACT 300
DB	241 TTCAATGGCATTAAGTGTGCTTACCAATATTTAATGATATTTACAGACCGAAGCGACT 300
QY	301 GATGAGGAATPACCTTGTGCAAGTCTAGTCTCGTGTGCAATGTCATTAACCTAC 360
DB	301 GATGAGGAATPACCTTGTGCAAGTCTAGTCTCGTGTGCAATGTCATTAACCTAC 360
QY	361 AATAGCTTATATCCGACCATGGAAGAAAGACAGAAAGTAACTCAAGAAATCAAGTCCA 420
DB	361 AATAGCTTATATCCGACCATGGAAGAAAGACAGAAAGTAACTCAAGAAATCAAGTCCA 420
QY	421 TTGGGAATTCAAATACTCAGCATGAGCATTTGGAAAAATCTCTTAA 465
DB	421 TTGGGAATTCAAATACTCAGCATGAGCATTTGGAAAAATCTCTTAA 465
RESULT 2	
AADD42716	
ID	AAD42716 standard; DNA; 792 BP.
XX	
XX	AAD42716;
XX	
XX	15-NOV-2002 (first entry)
XX	
DE	Pokeweed mature PAP-S protein encoding DNA.
KW	Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KW	gene; ds.
OS	
OS	Phytolacca americana.
XX	
XX	
Key	Location/Qualifiers
FT	1..792
FT	/tag= a
FT	/product= "Mature PAP-S protein"
FT	1..29
FT	/tag= b
FT	/bound_molety= "Primer PS1BP"
FT	complement(436..462)
FT	/tag= c
FT	/bound_molety= "Primer PS1SR"

PT	primer_bind	463..492	/tag= d	/bound_moiety= "Primer pS2BP"
PT				
PT	misc_feature	681..686	/tag= e	/note= "Sequence replacing removed XbaI site"
PT				
PT	primer_bind		/tag= f	/bound_moiety= "Primer pS2SR"
PT				
PN	WO20023107-A2.			
PD	25-APR-2002.			
XX				
PR	15-OCT-2001; 2001WO-GB004593.			
XX				
PR	14-OCT-2000; 2000GB-00025217.			
PA	(ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.			
PI	Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;			
XX				
DR	WPI; 2002-489691/52.			
XX				
DR	P-PSDB; AAE25919.			
PT				
PT	Inducing necrotic effect in specific cells of plant by transforming plant			
PT	with a chimeric gene encoding pokeweed antiviral protein and a promoter			
PT	which acts in response to application of specific stimulus to plant.			
PS	Claim 2; Page 76; 87pp; English.			
XX				
CC	The invention relates to a method of inducing a necrotic effect in			
CC	specific cells of a plant. The method involves transforming the plant			
CC	with chimeric gene(s), which encodes a pokeweed antiviral protein namely			
CC	PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts			
CC	in response to the application of a specific stimulus to the plant so as			
CC	to facilitate expression of the pokeweed antiviral protein in specific			
CC	cells of the plant. The method is useful for inducing a necrotic effect			
CC	in specific cells of a plant. The present sequence is pokeweed mature PAP			
CC	-S protein encoding DNA			
SQ	Sequence 792 BP; 268 A; 161 C; 151 G; 212 T; 0 U; 0 Other;			
Query Match	99.4%; Score 462; DB 6; Length 792;			
Best Local Similarity	100.0%; Pred. No. 4.1e-123;			
Matches 462; Conservative	0; Mismatches 0; Indels 0; Gaps 0			
OY	1 ATGATTAATTCAGATCACCCTTGATCTGCTGGAATGCGACCATTAACAAATATGCGACCTT	60		
DB	1 ATGATTAATTCAGATCACCCTTGATCTGGAATGCGACCATTAACAAATATGCGACCTT	60		
OY	61 ATGGAATCTCTTGATCAAGCGAAGATCCAAAATCTAAATGCTATGCGATCAATG	120		
DB	61 ATGGAATCTCTTGATCAAGCGAAGATCCAAAATCTAAATGCTATGCGATCAATG	120		
OY	121 CTACCTGATCTAATTCGACCCCTTAAGTACTTATTGTTAAAGCTCCAAAGTCAAACTTA	180		
DB	121 CTACCTGATCTAATTCGACCCCTTAAGTACTTATTGTTAAAGCTCCAAAGTCAAACTTA	180		
OY	181 AAAACCATTAACATTAAGTCTGAGCGAAATTAATTAAGTATGAGTATTCGATCC	240		
DB	181 AAAACCATTAACATTAAGTCTGAGCGAAATTAATTAAGTATGAGTATTCGATCC	240		
OY	241 TTCAATGCGAATTAAGTCTGATTAACATATTTATGATTTATTAACAAGCAGCGACT	300		
DB	241 TTCAATGCGAATTAAGTCTGATTAACATATTTATGATTTATTAACAAGCAGCGACT	300		
OY	301 GATGTGAGAAATCTTTGCTCAAGTTCTAAGTTCTGCTGTTGCAATGTCATTAACTAC	360		
DB	301 GATGTGAGAAATCTTTGCTCAAGTTCTAAGTTCTGCTGTTGCAATGTCATTAACTAC	360		
OY	361 AATGCTTATTCGACCATGGAAGAAAGAGAGAGAACTCAAGAAATCAAGTCCAA	420		
DB	361 AATGCTTATTCGACCATGGAAGAAAGAGAGAGAACTCAAGAAATCAAGTCCAA	420		

Db 361 AATAGCTTATATCCGACCATGAGAAAAGACAGAACTAACTCAAGAAATCAAGTCCAA 420
Oy 421 TTGGGAATTCAAATPACTCAGCAGTGACATTGGAAATATCTCT 462
Db 421 TTGGGAATTCAAATPACTCAGCAGTGACATTGGAAATATCTCT 462

RESULT 3
AAD42729
ID AAD42729 standard; DNA; 1092 BP.
XX
AC AAD42729;
XX 29-AUG-2003 (revised)
DT 15-NOV-2002 (first entry)
XX
DB Pokeweed PAP-S/TEV PCS/rice cystatin delta D86 fusion DNA.
XX
KM Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KM chimeric; rice; cystatin delta D86; NIA protease cleavage site; PCS; ds.
XX
OS Phytothacca americana.
OS Oryza sativa.
OS Tobacco; Etch virus.
OS Chimeric.
XX
FH Key
FT primer_bind 1..29 location/Qualifiers
FT /*tag= a
FT /bound_molecy= "Primer PS1BP"
FT misc_feature 681..686
FT /*tag= b
FT /note= "Modified XbaI site"
FT primer_bind complement(742..786)
FT /*tag= c
FT /bound_molecy= "Primer PCS-PAPSR"
FT primer_bind 766..806
FT /*tag= d
FT /bound_molecy= "Primer PCS-Delta86P"
FT misc_feature 766..786
FT /*tag= e
FT /note= "TEV NIA protease cleavage site"
FT primer_bind complement(1066..1092)
FT /*tag= f
FT /bound_molecy= "Primer SYNPOTDelta86P"
XX
PN W0200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-GB004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADTE-) ADVANCBED TECHNOLOGIES CAMBRIDGE LTD.
XX
PI Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A,
XX
XX WPI; 2002-489891/52.
XX
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX which acts in response to application of specific stimulus to plant.
XX
XX Disclosure; Page 83; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
XX specific cells of a plant. The method involves transforming the plant
XX with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX PAP', PAPRI and PAP-S, where the gene(s) comprises a promoter which acts
XX in response to the application of a specific stimulus to the plant so as
XX to facilitate expression of the pokeweed antiviral protein in specific
XX cells of the plant. The method is useful for inducing a necrotic effect

CC in specific cells of a plant. The present sequence is a fusion DNA. This
CC sequence comprises pokeweed pro-PAP-S DNA, rice cystatin delta D86 DNA
CC and Tobacco Etch virus (TEV) NIA protease cleavage site (PCS). (Updated
CC on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 1092 BP; 369 A; 195 C; 222 G; 306 T; 0 U; 0 Other;
Query Match 99.4%; Score 462; DB 6; Length 1092;
Best Local Similarity 100.0%; Pred. No. 4.5e-123; Indels 0; Gaps 0;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ATGATTAATACGATCACCCTTGTGATGCTGAATGCCACATTAACTAATATGCCACTTT 60
Db 1 ATGATTAATACGATCACCCTTGTGATGCTGAATGCCACATTAACTAATATGCCACTTT 60
Oy 61 ATGGAATCTCTTGCTATCAAGCGAAGATCCAAACTAAATGCTATGCGATACCAATG 120
Db 61 ATGGAATCTCTTGCTATCAAGCGAAGATCCAAACTAAATGCTATGCGATACCAATG 120
Oy 121 CTACCTGATTAATTTGACCCCTTAAGTACTTATTTGTTAGCTCCAAAGTGCAAACTTA 180
Db 121 CTACCTGATTAATTTGACCCCTTAAGTACTTATTTGTTAGCTCCAAAGTGCAAACTTA 180
Oy 181 AAAACATTACATTAATGCTGAGACGAAATTAATTAATGATGAGGCTATTGATCC 240
Db 181 AAAACATTACATTAATGCTGAGACGAAATTAATTAATGATGAGGCTATTGATCC 240
Oy 241 TTCAATGCAATTAAGTGTCTTACCATATATTTAATGATTTACAGACCGAACT 300
Db 241 TTCAATGCAATTAAGTGTCTTACCATATATTTAATGATTTACAGACCGAACT 300
Oy 301 GATGTGAGAAATATCTTTTGTGCAAGTTCTGCTGATGCTGCAATGTCATTAACTAC 360
Db 301 GATGTGAGAAATATCTTTTGTGCAAGTTCTGCTGATGCTGCAATGTCATTAACTAC 360
Oy 361 AATAGCTTATATCCGACCATGAGAAAAGACAGAACTAACTCAAGAAATCAAGTCCAA 420
Db 361 AATAGCTTATATCCGACCATGAGAAAAGACAGAACTAACTCAAGAAATCAAGTCCAA 420
Oy 421 TTGGGAATTCAAATPACTCAGCAGTGACATTGGAAAAATCTCT 462
Db 421 TTGGGAATTCAAATPACTCAGCAGTGACATTGGAAAAATCTCT 462

RESULT 4
AAD42715
ID AAD42715 standard; DNA; 945 BP.
XX
XX AAD42715;
XX
XX 15-NOV-2002 (first entry)
XX
XX Pokeweed pro-PAP-S protein encoding DNA.
XX
XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
XX gene; ds.
XX
XX Phytothacca americana.
XX
XX
XX Key
XX CDS 1..945 location/Qualifiers
XX primer_bind 1..24 /*tag= a
XX /product= "Pro-PAP-S protein"
XX primer_bind 1..24 /*tag= b
XX /bound_molecy= "Primer PPS1BP"
XX primer_bind complement(735..776) /*tag= c
XX /bound_molecy= "Primer PSXDR"
XX primer_bind 736..777 /*tag= d
XX /bound_molecy= "Primer PSXDF"
XX misc_feature 750..759

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FT      /*cag= e
FT      /note= "Sequence replacing removed XbaI site"
FT      primer_bind
FT      complement(922..945)
FT      /*cag= f
FT      /bound_moiety= "Primer PP52BR"
XX      NO200233107-A2.
XX      25-APR-2002.
XX      15-OCT-2001; 2001WO-GB004593.
XX      14-OCT-2000; 2000GB-00025217.
XX      (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX      Thomas CJR, McPherson MJ, Atkinson HJ, Neelam A;
XX      WPI; 2002-489891/52.
XX      P-PSDB; AAE25918.
XX      Inducing necrotic effect in specific cells of plant by transforming plant
XX      with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX      which acts in response to application of specific stimulus to plant.
XX      Claim 24; Page 73-74; 87pp; English.
XX      The invention relates to a method of inducing a necrotic effect in
XX      specific cells of a plant. The method involves transforming the plant
XX      with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX      PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
XX      in response to the application of a specific stimulus to the plant so as
XX      to facilitate expression of the pokeweed antiviral protein in specific
XX      cells of the plant. The method is useful for inducing a necrotic effect
XX      in specific cells of a plant. The present sequence is pokeweed pro-PAP-S
XX      protein encoding DNA
XX      Sequence 945 BP; 307 A; 187 C; 180 G; 271 T; 0 U; 0 Other;
SQ
Query Match      98.7%; Score 459; DB 6; Length 945;
Best Local Similarity 100.0%; Pred. No. 3.2e-122;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      4 ATAAATACGATCACTTGTGATGCTGGAATGCCACATTAACAATATGCCACTTTATG 63
XX      73 ATAAATACGATCACTTGTGATGCTGGAATGCCACATTAACAATATGCCACTTTATG 122
XX      64 GAATCTTGTGATCAAGGAAAGATCCAAACTAAATATGCTATGCCATACCAATGCTTA 123
XX      133 GAATCTTGTGATCAAGGAAAGATCCAAACTAAATATGCTATGCCATACCAATGCTTA 192
XX      124 CCGATATCAATTCGACCCCTTAAGTACTTATGTTAAGCTCCAAAGGTGCAAACTTAAA 183
XX      193 CCGATATCAATTCGACCCCTTAAGTACTTATGTTAAGCTCCAAAGGTGCAAACTTAAA 252
XX      184 ACCATTAACCTAATGCTGAGACGAAATTAATTAACGTAATGCGCTATTCGATCCCTTC 243
XX      253 ACCATTAACCTAATGCTGAGACGAAATTAATTAACGTAATGCGCTATTCGATCCCTTC 312
XX      244 AATGCGAATAAGTGCTTACCATATTTTAATGATATTAACAGCACCGAAGCACTGAT 303
XX      313 AATGCGAATAAGTGCTTACCATATTTTAATGATATTAACAGCACCGAAGCACTGAT 372
XX      304 GTGAGAAATCTCTTTGCTCAAGTTCAGTTCGTGTGCAATGTCATTAACTAACAAT 363
XX      373 GTGAGAAATCTCTTTGCTCAAGTTCAGTTCGTGTGCAATGTCATTAACTAACAAT 432
XX      364 AGCTTATATCGACCATGAAAAAGAAAGCAAGTAATCAAGAAATCAAGTCCAAATG 423
XX      433 AGCTTATATCGACCATGAAAAAGAAAGCAAGTAATCAAGAAATCAAGTCCAAATG 492
XX      424 GGAATTCAAATATCTCGACGATGACATTGGAAAAATCTCT 462

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Db      493 GGAATTCAAATATCTACGACGATGACATTTGAAAAATCTCT 531
RESULT 5
AAT99556
ID      AAT99556 standard; DNA; 882 BP.
XX      AAT99556;
XX      17-OCT-2003 (revised)
XX      08-JUN-1998 (first entry)
XX      Phytoacca insularis antiviral protein gpIP2 gene.
XX      Antiviral protein; gpIP2 gene; virulence; transgenic plant;
XX      virus resistance; immunocjugate; AIDS; cancer; therapy; ss.
XX      Phytoacca insularis; Nakai.
XX      OS
XX      FH      Location/Qualifiers
XX      FT      1..882
XX      FT      CDS
XX      FT      /*cag= a
XX      FT      /transl_except= (pos:715..717, aa:Ile)
XX      EPP08902-A2.
XX      26-NOV-1997.
XX      30-SEP-1996; 96EP-00307159.
XX      22-MAY-1996; 96KR-00017404.
XX      (JINR-) JIN RO LTD.
XX      Moon Y, Choi J, Yun Y, Jin J, Hong B, Lee J, Choi K, Lee J;
XX      Song S, Choi Y, Kim C, Kim M;
XX      WPI; 1998-001788/01.
XX      P-PSDB; AAW26773.
XX      Antiviral proteins of Phytoacca insularis Nakai and their genes - useful
XX      in plant antiviral agents and immunocjugates for the treatment of AIDS
XX      and cancer.
XX      Claim 2; Page 10-12; 26pp; English.
XX      This polynucleotide comprises the coding region of the Phytoacca
XX      insularis Nakai gene coding for a 32.8 kDa novel antiviral protein
XX      designated gpIP2 (see AAW26773). The gpIP2 gene was isolated from leaf
XX      genomic DNA by PCR amplification (see AAT99558-59). Another gene (see
XX      CC AAT99557), encoding a 35.7 kDa protein (see AAW26774) designated gpIP50,
XX      has also been isolated from P. insularis Nakai. Also claimed are vectors
XX      encoding these antiviral proteins and host cells transformed or
XX      transduced with these vectors. E. coli XL1-Blue MRP. gpIP2 (RCM-10080)
XX      host cells are claimed, as is a process for preparing antiviral protein
XX      by culturing these cells and purifying the protein from inclusion
XX      bodies. The antiviral proteins and recombinant proteins inhibit protein
XX      synthesis. They can be used as active ingredients of antiviral agents of
XX      plant viruses, and employed in the manufacture of immunocjugates for
XX      the treatment of AIDS and cancer. The isolated genes can be used in the
XX      breeding of transgenic plants having viral resistance. (Updated on 17-OCT
XX      -2003 to standardise OS field)
XX      Sequence 882 BP; 301 A; 164 C; 174 G; 243 T; 0 U; 0 Other;
SQ
Query Match      67.4%; Score 313.2; DB 2; Length 882;
Best Local Similarity 79.9%; Pred. No. 4.1e-80;
Matches 369; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
XX      1 ATGATTAATACGATCACTTGTGATGCTGGAATGCCACATTAACAATATGCCACTTT 60
XX      1 ATGATTAATACGATCACTTGTGATGCTGGAATGCCACATTAACAATATGCCACTTT 60

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PR 02-AUG-2001; 2001CN-00123911.
XX (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
XX Peng X, Bai L, Yin B,
XX WPI; 2003-469263/45.
DR P-PSDB; ADM74752.
XX
XX Two kinds of cDNA with activity capable of extensively inhibiting HIV and
PT its expression, separation and purification method in protokaryon.
XX
PS Example 8; Page 9-10; 17pp; Chinese.
XX
XX The present invention relates to two kinds of cDNA which can inhibit
CC human immunodeficiency virus (HIV-1) activity, including separation clone
CC of two kinds of cDNA, external mutation, fusion expression in prokaryons
CC and application of the cDNA in preparation of preparation for curing the
CC virus and tumours. One of the described cDNAs is obtained by separation
CC and cloned from a plant Chinese phytolacca leaf, and one from the trans-
CC acting activation factor (Tat) mutant coded by human immunodeficiency
CC virus HIV-1 gene. This polynucleotide sequence represents a cDNA used in
CC the HIV-1 inhibition activity of the invention.
XX
SQ Sequence 1164 BP; 379 A; 239 C; 248 G; 298 T; 0 U; 0 Other;
Query Match 65.5%; Score 304.4; DB 11; Length 1164;
Best Local Similarity 79.0%; Pred. No. 1.5e-77;
Matches 362; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
QY 5 TAAATACGATCAGCTTGTGATGCTGGAATGCCACATTAAACAAATATGCCACCTTATGG 64
DB 290 TGAATACATCATCTCAATGTTGGAATGACACCATTAACCAATACGCCATTTCTGG 349
QY 65 AATCTCTGTATCAAGCGAAGATCCAAATCTAAATGCTATGCAATGCTAC 124
DB 350 ATATCTTCTGTATGAGGAGGAGATCCAGTTTAAATGCTATGGAATCCAAATGTTGC 409
QY 125 CTGATATTAATGACCCCTTAAGTACTTATGTTAGTTCAGTCCAAAGTCCAACTTAAAA 184
DB 410 CCAATCAAAATCCAAATCCAAAGTACGTTGGTGGTCCAAAGTTCAATTAATAAAAA 469
QY 185 CCATTACATTAATGCTGAGCGAATTAATTAATGATGGGCTATTCGATCCCTCA 244
DB 470 CCAATCACTAAATGCTGAGCGAATTAATTAATGATGGGCTATTCGATCCCTTGG 529
QY 245 ATGCAATTAAGTCTGTTACCATATATTAATTAATTAACAGCAGGACGATGATG 304
DB 530 ATACCAATTAAGTCTGTTACCATATCTTTAGTATATCTCAAGTACGAGCCAGATG 589
QY 305 TGGAGAAATCTCTTCTCAAGTTCTAGTCTGCTGTTGCAATGTCATTAACTACATA 364
DB 590 TAGAGACTACTGTTTCCCAATCCCAATCTGCTGTAGTAAACATTAACATGATGATA 649
QY 365 GCTTAATTCGACATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 424
DB 650 GTCGATATCCAAATGATGATCAAAAGCGGAGATTAATCAAGAGATCAAGTCAACTGG 709
QY 425 GAATTCAAATTAATCAGAGATGATCAATTTGAAAAATCTCT 462
DB 710 GAATTCAAATTAATCAGAGATGATTAATTTGAAAAATTTCT 747
RESULT 8
ADG76061
ID ADG76061 standard; DNA; 1378 BP.
XX
XX ADG76061;
XX
XX 11-MAR-2004 (first entry)
XX
XX American pokeweed antiviral protein (PAP) DNA Segid 1.
XX

KM gene; ds; pokeweed antiviral protein; PAP; HIV-1; anti-HIV; antiviral;
KM nucleoside analogue inhibitor; viral protease inhibitor; viral infection;
KM american pokeweed; retroviral.
XX
XX Phytolacca americana.
XX
XX WO2003106479-A2.
XX
XX 24-DEC-2003.
XX
XX 17-JUN-2003; 2003WO-US019141.
XX
XX 17-JUN-2002; 2002US-0389649P.
XX
XX (PARK-) PARKER HUGHES INST.
XX
XX Uckun FM;
XX
XX WPI; 2004-082156/08.
XX
XX P-PSDB; ADG76064.
XX
XX Novel modified pokeweed antiviral protein useful for inhibiting viral
PT replication, for inducing depurination of viral RNA, or for treating
PT viral infection in subject.
XX
XX
XX Example 2; SEQ ID NO 1; 62pp; English.
XX
XX This invention relates to novel modified pokeweed antiviral proteins
CC (PAPs). Specifically, it refers to modifications relative to wild-type
CC PAP that confer increased activity towards viral RNA, particularly
CC retroviral RNA such as HIV-1 and drug resistant HIV-1. Furthermore,
CC modified PAP also exhibits decreased activity towards ribosomal RNA
CC relative to wild-type PAP. The present invention describes a molecular
CC model of PAP-HIV RNA interactions that have been used for the rational
CC redesign of PAP mutants with potent anti-HIV activity, where
CC modifications have been introduced in regions other than the active site.
CC Accordingly, these mutants represent antiviral agents that can work as
CC nucleoside analogue inhibitors of reverse transcriptase, as well as viral
CC protease inhibitors that can be used for treating viral infections. As
CC such, they are useful for inhibiting viral replication and for
CC depurinating viral RNA. This polynucleotide sequence is the DNA encoding
CC the wild type american pokeweed antiviral protein (PAP) of the invention.
XX
SQ Sequence 1378 BP; 487 A; 234 C; 268 G; 389 T; 0 U; 0 Other;
Query Match 64.8%; Score 301.2; DB 12; Length 1378;
Best Local Similarity 78.6%; Pred. No. 1.4e-76;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
QY 5 TAAATACGATCAGCTTGTGATGCTGGAATGCCACATTAAACAAATATGCCACCTTATGG 64
DB 291 TGAATACATCATCTCAATGTTGGAATGACACCATTAACCAATACGCCATTTCTGTA 350
QY 65 AATCTCTGTATCAAGCGAAGATCCAAATCTAAATGCTATGCAATGCTAC 124
DB 351 ATGATCTTGTATGAGGAGAGATCCAAATGTTTAAATGCTATGGAATCCAAATGCTGC 410
QY 125 CTGATATTAATGACCCCTTAAGTACTTATGTTAGTTCAGGTTGCAAACTTAAAA 184
DB 411 CCAATCAAAATCCAAATCCAAATGATGCTGTTGTTAGCTCCAAAGTTCAATTAATAAAAA 470
QY 411 CCAATCAAAATCCAAATCCAAATGATGCTGTTGTTAGCTCCAAAGTTCAATTAATAAAAA 470
DB 185 CCATTACATTAATGCTGAGCGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 244
DB 471 CCAATCACTAAATGCTGAGCGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 530
QY 245 ATGCAATTAAGTCTGTTACCATATATTAATTAATTAATTAATTAATTAATTAATTAAT 304
DB 531 AAACCAATTAATGCTGTTACCATATCTTTAATGATATCTCAAGTACGAGCCAGATG 590
QY 305 TGGAGAAATCTCTTCTCAAGTTCTAGTCTGCTGTTGCAATGTCATTAACTACATA 364
DB 591 TAGAGACTACTGTTTCCCAATCCCAATTTCTGTTTATTAATAACATTAACCTTGTGATA 650

OY 365 GCTTATATCCAGCATGGAAAAAGAGAAAGTAAGTCAAGAAATCAAGTCCATTGG 424
 DB 651 GTGATATCCAACTGGAATGAAACGCGAGTAATAATCAAGAAAGTCAAGTCCAACTGG 710
 OY 425 GAATTCAAATATCTGACGATGATTCATTTGAAAAATCTCT 462
 DB 711 GAATTCAAATATCTGACGATATATTGAAAAAGATTCT 748
 RESULT 9
 AAZ45197
 ID AAZ45197 standard; DNA; 1379 BP.
 AC AAZ45197;
 XX
 DT 29-FEB-2000 (first entry)
 DB Wild-type pokeweed antiviral protein (PAP) nucleotide sequence.
 XX
 KW Pokeweed antiviral protein; PAP; PAP II; antifungal; transgenic plant;
 KM ribosome inhibiting protein; RIP; cereal crop; viral resistance; PVX;
 KM potato virus X; cucumber mosaic virus; CMV; ss;
 KM tomato yellow leaf curl virus.
 XX
 OS PhytoIacca americana.
 FH
 FH Key Location/Qualifiers
 FT CDS 225..1166
 FT /*tag= a
 FT /product= "PAP"
 FT /note= "Pokeweed antiviral protein"
 FT
 XX
 PN MO9960843-A1.
 PD 02-DEC-1999.
 XX
 PF 21-MAY-1999; 99WO-US011301.
 XX
 PR 22-MAY-1998; 98US-0086374P.
 XX
 PA (RUTP) UNIV RUTGERS STATE NEW JERSEY.
 PI Turner NE, Wang P;
 DR WPI; 2000-062555/05.
 DR P-PSDB; AAY58025.
 XX
 PT New antiviral DNA useful for generating transgenic plants resistant to
 PT viruses and/or fungi.
 XX
 PS Example; Page 4-5; 43pp; English.
 XX
 CC This is the Pokeweed antiviral protein (PAP) nucleotide sequence. PAP is
 CC a type I ribosome-inhibiting protein (RIP) found in the cell walls of
 CC PhytoIacca americana (pokeweed). It is a single polypeptide chain that
 CC catalytically removes a specific adenine residue from a highly conserved
 CC stem-loop structure in the 26S rRNA of eukaryotic ribosomes. The pokeweed
 CC antiviral protein II (PAP II) protein confers antiviral and or antifungal
 CC activities to plants. A DNA molecule encoding a PAP II protein with an
 CC intact catalytic active site amino acid residue (S172) is useful for
 CC generating transgenic plants. PAP II DNA is useful for generating a
 CC protoplast or introducing the DNA directly into a plant part prior to
 CC regeneration. Cells and seeds which exhibit anti-viral and/or anti-fungal
 CC activity thus have increased resistance to viruses and/or fungi. Viruses
 CC include potato virus X (PVX), cucumber mosaic virus (CMV), and tomato
 CC yellow leaf curl virus, and fungi include Pythium, Phytophthora,
 CC Sclerotinia and Aspergillus. PAP II proteins also confer resistance to
 CC other plants pests including insects, bacteria and nematodes. PAP II DNA
 CC is also useful for identifying a PAP II protein having reduced
 CC cytotoxicity. PAP II has a reduced cytotoxicity compared to PAP, so
 CC unlike PAP transgenic plants which are stunted and sterile, PAP II
 CC transgenic plants have a normal and fertile phenotype

XX
 SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
 Query Match 64.8%; Score 301.2; DB 3; Length 1379;
 Best Local Similarity 78.6%; Pred. No. 1.4e-76;
 Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
 OY 5 TAAATAGCATCACTTGTATGCTGGAATGACCACTTAATCAAAATATGCACTTATG 64
 DB 292 TGAATACAAATCTTCAATGATGTTGAGATACCACTTAATGCAATATGCACTTCTGA 351
 OY 65 AATCTCTTGTATTCAGCAAGAGATCCAAATCTAAATGCTATGCAATACCAATGCTAC 124
 DB 352 ATGATCTTGTATGATGAGCGAAAGATCCAAAGTTTAAATGCTATGCAATACCAATGCTGC 411
 OY 125 CTGATACATTAATTCGACCCCTTAAGTACTTATGTTAGCTCCAGGTGCAAACTTAAAA 184
 DB 412 CCAATACAAATACAAATTCAAAGTACGTTGTTGAGCTCCAAAGTTCAAAATAAAAAA 471
 OY 185 CCATTACACTAATGCTGAGAGAAATATCTATACGATGAGGCTATTCTGATCCCTTCA 244
 DB 472 CCAATCACTAATGCTGAGAGAAATCTTATGATGATGATGATGATGATGATGATGATG 531
 OY 245 ATGCAATATAGTGTCTGTTACCATATATTATTAATGATTAACAAGACCGAAGCACTGATG 304
 DB 532 AAACCAATTAATGTGCTTACCATATCTTATGATGATGATGATGATGATGATGATGATG 591
 OY 305 TGGAGAAATCTCTTGTCTGCAAGTTCTAGTTCTGCTGTTGCAATGCTCAATTAACATA 364
 DB 592 TAGAGACTACTCTTGTGCGCAATTCCTGCTGTTAGTAAACATTAACCTTGTGATA 651
 OY 365 GCTTATATCCGACCATGGAAAAAGAGAGAAATCTCAAGAAATCAAGTCCAAATGG 424
 DB 652 GTGATATCCAACTGGAATGAAACGCGAGTAATAATCAAGAAAGTCAAGTCCAACTGG 711
 OY 425 GAATTCAAATATCTGACGATGATTCATTTGAAAAATCTCT 462
 DB 712 GAATTCAAATATCTGACGATATATTGAAAAAGATTCT 749
 RESULT 10
 AAZ59220
 ID AAZ59220 standard; cDNA; 1379 BP.
 AC AAZ59220;
 XX
 DT 20-APR-2000 (first entry)
 DB Pokeweed antiviral protein coding sequence spring leaf form.
 XX
 KW Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
 KM resistance; potato virus X; potato virus Y; potato leaf roll virus;
 KM tuber; ss.
 XX
 OS PhytoIacca americana.
 FH
 FH US6015940-A.
 PD 18-JAN-2000.
 XX
 PF 07-APR-1992; 92US-00865169.
 XX
 PR 07-APR-1992; 92US-00865169.
 XX
 PA (MONS) MONSANTO CO.
 PI Kaniewski WK, Turner NE, Lodge JK;
 DR WPI; 2000-126326/11.
 XX
 PT Production of transgenic potato plants or tubers expressing pokeweed
 PT antiviral protein which are resistant to potato virus X or Y.
 XX

PS Claim 6; Fig 4; 30pp; English.

XX This is the coding sequence for the spring leaf form of the pokeweed
CC antiviral protein (PAP) which is used to generate transgenic potato
CC plants. PAP is able to confer resistance to infection by potato virus X
CC (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in the
CC potato plant or tuber expressing PAP

XX Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Query Match 64.8%; Score 301.2; DB 3; Length 1379;

Best Local Similarity 78.6%; Pred. No. 1.4e-76;

Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 5 TAAATACGATCACCTTGATGCTGGAATGCGACCATTAACAATATGCACTTTATG 64

DB 292 TGAATACATCTCTACATCTGTTGAGAGTACACCATTTAGCAATAGCCCTTTCTGA 351

QY 65 AATCTCTTGTAAATCAAGCGAAGATCCAAACTAAATGCTATGCGATACCATGCTAC 124

DB 352 ATGATCTTGTAAATGAGCGAAGATCCAACTTAAATGCTATGGAATGCAATGCTGC 411

QY 125 CTGATCTAATTTGACCCCTTAAGTCTTATTTGTTAGCTTCAAGTGCACCTTAAAA 184

DB 412 CCAATCAAAATACAAATCCAAAGTACGTGTGTTGAGCTCCAAAGTTCAAAATAAAAA 471

QY 185 CCATTACACTAATGCTGAGACGAATACTATACGTAGTGGCTATTTGATCCCTTCA 244

DB 472 CCATCACACTAATGCTGAGACGAATACTATACGTAGTGGCTATTTGATCCCTTCA 531

QY 245 ATGGCAATTAAGTGTGCTTACCATATATTATATATACAGACCGAAGCGACGTAGT 304

DB 532 AAACCAATTAATGCTGTTACCATATCTTTATGATATCTCAGGATCGAAGCGCAAGATG 591

QY 305 TGGAGAAATCTCTTTGCTCAAGTTCTAGTCTGTTGCAATGTCATTACTACATA 364

DB 592 TAGAGCTACTCTTTGCTCAAGTTCTAGTCTGTTGCAATGTCATTACTACATA 651

QY 365 GCTTATATCCGACCATGGAAGAAAGCAGAGTAATCAAGAAATCAAGTCCAAATGG 424

DB 652 GTGATATTCACATTTGGAATCAAAAGCGGAGTAAATCAAGAGTCAAGTCCAACTGG 711

QY 425 GAATTCAAATACTCAGACGTGACATTTGAAAAATCTCT 462

DB 712 GAATTCAAATACTCAGACGTGATATTTGAAAAATTTCT 749

RESULT 11

AAC87929 standard; DNA; 1379 BP.

XX AAC87929;

DT 06-MAR-2001 (first entry)

DE P. americana pokeweed antiviral protein encoding DNA SEQ ID NO:1.

XX Phytolacca americana; pokeweed; pokeweed antiviral protein; PAP; cancer;

KW biotransferase; fusion protein; immunoglobulin; mutant; cytotoxic;

KW anti-HIV; human immunodeficiency virus; AIDS; leukemia; lymphoma;

KW brain tumour; neuroblastoma; soft tissue sarcoma; osteosarcoma; 89.

OS Phytolacca americana.

XX Key Location/Qualifiers

FT CDS 225..1166

FT /tag= a /product= "pokeweed antiviral protein (PAP)"

PN US6146628-A.

XX 14-NOV-2000.

XX

PF 11-JUL-1995; 95US-00501253.

XX 11-JUL-1995; 95US-00501253.

XX (MINTU) UNIV MINNESOTA & RUTGERS.

PA (VINE-) UNIV STATE NEW JERSEY.

PI Uckun FM, Turner NE;

DR WPI; 2001-040422/05.

DR P-PSDB; AAB36500.

PT Immunoglobulins useful for treating cancer and acquired immunodeficiency

XX syndrome, comprises mutant pokeweed anti-viral protein and a targeting

XX moiety that binds a cell surface receptor.

XX Disclosure; Col 47-50; 32pp; English.

XX The present invention describes a fusion protein or an immunoglobulin

XX (1), comprising mutant Pokeweed Anti-viral Protein (PAP) having an amino

XX acid substitution at residue 75, 97 or 176 of native PAP and a targeting

XX moiety that binds a cell surface receptor. (1) can have cytosolic and

XX anti-HIV activities, and is an inhibitor of cellular RNA or protein

XX synthesis. (1) is useful for treating AIDS and cancers including

XX leukemia, lymphoma, a brain tumour, neuroblastoma, osteosarcoma, soft

XX tissue sarcoma, breast, prostate, ovarian, testicular, melanoma, lung, or

XX colon cancer. Immunoglobulins prepared using PAP mutants exhibit an

XX improved therapeutic index over immunoglobulins containing either wild-

XX type PAP or variant PAP. The present sequence encodes the wild-type PAP,

XX which is given in the exemplification of the present invention

XX Sequence 1379 BP; 488 A; 234 C; 268 G; 389 T; 0 U; 0 Other;

Query Match 64.8%; Score 301.2; DB 4; Length 1379;

Best Local Similarity 78.6%; Pred. No. 1.4e-76;

Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 5 TAAATACGATCACCTTGATGCTGGAATGCGACCATTAACAATATGCACTTTATG 64

DB 292 TGAATACATCTCTACATCTGTTGAGAGTACACCATTTAGCAATAGCCCTTTCTGA 351

QY 65 AATCTCTTGTAAATCAAGCGAAGATCCAAACTAAATGCTATGCGATACCATGCTAC 124

DB 352 ATGATCTTGTAAATGAGCGAAGATCCAACTTAAATGCTATGGAATGCAATGCTGC 411

QY 125 CTGATCTAATTTGACCCCTTAAGTCTTATTTGTTAGCTTCAAGTGCACCTTAAAA 184

DB 412 CCAATCAAAATACAAATCCAAAGTACGTGTGTTGAGCTCCAAAGTTCAAAATAAAAA 471

QY 185 CCATTACACTAATGCTGAGACGAATACTATACGTAGTGGCTATTTGATCCCTTCA 244

DB 472 CCATCACACTAATGCTGAGACGAATACTATACGTAGTGGCTATTTGATCCCTTCA 531

QY 245 ATGGCAATTAAGTGTGCTTACCATATATTATATATTAACAGACCGAAGCGACGTAGT 304

DB 532 AAACCAATTAATGCTGTTACCATATCTTTATGATATCTCAGGATCGAAGCGCAAGATG 591

QY 305 TGGAGAAATCTCTTTGCTCAAGTTCTAGTCTGTTGCAATGTCATTACTACATA 364

DB 592 TAGAGCTACTCTTTGCTCAAGTTCTAGTCTGTTGCAATGTCATTACTACATA 651

QY 365 GCTTATATCCGACCATGGAAGAAAGCAGAGTAATCAAGAAATCAAGTCCAAATGG 424

DB 652 GTGATATTCACATTTGGAATCAAAAGCGGAGTAAATCAAGAGTCAAGTCCAACTGG 711

QY 425 GAATTCAAATACTCAGACGTGACATTTGAAAAATCTCT 462

DB 712 GAATTCAAATACTCAGACGTGATATTTGAAAAATTTCT 749

RESULT 12

AAD42738 standard; DNA; 1379 BP.

XX AAD42738

XX	AAD42738;
AC	
XX	15-NOV-2002 (first entry)
DT	
XX	Pokeweed PAP' DNA #1.
DE	
XX	Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds.
KW	
XX	Phytolacca americana.
OS	
FH	Key Location/Qualifiers
FT	misc_feature 290..1076
PT	/tag= a
FT	/note= "Mature PAP' sequence"
XX	
PN	WO20023107-A2.
PD	
XX	25-APR-2002.
PP	
XX	15-OCT-2001; 2001WO-GB004593.
PR	
XX	14-OCT-2000; 2000GB-00025217.
PA	(ADPTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX	
PL	Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX	
DR	WPI; 2002-489891/52.
XX	
PT	Inducing necrotic effect in specific cells of plant by transforming plant
PT	with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX	which acts in response to application of specific stimulus to plant.
PS	Claim 5; Page 86; 87pp; English.
XX	
CC	The invention relates to a method of inducing a necrotic effect in
CC	specific cells of a plant. The method involves transforming the plant
CC	with chimeric gene(s), which encodes a pokeweed antiviral protein namely
CC	PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
CC	in response to the application of a specific stimulus to the plant so as
CC	to facilitate expression of the induced pokeweed antiviral protein in specific
CC	cells of the plant. The method is useful for inducing a necrotic effect
CC	in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX	
SQ	Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
Query Match	64.8%; Score 301.2; DB 6; Length 1379;
Beet Local Similarity	78.6%; Pred. No. 1.4e-76;
Matches 360; Conservative	0; Mismatches 98; Indels 0; Gaps 0
Dy	5 TAAATACGATCACTTGTAGTCGTGAATAATGCCACATTAAACAATATGGCACCTTTATGG 64
Dd	292 TGATACATCATCTCAATGTTTGAGAATGCACCACTTAAGCAAATATGCGCACCCTTTCGA 351
Dy	65 AATCTTGTGATATCAGCGAAGATCCAAAATAAATGCTATGSGATATCCATGACTAC 124
Dd	352 ATGATCTTGTGATATGAGCGAAGATCCAAAGTTTAAATGCTATGGAATACCAATGCTGC 411
Dy	125 CTGATACCTAATTCGACCCCTTAAGTACTAATGTTTAGTCCAGGTGCAAACTTAAAAA 184
Dd	412 CCAATATCAAAATCAAAATCCAAAGTACGTTGGTGAAGCTCCAAAGTTCCAATTAATAAAA 471
Dy	185 CCATTACACTATGCTGAGACGAATTAATCTTATATGATGAGGCTATTCGATCCCTTCA 244
Dd	472 CCAATCACTATGCTGAGACGAACAAATTTGTAATGATGAGGTTATTTCTGATCCCTTGG 531
Dy	245 ATGCAATATAGTGTCTTACCAATATATTTAATGATATTTACAGAACCGAAGCACTGATG 304
Dd	532 AAACCAATTAATATGTTTACCAATATCTTTAATGATATCTCAAGTACTGAACCGCAAGATG 591
Dy	305 TGGAAATATCTTGTCTCAAGTTTATGTTCTGCTGTTGCAATGTCATTAATCTAATTA 364

Db	592	TAGAGCTACTCTTTGCCCAATTCGATTCGTGTAGTAAACATTAACCTTTGATA	65
Qy	365	GCTTATATCCGACCATGAGAAAGAGAGATTAACCTCAAGAAATCAAGTCCAAATTGG	424
Db	652	GTCGATATCCACATTGGATTCAGAAAGGGGGAGTAAATCAAGAAGTCAGGTCCAACGTGG	711
Qy	425	GAATTCAATATCTCAGCAGTGCATTGGAAAAATCTCT	462
Db	712	GAATCAATACTCGACAGTAAATATGGAAAGATTCTT	749

RESULT_13

ID	AD105787	standard; DNA; 1379 BP.
XX	AC	
XX	AD105787;	
DT	15-APR-2004	(first entry)
XX		
XX		DNA encoding the wild-type pokeweed antiviral protein.
XX		ribosome depuration; antifungal; antiviral; virucide; anti-HIV;
XX		cytostatic; immunosuppressive; agricultural biotechnology; pharmaceuticals
XX		medicine; cancer; AIDS; viral infection; autoimmune disease; T-cell;
XX		B-cell; transgenic; plant; wild-type; pokeweed antiviral protein; gene;
XX		ds.
OS		Phytolacca americana.
XX		
XX	Key	Location/Qualifiers
FT	CDS	225..1166
FT		/tag= a
XX		/product= "wild-type pokeweed antiviral protein"
XX	W0200262952-A2.	
XX	15-AUG-2002.	
XX		
XX	01-FEB-2002; 2002WO-US002792.	
PP		
PR	02-FEB-2001; 2001US-0266396P.	
XX		
XX	(RUTP) UNIV RUTGERS STATE NEW JERSEY.	
XX		
XX	Turner NR, Hudak KA, Parikh B;	
XX		
DR	WPI; 2003-156656/15.	
XX	P-PSDB; AD105788.	
XX		
PT		New Pokeweed Antiviral Protein (PAP) mutant that is less toxic than wild-
PT		type PAP, useful in agricultural biotechnology or in the fields of
PT		pharmaceutics and medicine, e.g. treating cancer, AIDS, viral infection
PT		or autoimmune disease.
XX		
PS		Disclosure; SEQ ID NO 1; 51bp; English.
XX		
CC		The invention relates to a novel Pokeweed Antiviral Protein (PAP) mutant
CC		that is less toxic than wild-type PAP and exhibits ribosome depuration
CC		activity, where the mutant is a central domain mutant or N-terminal
CC		domain mutant. The PAP mutants have the following activities: antifungal,
CC		antiviral, virucide, anti-HIV, cytostatic and immunosuppressive. The PAP
CC		mutants are useful in agricultural biotechnology as well as in the fields
CC		of pharmaceutics and medicine. The PAP mutants and methods are useful in
CC		treating mammals with cancer, AIDS, viral infection or autoimmune
CC		diseases associated with proliferations of unwanted T-cells or B-cells.
CC		The transgenic plants are useful in exhibiting resistance to a broad
CC		spectrum of plant pests e.g. viruses and fungi. This polynucleotide
CC		sequence represents the DNA encoding the wild-type pokeweed antiviral
CC		protein of the invention.
XX		
XX		
Q0	Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;	

Query Match 64.8%; Score 301.2; DB 10; Length 1379;

Best Local Similarity 78.4%; Pred. No. 1.4e-76;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

```
OY 5 TAAATACGATCACCCTTGATGCTGGAATGCGCAATTAACAATATGCGCCTTTATG 64
   |||||
DB 292 TGAATACATCATTTACATAGTTGGAAGTACACCATTAAGCAATAGCCCTTTG 351
   |||||
OY 65 AATCTCTGTAATCAAGCGAAGATCCAAACTTAAATGCTATGCAATACCAATGCTAC 124
   |||||
DB 352 ATGATCTTCGTAATGAGCGAAGATCCAAAGTTTAAATGCTATGCAATACCAATGCTGC 411
   |||||
OY 125 CTGATATATATGACCCCTTAAGTACTTATGTTAGCTTCAAGGTCGAACCTTAAAA 184
   |||||
DB 412 CCAATACAAATATCAAAATCCAAAGTACGTGTGTTGAGCTCCAAAGTTCAAATAAAAA 471
   |||||
OY 185 CCAATACATTAATGCTGAGAGCAAAATTAATATATGATGAGGCTATTCGATCCCTTCA 244
   |||||
DB 472 CCAATACATTAATGCTGAGAGCAAAATTAATATGATGAGGCTATTCGATCCCTTGC 531
   |||||
OY 245 ATGCAATTAAGTGTCTTACCATATATTTATGATATTAATCAAGCAGCACTGATG 304
   |||||
DB 532 AAACCAATTAATATGCTTACCATATCTTTATGATATCTGAGTACTGAAAGCCAAATG 591
   |||||
OY 305 TGAAGATATCTCTTGTCTCAAGTTCTAGTCTGCTGTTGCAATGCCATTAATCAATA 364
   |||||
DB 592 TAGAGACTACTCTTGTGCGCAATGCAATCTCGTGTATGTAATCAATAACTTTGATA 651
   |||||
OY 365 GCTTATATCCGACCATGAGAAAGAAAGAGTAATCTCAAGAAATCAAGTCCAAATG 424
   |||||
DB 652 GTGATATCCAACTTGAATCAAAAGCGGAGTAATCAAGAGTCAAGTCCAACTGG 711
   |||||
OY 425 GAATTCAAATATCTGACGATGACATTTGAAAAATCTCT 462
   |||||
DB 712 GAATTCAAATATCTGACGATGATATTTGAAAAATTTCT 749
   |||||
```

RESULT 14

AA056672
ID AA056672 standard; cDNA; 1195 BP.

XX AC AA056672;

XX DT 16-OCT-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 04-SEP-1994 (first entry)

XX DE Sequence of Phytolecta antiviral protein (PAP) cDNA.

XX KW Antiviral protein; PAP; virus-resistance; transgenic plant; ss.

XX OS Phytolecta americana; L.

XX FH Key Location/Qualifiers
XX FT CDS 33..974
XX FT /*tag= a

XX PN EP585554-A1.

XX PD 09-MAR-1994.

XX PF 30-JUN-1993; 93EP-00110445.

XX PR 16-AUG-1992; 92KR-00014895.

XX PA (JINR-) JIN RO LTD.

XX PI Kim M, Lee K, Na B, Jeong H, Choi K, Moon Y, Jeon H;

XX DR WPI; 1994-076002/10.

XX DR P-PSDB; AAR48548.

XX PT Expression vector for phytolecta antiviral protein - used for producing
XX transgenic virus-resistant plants and for producing the antiviral agent.
XX PA

XX XX Disclosure; Fig 1; 15pp; English.

PS CC To isolate PAP gene, total cellular mRNA was purified from leaves of
XX CC Phytolecta americana L. obtd. in Korea. A cDNA library was constructed.
CC The PAP gene was selected by immunoscreening employing anti-PAP antibody.
CC A deletion mutant was prepd. from the isolated PAP gene, and the DNA
CC sequence of the PAP genome was determined. (Updated on 25-MAR-2003 to
XX CC correct FN field.) (Updated on 16-OCT-2003 to standardise OS field)

SO Sequence 1195 BP; 420 A; 201 C; 230 G; 344 T; 0 U; 0 Other;

Query Match 64.4%; Score 299.6; DB 2; Length 1195;

Best Local Similarity 78.4%; Pred. No. 3.8e-76;
Matches 359; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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OY 5 TAAATACGATCACCCTTGATGCTGGAATGCGCAATTAACAATATGCGCCTTTATG 64
   |||||
DB 100 TGAATACAAATCATCTACATAGTTGGAAGTACCAATTAAGCAATAGCCACTTTTCTGA 159
   |||||
OY 65 AATCTCTGTAATCAAGCGAAGATCCAAACTTAAATGCTATGCAATACCAATGCTAC 124
   |||||
DB 160 ATGATCTTCGTAATGAGCGAAGATCCAAAGTTTAAATGCTATGCAATACCAATGCTGC 219
   |||||
OY 125 CTGATATATATGACCCCTTAAGTACTTATGTTAGCTTCAAGGTCGAACCTTAAAA 184
   |||||
DB 220 CCAATACAAATATCAAAATCCAAAGTACGTGTGTTGAGCTCCAAAGTTCAAATAAAAA 279
   |||||
OY 185 CCAATACATTAATGCTGAGAGCAAAATTAATATGATGAGGCTATTCGATCCCTTCA 244
   |||||
DB 280 CCAATACATTAATGCTGAGAGCAAAATTAATGATGAGGCTATTCGATCCCTTGC 339
   |||||
OY 245 ATGCAATTAAGTGTCTTACCATATATTTATGATATTAATCAAGCAGCACTGATG 304
   |||||
DB 340 AAACCAATTAATATGCTTACCATATCTTTATGATATCTGAGTACTGAAAGCCAAATG 399
   |||||
OY 305 TGAAGATATCTCTTGTCTCAAGTTCTAGTCTGCTGTTGCAATGCCATTAATCAATA 364
   |||||
DB 400 TAGAGACTACTCTTGTGCGCAATGCAATCTCGTGTATGTAATCAATAACTTTGATA 459
   |||||
OY 365 GCTTATATCCGACCATGAGAAAGAAAGAGTAATCTCAAGAAATCAAGTCCAAATG 424
   |||||
DB 460 GTGATATCCAACTTGAATCAAAAGCGGAGTAATCAAGAGTCAAGTCCAACTGG 519
   |||||
OY 425 GAATTCAAATATCTGACGATGACATTTGAAAAATCTCT 462
   |||||
DB 520 GAATTCAAATATCTGACGATGATATTTGAAAAATTTCT 557
   |||||
```

RESULT 15

AA081457
ID AA081457 standard; cDNA; 1195 BP.

XX AC AA081457;

XX DT 16-OCT-2003 (revised)
XX DT 25-AUG-1995 (first entry)

XX DE Phytolecta antiviral protein (PAP) cDNA.

XX KW Antiviral protein; vector PMJ12; KCCM 10037; PAP; ss.

XX OS Phytolecta americana; L.

XX PN AU9350642-A.

XX PD 19-JAN-1995.

XX PF 11-NOV-1993; 93AU-00050642.

XX PR 02-JUL-1993; 93KR-00012360.

XX PA (JINR-) JIN RO LTD.

XX Lee K, Choi K, Jeon H, Kim M, Moon Y;
PI
XX
DR WPI, 1995-067518/10.

XX Recombinant vector for producing Phytolecta anti-viral protein - and
PT transformed E. coli useful for making immunoconjugates for treatment of
PT AIDS.

XX
PS Claim 1; Fig 1; 27pp; English.

XX
CC Total cellular mRNA from leaves of P. americana was used to produce a
CC cDNA library and this screened with anti-PAP antibody raised in rabbits
CC against purified PAP. Inserts were isolated from 2 clones and sequenced
CC to identify a 1195 ORF (AA081457) that encodes a 313 AA PAP including a
CC 22 AA signal peptide. The mature PAP gene was subjected to PCR
CC amplification using primers AA081458 and AA081459. The amplification
CC product was cut with Hind III and inserted into the commercial FLAG (RTM)
CC vector cut with the same enzyme to form pmJ12. pmJ12 is deposited with
CC the Korean Collection of Culture and Microorganism (KCCM), an
CC International Depository Authority, on June 30 1993, as deposition No.
CC KCCM 10037, and claimed. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 1195 BP, 420 A; 203 C; 229 G; 343 T; 0 U; 0 Other;

Query Match 64.1%; Score 298; DB 2; Length 1195;

Best Local Similarity 78.2%; Pred. No. 1,1e-75;

Matches 358; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 5 TAAATACGATCCTTGTGATGCGAATGCGACCATTAACAATATGCGACCTTATG 64
Db 100 TGAATACATCATCTACATGATGAGAGACCATTAAGCAATATGCGACCTTATG 159
QY 65 AATCTCTGATATGAGCGAAGATCCAAACTAAATGCTATGCGATACCATGCTAC 124
Db 160 ATGATCTTCTGTAATGAGCGAAGATCCAAAGTTTAAATCTATGAAATACCATGCTGC 219
QY 125 CTGATACTAATTCGACCCCTAAGTACTTATGTTAGTCCAAAGTGCAAACTAAAA 184
Db 220 CCAATACAAATACAAATCCAAAGTACGTGTGTGAGCTCCAAAGTCCAAATAAAAA 279
QY 185 CCATTACATATGCTGAGAGCAATTAATACGTATGCGCTATTCGATCCCTCA 244
Db 280 CCATCAGCTATATGCTGAGAGCAATTAATGATGATGATGATGATGATGATGATG 339
QY 245 ATGCAATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 304
Db 340 AAACCACTAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 399
QY 305 TGAAGATATCTCTTGTGCTCAAGTCTAGTCTGCTGCTGCAATGCTCAATTA 364
Db 400 TGAAGATATCTCTTGTGCTCAAGTCTAGTCTGCTGCTGCAATGCTCAATTA 459
QY 365 GCTTATATCCGACATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 424
Db 460 GTGATATCCGACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 519
QY 425 GAATTCAAATCTGACGATGATGATGATGATGATGATGATGATGATGATGATG 462
Db 520 GAATTCAAATCTGACGATGATGATGATGATGATGATGATGATGATGATGATG 557

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:25:18 ; Search time 2202.83 Seconds
(without alignments)
9876.364 Million cell updates/sec

Title: US-09-978-274a-5

Perfect score: 465

Sequence: 1 atgataaatacagatcacctt.....acattgaaaaatctttaa 465

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hrc:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_g881:*

10: gb_g882:*

11: gb_g883:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62.2	13.4	498	5	BQ588134 E012337-0
2	47.8	10.3	829	7	CN782289 EST00385
3	46.6	10.0	489	2	BE130330 L48-484T3
4	44	9.5	701	9	BZ031330 ce124f09.
5	42.4	9.1	561	9	AO156306
6	41.8	9.0	658	10	C2857242
7	41	8.8	788	10	CG690741
8	40.4	8.7	563	9	AO670952
9	40.4	8.7	630	7	CO102355
10	40	8.6	528	10	AG960279
11	39.6	8.5	878	10	CNS01878
12	39.6	8.5	913	10	CNS00C20
13	39.6	8.5	1204	10	CNS016E2
14	39.4	8.5	880	10	CL848175
15	39.2	8.4	473	7	CN466064
16	39.2	8.4	853	10	BN147963
17	39	8.4	1019	10	CNS006FW
18	38.6	8.3	707	5	BQ545338
19	38.4	8.3	879	10	C2945561
20	38.2	8.2	456	2	BQ555640
21	38.2	8.2	739	8	DR166187
22	38	8.2	586	7	CK768171

23	37.8	8.1	946	4	AK015929
24	37.8	8.1	959	5	BY116082
25	37.8	8.1	964	5	BY115491
26	37.8	8.1	1382	4	AK016430
27	37.4	8.0	492	3	BM967727
28	37.4	8.0	613	7	CK133860
29	37.2	8.0	472	3	BO133949
30	37.2	8.0	543	3	BO134091
31	37.2	8.0	580	6	CD408931
32	37.2	8.0	715	9	CC004347
33	37.2	8.0	1146	10	CNS021G2
34	37	8.0	343	7	CV500814
35	37	8.0	410	7	CV292656
36	37	8.0	937	7	CK282629
37	36.8	7.9	317	7	CK632351
38	36.8	7.9	947	10	C2944913
39	36.6	7.9	315	7	CK632387
40	36.6	7.9	410	7	CK495303
41	36.6	7.9	512	1	AM199192
42	36.6	7.9	664	9	BZ003153
43	36.6	7.9	670	10	AG073512
44	36.6	7.9	680	3	B078909
45	36.6	7.9	854	10	D0089625

ALIGNMENTS

RESULT 1
BQ588134
LOCUS
DEFINITION
024-009-G14 5-PRIME, mRNA sequence.
ACCESSION
BQ588134
VERSION
BQ588134.1 GI:26117717
KEYWORDS
SOURCE
ORGANISM
Beta vulgaris
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.

REFERENCE
AUTHORS
Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Leinrich, H. and Kadetoff, U.
TITLE
Construction of a 'uniGene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
PUBMED
12472698
Contact: Weishaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpz-koeln.mpg.de
Insert length: 498 Std Error: 0.00
Plate: 9 row: G column: 14
Seq primer: SP6; CATACGATTGCTGACACTTAG.

FEATURES
source
1..498
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultiVar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:184726"
/db_xref="taxon:161934"
/clone="024-009-G14"
/tissue_type="leaf"
/lab_host="BMDH10B"
/clone_id="MPZ-ADIS-024-leaf"
/note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinfanzlebener Saatnucht AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites SalI-NciI, primer sites and orientation:
SP6-SalI-CCAGCGCTCCG-5prime-cDNA-polyA-CC-NciI-T7; Note:
Sequencing granted in the context of the GABI-beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

ORIGIN

Query Match 13.4%; Score 62.2; DB 5; Length 498;
Best Local Similarity 56.7%; Pred. No. 4e-06;
Matches 140; Conservative 0; Mismatches 98; Indels 9; Gaps 1;

QY 14 TCACCTTGATGCGGAAATGCGACCATTAACAATATGCAACCTTATGGAATCTCTC 73
DB 169 TAACTTTGACCTTGAAACAGCTTCAAGACAAATATGCACTTTTCTAAGCAATCTAC 228
QY 74 GTATCAAGCGAAAGATCCAAACTAAATGCTATGCAATCAATGCTACTGANTACTA 133
DB 229 GCACAAATGTGAAGGATTCAAAGCTATGATAGAGAAATTCATGCTCCCTGCACAT 288
QY 134 ATTCAGACCCCTAAGTACTTATGTTAGCTCCAAAGTGCAGAA-----CCTAAAA 184
DB 289 CAAACACGCAAAATACCTTTTACCGAGCTAAAGCTAAAAAGCCGCTACTGACATTA 348
QY 185 CCATTACACTAATGCTGACGAAATTAATTAATGATGAGGCTATTCTGATCCCTTCA 244
DB 349 CCATCAACCTTGCTGTTAGCAAAATGACTTATATGATGAGCTTTTACTATCAAGTAG 408
QY 245 ATGGCAA 251
DB 409 CAGGTAA 415

RESULT 2 829 bp mRNA linear EST 21-MAY-2004
CN782289
LOCUS CN782289
DEFINITION EST00385 cgsed Chenopodium quinoa cDNA clone S02J22 5' similar to
antiviral ribosome-inactivating protein CAP30B (Chenopodium album),
mRNA sequence.

ACCESSION CN782289
VERSION CN782289.1 GI:47561753
KEYWORDS EST.

SOURCE Chenopodium quinoa (quinoa)

ORGANISM Chenopodium quinoa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Chenopodium.

REFERENCE 1 (bases 1 to 829)
Coles, N.D., Coleman, C.E., Christensen, S.A., Jellen, B.N.,
Stevens, M.R., Bonifacio, A., Rojas-Beltran, J.A., Fairbanks, D.J. and
Maughan, P.J.

TITLE Development and use of an expressed sequence tag library in quinoa
(Chenopodium quinoa Willd.) for the discovery of single nucleotide
polymorphisms

JOURNAL Plant Sci. 168 (2), 439-447 (2005)

COMMENT Contact: Coleman, Craig E.
Department of Plant and Animal Sciences
Brigham Young University
275 WIDB, Brigham Young University, Provo, UT 84602, USA
Tel: (801) 422-5145
Fax: (801) 422-0008
Email: craig.coleman@byu.edu

Plate: 02 row: J column: 22
Seq primer: M13 Forward
High quality sequence stop: 829.

FEATURES

source

1..829
Location/Qualifiers

/organism="Chenopodium quinoa"
/mol_type="mRNA"
/cultivar="Real"
/db_xref="taxon:63459"
/clone="S02J22"

/tissue_type="Developing Seed"
/lab_host="XL-1 Blue"
/clone_lib="cgsed"
/note="Vector: pTrp1Bx2; Site_1: SfiI; Site_2: SfiI;
Developing Seed cDNA Library from Chenopodium quinoa"

ORIGIN

Query Match 10.3%; Score 47.8; DB 7; Length 829;
Best Local Similarity 51.7%; Pred. No. 0.041;
Matches 140; Conservative 0; Mismatches 122; Indels 9; Gaps 1;

QY 30 AATGCCACCATTAACAATATGCGACCTTATGGAATCTCTTGATATCAAGCGAAGA 89
DB 115 AAAACCTACACAGAACTTATTAACACTTTCTGCAAGATAGCGACCAACTAAGA 174
QY 90 TCCAAACTAAATGCTATGCAATCAATGCTACTGATATTAATTCGACCCCTAAGTA 149
DB 175 TCCAAAGCTTATGATAGAGAAATCCCAATGATCCGACCAACCAACCAATACATA 234
QY 150 CTTATGTTAAGCTCCAAAGTGCAGAACTTAAAC-----CATTAACATATAGCT 200
DB 235 TCTTTGCTGACCTTGAAATCTTAAAGATAGATAGATATTCATTAACCTTGCTT 294
QY 201 GAGACGAATTAATTAATGATATGATGAGGCTATTTGATCCCTCAATGCAATTAAGTGC 260
DB 295 AAGTAGAAGACGACTTGATGATAGAGGCTTTGCTGATTAATTTGAGGCAAGTTCCGG 354
QY 261 TTACCATATTAATTAATGATATTAACAACACC 291
DB 355 CCATTTCTTTCCACTTAAACATTAACATGAACC 385

RESULT 3 489 bp mRNA linear EST 20-FEB-2001
BE130330
LOCUS BE130330
DEFINITION L48-484T3 Ice plant Lambda Uni-Zap XR expression library, 48 hours
NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-484 5',
mRNA sequence.

ACCESSION BE130330
VERSION BE130330.1 GI:8577693
KEYWORDS EST.

SOURCE Mesembryanthemum crystallinum (common iceplant)

ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Aizoaceae; Mesembryanthemum.

REFERENCE 1 (bases 1 to 489)
Cushman, J.C.

TITLE An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum

JOURNAL Unpublished (1997)

COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

PCR primers
FORWARD: T7
BACKWARD: T3
Plate: L48-5 row: G column: 12
Seq primer: T3
High quality sequence stop: 350
POLYA=No.

Location/Qualifiers

FEATURES

source

1..489
Location/Qualifiers

/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="L48-484"
/tissue_type="Leaf", 48 h 0.4M NaCl"
/dev_stage="Six week old"

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/clone_lib="rice plant lambda Uni-Zap XR expression  
library, 48 hours NaCl treatment"  
/note=Vector: Lambda Uni-Zap XR, Bluescript SK-, Site_1:  
EcoRI, Site_2: XhoI"
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Qy 112 ATCCAAATCTGACCTGATATCTAAATTCGACCCCTTAAGTACTAATGGTATTAAGTCCAAAGT 171

Db 322 ATCCAAATCTAAATTAATTAACCTTAACAAACCCAGTGTAATACCTGTAAACCGCMAACA 263

Qy 172 GCAAACTTAAACCACTTACACTAATGCTGAGACGAATAACTATACGTGATGGGCTAT 231

Db 262 CCAAACTCTAAATCTTTTACCAATAATCTCGAAAAAACAATTTTTTAAAAAATAATCATTA 203

Qy 232 TCTGATCCCTTCATATGGCAATTAAGTGTGCTACCATATATTTATATGATATTTA 283

Accession	A0156306.1	GI:355331
Version	GSS.	
Keywords	Oryza sativa (japonica cultivar-group)	
Source	Oryza sativa (japonica cultivar-group)	
Organism	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
Definition	561 bp DNA linear GSS 12-SRP-1999	
Locusts	ncbi000707076 CUGI Rice BAC library Oryza sativa (japonica	
Accession	sequence. A0156306	

1 (baber 1 to 561)

TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288

High quality sequence stop: 262.

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Source
Location/Qualifiers
1. .561
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="japonica"

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/lab host="E. coli DH10B"
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/note=Vector: pBel0BACII, Site 1: HindIII, Site 2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics

genome of rice, three times larger than that of

microarrays, makes it valuable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from *Oryza sativa*, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The

deep coverage allows the isolation a particular sequence

each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

Query Match	9.1%;	Score 42.4;	DB 9;	Length 561;
Best Local Similarity	51.0%;	Pred. No.1.2;		
Matches 100;	Conservative 0;	Mismatches 96;	Indels 0;	Gaps 0;
Qy	76	AATCAAGCGAAGATCCAAAACCTAAATVGTCTATGCGATACCAATGCTACTGATACTAAT	135	
Db	392	AATTATATAAATTTATTCABAAAATAATCAACAATGAATTTAAAATATATTAATATTGAT	333	
Qy	136	TCGACCCCTTAAGTACTATTGGTTAAGTCCAGGTGCAACCTTAAAACCTATACACTA	195	
Db	332	TCCAAAACGACCACTAATTAATCAACCAAAACAATGGGTAACTGATCAATCAACCCAAATC	273	
Qy	196	ATGCGAGAGCAATTAATTAATTAATGATGGAGCTATTGATCCCTTCAATGGCAATTAAG	255	
Db	272	ATCGCAATTAATTAATTAATTAATTTCTTTTTCCAAAACTCTCCCTTTTTCATGAT	213	
Qy	256	TGTCGTTACCATATAT	271	
Db	212	TTTGTTTTCTTAAT	197	
RESULT 6				
LOCUS	CZ857242/c	658 bp	DNA	linear
DEFINITION	OC__Ba0248N02.r OC__Ba Oryza coarctata genomic clone OC__Ba0248N02			
ACCESSION	CZ857242			
VERSION	CZ857242.1			
KEYWORDS	GSF.			
SOURCE	Oryza coarctata (Porteresia coarctata)			
ORGANISM	Oryza coarctata			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.			
AUTHORS	1. (bases 1 to 658) Kim,H., Collura,K., Wiscocki,M., Byrne,M., Stum,D., Smart,D., Rao,K., Luo,M., Jelic,R., Kudrna,D., Muller,C., Soderlund,C. and Wang,R.			
JOURNAL	OMG (Oryza Map Alignment Project) - Arizona Genomics Institute			
COMMENT	Unpublished (2005) Contact: Rod A. Wing Arizona Genomics Institute University of Arizona Forbes Building Room 303, Tucson, AZ 85721-0036, USA Tel: 520 626 9595 Fax: 520 621 1259 Email: rwing@genome.arizona.edu PCR primers FORWARD: TBA TAC GAC TCA CTA TAG GG BACKWARD: CAC TCA TTA GGC ACC CCA Plate: 0248 row: N column: 02 Seq primer: CAC TCA TTA GGC ACC CCA Class: BAC ends.			
FEATURES				
source	Location/Qualifiers 1..658 /organism="Oryza coarctata" /mol_type="genomic DNA" /db_xref="taxon:77588" /clone="OC_Ba0248N02" /tissue_type="leaves" /dev_stage="mature" /lab_host="DH10B" /clone_1fb="OC_Ba" /note="Vector: pAGHBact1; site_1: HindIII; site_2: HindIII"			
ORIGIN				
Query Match	9.0%;	Score 41.8;	DB 10;	Length 658;
Best Local Similarity	52.6%;	Pred. No.1.8;		
Matches 91;	Conservative 0;	Mismatches 82;	Indels 0;	Gaps 0
Qy	247	GGCAATTAAGTGCCTTACCATATATTATGATATTACAGACGCAAGCACTGATG	306	
Db	478	GGACAAAGATGTTGGCAAAAATGTGACGATGACCTTTATGCGACACGGTGCTG	419	

Qy	307	GAGAAATCTCTTTGGTCACAGTTCTAGTCTCGGTTGCAATGCCATTAACCTACCAATAGC	366
Db	418	GGAGATCTGCTTAACCTCAAGTAGAGTTCTTAGCTTTGTCCTTAGAGGATAGACATTAA	359
Qy	367	TTATATCCGACCATGTGMAAAGAAAGCAAGATTAACCTCAAGAAATCAAGTCCA	419
Db	358	TTTGATCTCTACATTTGACAAAGAAACATAGCAAAAGTAAGGACCTTAGACCAA	306
RESULT 7			
LOCUS	CG690741/c	788 bp	DNA linear
DEFINITION	ZMMBc0135P02r ZMMBc (EcoRI) Zea mays genomic clone ZMMBc0135P02		
ACCESSION	CG690741		
VERSION	CG690741.1		
KEYWORDS	3', genomic survey sequence.		
SOURCE	GS.		
ORGANISM	Zea mays		
	Zea mays		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.		
REFERENCE	1 (bases 1 to 788)		
AUTHORS	Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C., Zolovetz,V., Fuks,G., Yu,Y., Ming,R. and Messing,J.		
TITLE	Sequencing of the maize genome at PCR (2003c)		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Bharti,A.K. Dr. Joseph Messing's lab The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers University 190 Frelinghuysen Road, Piscataway, NJ 08854, USA Tel: 732 445 3801 Fax: 732 445 5735 Email: bharti@waksman.rutgers.edu Seq primer: SP6 Class: BAC ends High quality sequence start: 88. Location/Qualifiers 1..788 /organism="Zea mays" /mol_type="genomic DNA" /cultivar="B73" /db_xref="taxon:4577" /clone="ZMMBc0135P02" /lab_host="E. coli DH10B" /clone_lib="ZMMBc (EcoRI)" /note="Vector: pTARAC2.1; Site_1: EcoRI; Site_2: EcoRI"		
FEATURES			
source			
ORIGIN			
Query Match	8.8%;	Score 41;	DB 10;
Best Local Similarity	55.2%;	Pred. No. 3;	
Matches	80;	Conservative	0;
		Mismatches	65;
		Indels	0;
		Gaps	0;
Qy	317	TTTGCTCAAGTTCAGTTCCTCGTGTGCAATGCCATTAACCTACAAATGCTTAATCCGA	376
Db	470	TGTTTCAACTTAATGCTGTTGTTTGCACTGTGACAAATTAATCTCCGTAAATATTTT	411
Qy	377	CCATGGAAAAGAAAGCAAGATTAACCAAAATCAAGTCCATTTGGGAATTCAAATAC	436
Db	410	CCATGGAAAGAAATTAATTAATGTCATTTTCATTAACCAATGCCAAAGATGATCATGTTT	351
Qy	437	TCAGCAATGACATTTGAAAAATCTC	461
Db	350	CTTACTTGGAAACTGAAACAAC	326
RESULT 8			
LOCUS	AO670952	563 bp	DNA linear
DEFINITION	HS 5429 B2 B06 TRA RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=1005 Col=12 Row=J, genomic survey sequence.		

JOURNAL

Submitted (19-JAN-2005) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: hattori@gscc.riken.jp, URL: http://hgp.gscc.riken.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the BAC library D581
For BAC library availability, please contact Masa-Toshi Yamamoto (Yamamoto@kit.jp).
Submitted (30-11-2004) by Masahira Hattori,
RIKEN, Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: hattori@gscc.riken.jp, Tel: 81-45-503-9111,
Fax: 81-45-503-9170)

COMMENT

This work was done in collaboration with Yamamoto, M-T. Drosophila Genetic Resource Center
Saga Ippongi-cho, Ukyo-ku, Kyoto 616-8354, Japan
Tel: 81-75-873-2660 FAX: 81-75-861-0881
PRIMERS

Sequencing : R

LIBRARY

Vector : pKS150
R.Site 1 : SacI
R.Site 2 : SacI

Location/Qualifiers

1..528
/organism="Drosophila sechellia"
/mol_type="genomic DNA"
/db_xref="taxon:7238"
/clone="DSB1-018H10.R.fa"
/clone_lib="DSB1 Drosophila BAC library"

ORIGIN

Query Match 8.6%; Score 40; DB 10; Length 528;
Best Local Similarity 51.7%; Pred. No. 5.3;
Matches 91; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

FEATURES

source

172 GCAACCTGAAACCATCTACCTAATGCTGAGCAAGTAATCTTACGTAGGGCTAT 231
117 GCAGAGTTATATCATCTTATTAATTAAGTGAAGTATTTGGAATTAATTTAT 176
232 TCTGATCCCTCAATGCAATAGAGTGTACCATATATTAATGATATTAACAAGC 291
177 GCGAGTTTGTGCTTTATTAAGTTCGTTTAAATTTGGAGCTGATATTAAG 236
292 GAAGCAGCTGATGTGAGAAATCTTGTCTCAAGTTCTAGTTCGTGTCAT 347
237 ACACATATGATTAGGCGAATAGCATTCACAAAGTAATTCGTTATATTTTAT 292

RESULT 11

CNS0187R 878 bp DNA linear GSS 26-JUL-1999

LOCUS

Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN04E04 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION

AL108993 GI:5629297

VERSION

AL108993.1 GI:5629297

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 878)

REFERENCE

AUTHORS

JOURNAL

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (BDGP) -
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billand at CEPH (Centre

d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
peloBAC11.

FEATURES

source

Location/Qualifiers
1..878
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN04E04"
/clone_lib="DrosBAC"
/plasmid="peloBAC11"
/note="end : SP6"

ORIGIN

Query Match 8.5%; Score 39.6; DB 10; Length 878;
Best Local Similarity 23.1%; Pred. No. 7.5;
Matches 48; Conservative 73; Mismatches 87; Indels 0; Gaps 0;

250 AATAAGTGTGTTACATATATTTAATGATATTAACAAGCAGCAAGCACTGATGTGAG 309
92 WAAAAAAMWMAAAAAAAMWMAAAGAMWGMWGAAMWMAAMRGMAAMWMAAAAA 151
310 AATACCTTTGCTCAAGTTCTAGTTCGTGTTGCAATGTCATTAACTACATAGCTTA 369
152 AAAAAWCTTTCMCTGATWRTTGTWTAAMWMTTBAAMWMAAMWMAAMWMAARG 211
370 TATCCGACATGAAAAAAGCAAGTAATCAAGAAATCAAGCCATATGGAAAT 429
212 WAAAAWMAAAAAAAMWMAAMWMAAMWMAAMWMAAMWMAAMWMAAMWMAAMWMA 271
430 CAATACCTCAGCAGTGCATGAGAAAA 457
272 WMAAMWMAAMWMAAMWMAAMWMAAMWMAAMWMAAMWMAAMWMAAMWMAAMWMA 299

RESULT 12

CNS00C20 913 bp DNA linear GSS 04-JUN-1999

LOCUS

Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR26P05 of RPI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION

AL059715 GI:4947359

VERSION

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 913)

REFERENCE

AUTHORS

JOURNAL

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazuo Oosawa and
Aaron Mammoxer in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
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/mol_type="genomic DNA"
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/clone="BACR26R05"
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/note="end : TET3"

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/db_xref="taxon:7227"
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			Gaps 1	
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QY	65	AATCTCTTGCGTAAATCGAAGCAAGATCCAAATACTAAATATGATGCGATGCAATGCTAC	124	
DB	939	TTTTTTTMMTTTTMMMMMMTTTTMMMMMMMMMMMMMMMMMMTTTTMMTTTTMMTTTTMM	998	
QY	125	CTGATACATAATGACACCCCTAAGTACTTATTTGGTAAAGCTCCAAAGTGCAAACTAAAAA	184	
DB	999	TTTTTTTMMTTTTMMMMMMTTTTMMTTTTTMMTTTTMMMMHTTTTMMTTTTMMTTTTMM	1058	
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QY	245	ATGCAATATAGTGTGCTTACCATATATATTTATGATATT	282	
DB	1118	TTTTTTTMMTT	1155	

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CNS016E2		
LOCUS		
DEFINITION		
ACCESSION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
COMMENT		

CNS016E2 1204 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN15A12 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL106628
AL106628.1 GI:5622852
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Epiphydoidea; Drosophilidae; Drosophila.
1 (bases 1 to 1204)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segr@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dicos BAC) was made by Alain Billand at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Fayan. It has been constructed in the vector
pbeloBAC11.

RESULT	14
LOCUS	CL848175
DEFINITION	CL848175 880 bp DNA linear GSS 16-AUG-2004
ACCESSION	OR_CBA0075J06.f OR_CBA Oryza rufipogon genomic clone OR_CBA0075J06
VERSION	5 , genomic survey sequence.
KEYWORDS	CL848175 CL848175.1 GI:51251441
SOURCE	GSS.
ORGANISM	Oryza rufipogon
	Oryza rufipogon
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriarctoidae; Oryzaceae; Oryza. 1 (bases 1 to 880)
REFERENCE	Kim,H., Yu,Y., Wisotski,M., Yost,D., Stum,D., Rao,K., Luo,M., Jettly,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
AUTHORS	OMAP project
TITLE	Unpublished (2004)
JOURNAL	Contact: Rod A. Wing
COMMENT	Arizona Genomics Institute University of Arizona Forbes Building Room 303, Tucson, AZ 85721-0036, USA Tel: 520 626 9595 Fax: 520 621 1259 Email: rwing@genome.arizona.edu
	PCR Primers FORWARD: TAA TAC GAC TCA CTA TAG GG BACKWARD: CAC TCA TTA GGC ACC CCA. Plate: 0075 row: J column: 06 Seq primer: TAA TAC GAC TCA CTA TAG GG Class: BAC ends.
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using SW model

Run on: April 8, 2006, 09:19:56 ; Search time 161.42 Seconds
(without alignment)
5120.590 Million cell updates/sec

Title: US-09-978-274A-5

Perfect score: 465
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

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Issued Patents NA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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3	301.2	64.8	1379	2 US-08-500-611-1	Sequence 1, Appli
4	301.2	64.8	1379	2 US-08-500-694-1	Sequence 1, Appli
5	301.2	64.8	1379	2 US-07-865-169-1	Sequence 1, Appli
6	301.2	64.8	1379	3 US-09-005-273-1	Sequence 1, Appli
7	301.2	64.8	1379	3 US-08-501-253A-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1
US-08-373-858-1
; Sequence 1, Application US/08373858
; Patent No. 5633155
; GENERAL INFORMATION:
; APPLICANT: Kim, Man-Keun
; APPLICANT: Lee, Kwan-Ho
; APPLICANT: Na, Byeong-Kook
; APPLICANT: Jeong, Han-Seung
; APPLICANT: Choi, Kyu-Whan
; APPLICANT: Moon, Young-Ho
; APPLICANT: Jeon, Hong-Seob
; TITLE OF INVENTION: Expression Vector for Phytolecta
; TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
; TITLE OF INVENTION: Plant Transformed Thereof.
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Darby & Darby
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,858
; FILING DATE: 18-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0136/117986-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7770
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: *Phytolacca americana*
TISSUE TYPE: Leaf
US-08-373-858-1

Query Match 65.1%; Score 302.8; DB 2; Length 1195;
Best Local Similarity 78.8%; Pred. No. 1.3e-78;
Matches 361; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

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RESULT 2

US-08-342-786B-1

Sequence 1, Application US/08342786B

Patent No. 5648234

GENERAL INFORMATION:

APPLICANT: Moon, Young-Ho

APPLICANT: Jeon, Hong-Seob

APPLICANT: Choi, Kyu-Whan

APPLICANT: Lee, Kwan-Ho

APPLICANT: Kim, Man-Keun

TITLE OF INVENTION: A No. 5648234e1 Expression Vector for *Phytolacca*

TITLE OF INVENTION: Antiviral Protein

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Darby & Darby

STREET: 805 Third Ave.

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/342,786B

FILING DATE: 21-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/147,024

FILING DATE: 01-NOV-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, S. Peter

REGISTRATION NUMBER: 25,351

REFERENCE/DOCKET NUMBER: 0136/08862-US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)527-7700

TELEFAX: (212)753-6237

TELEX: 236687

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1195 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: *Phytolacca americana* L.

IMMEDIATE SOURCE:

CLONE: PAP

US-08-342-786B-1

Query Match 65.1%; Score 302.8; DB 2; Length 1195;
Best Local Similarity 78.8%; Pred. No. 1.3e-78;
Matches 361; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 5 TAAATAGATGACCTTTGATGCTGGAATGCGACCATTAACAATATGCGCCTTTATG 64
DB 100 TGAATACAAATCATCTACATGTTGAAATGACACCATTAAGCAATACCGCCTTTTGA 159
QY 65 AATCTCTGCTGATCAAGCGAAGATCAAACTAAATGCTATGCGCATACCATGCTAC 124
DB 160 ATGATCTTCTGTAAGAGCGAAGATCAAGTTTAAATGCTATGAAATACCAATGCTGC 219
QY 125 CTGATTAATTCGACCCCTTAAGTATGTTAGTTGTTAAGCTCAAGTCAAACTAAAA 184
DB 220 CCAATACAAATACAAATCCAAAGTACGTGTGTTAGCTCAAGTCAAACTAAAAA 279
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QY 365 GCTTATATCCGACCATGGAAGAAAGACGAAGTAACTCAAGAAATCAAGTCAATGG 424
DB 460 GTCGATATCCAACTTGAAATCAAAAGCGGAGTAAATCAAGAAATCAAGTCAATGG 519
QY 425 GAATTCAAATGCTGAGATGATGGAATTAATCTCT 462
DB 520 GAATTCAAATGCTGAGATGATGGAATTAATCTCT 557

RESULT 3

US-08-500-611-1

Sequence 1, Application US/08500611

Patent No. 5756322

GENERAL INFORMATION:

APPLICANT: Turner, Nijlun B.

TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leiner, David, Litlenberg, Krumholz & Mentlik

STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500.611
FILING DATE: 11-JUL-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-611-1

Query Match 64.8%; Score 301.2; DB 2; Length 1379;
Best Local Similarity 78.6%; Pred. No. 4.1e-78;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 5 TAAATACGATACCTTTGATGCTGGAATGCGACCATTAACAATAATGCGACCTTTATG 64
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RESULT 4
US-08-500-694-1
Sequence 1, Application US/08500694
Patent No. 580329
GENERAL INFORMATION:
APPLICANT: Tumei, Nilgun E.
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein
TITLE OF INVENTION: Mutants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500.694
FILING DATE: 11-JUL-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-694-1

Query Match 64.8%; Score 301.2; DB 2; Length 1379;
Best Local Similarity 78.6%; Pred. No. 4.1e-78;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 5 TAAATACGATACCTTTGATGCTGGAATGCGACCATTAACAATAATGCGACCTTTATG 64
DB 292 TGAATACATCATCTACCAATGTTGGAAGTACCACTTAAGCAAAATGCGACCTTTCTGA 351
QY 65 AATCTCTGTAATCAAGCGAAAGATCCAAACTAAATGCTATGCGATCAATGCTAC 124
DB 352 ATGATCTTCGTAATGAAGCGAAAGATCCAACTTTAAATGCTATGGAATACCAATGCTGC 411
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DB 472 CCATCACACTATCTGTGAGAGCAAAATTTGATGTGATGGGTTATCTGATCCCTTGG 531
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QY 305 TGAGAAATCTCTTGTGCTCAAGTTCTAGTTCTCGTGTGCAATGTCATTAACAATA 364
DB 592 TAGAGACTACTCTTTGCCCCAATGCAATTCCTGTTAGTAAAAACATTAACCTTTGATA 651
QY 365 GCTTATATCCGACATGGAAGAAAGCAAGATTAACCTCAAGAAATCAAGTCAATTGG 424
DB 652 GTCATATATCCAACTTGGAAATCAAAAGCGGAGTAAATCAAGAAAGTCAAGTCCAACTGG 711
QY 425 GAATTCAAATCTCAGACGATGACATTTGGAATAATCTCT 462
DB 712 GAATTCAAATCTCAGACGATTAATTTGGAAGATTTCT 749

RESULT 5

US-07-865-169-1
; Sequence 1, Application US/07865169
; Patent No. 6015940
; GENERAL INFORMATION:
; APPLICANT: Turner, Nilgun E.
; APPLICANT: Lodge, Jennifer K.
; APPLICANT: Kandlewski, Wojciech K.
; TITLE OF INVENTION: Virus Resistant Potato Plants
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
; STREET: 700 Chesterfield Parkway No. 6015940th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/865,169
; FILING DATE: 19920407
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10547)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1379 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-07-865-169-1

Query Match 64.8%; Score 301.2; DB 3; Length 1379;
Best Local Similarity 78.6%; Pred. No. 4,1e-78;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 5 TAAATAGATCACTTTGATGCTGGAATGCGACCATTAACAATATGCCACTTTATGG 64
DB 292 TGAATACATCATCTACCAATGTTGGAAGTACCACTATGCAATATAGCCGCACTTTTGA 351
QY 65 AATCTCTTGTGAATCAAGCGAAATCCAAACTAAATGTATGCGATACCATGCTAC 124

DB 352 ATGATCTTCGTAATGAGACGAAAGATCCAGTTTAAATCTATGNAATCAATGCTGCG 411
QY 125 CTGATCTAATATGAGACCCCTAAGACTTATTTGTTAAGTCCAAAGTGAACCTAATAAA 184
DB 412 CCATTAACAATATACAAATCCAAAGTACTGTGTTGAGCTCCAAAGTTCAATTAATAAAA 471
QY 185 CCATTACCTAATGCTGAGACGAAATTAATTATACGTATGAGGCTATTCTGATCCCTTCA 244
DB 472 CCATCACACTAATGCTGAGACGAAACAAATTTGATGTGATGGGTTATCTGATCCCTTGG 531
QY 245 ATGGCAATTAAGTGTGCTGATCAATATATTTATGATTTACAGACCGAAGCAGCTGATG 304
DB 532 AAACCAATTAATGTCGTTACCATATCTTTAATGATCTCAGGTAAGTGAAGCGCAAGATG 591
QY 305 TGAGAAATCTCTTGTGCTCAAGTTCTAGTTCTCGTGTGCAATGTCATTAACAATA 364
DB 592 TAGAGACTACTCTTTGCCCCAATGCAATTCCTGTTAGTAAAAACATTAACCTTTGATA 651
QY 365 GCTTATATCCGACATGGAAGAAAGCAAGATTAACCTCAAGAAATCAAGTCAATTGG 424
DB 652 GTCATATATCCAACTTGGAAATCAAAAGCGGAGTAAATCAAGAAAGTCAAGTCCAACTGG 711
QY 425 GAATTCAAATCTCAGACGATGACATTTGGAATAATCTCT 462
DB 712 GAATTCAAATCTCAGACGATTAATTTGGAAGATTTCT 749

RESULT 6

US-09-005-273-1
; Sequence 1, Application US/09005273
; Patent No. 6137030
; GENERAL INFORMATION:
; APPLICANT: Turner, Nilgun E.
; TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
; TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLTZ &
; ADDRESS: MENTILIK
; STREET: 600 South, Avenue West
; CITY: Westfield
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07090
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,273
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,611
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,694
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/11546
; FILING DATE: 11-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Foley, Shawn P.
; REGISTRATION NUMBER: 33,071
; REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-654-7866
; TELEFAX: 908-654-5000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1379 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 225..1163
 FRAMES:
 NAME/KEY: sig_peptide
 LOCATION: 225..230
 US-09-005-273-1

Query Match 64.8%; Score 301.2; DB 3; Length 1379;
 Best Local Similarity 78.6%; Pred. No. 4.1e-78;
 Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

5 TAAATAGATCACTTGAATGCTGAATGCAACATTAACAATAATGCACTTTATG 64
 292 TGAATCAATCATCTACATATGTAAGTACACCATTAAGCAACCTTTCTGA 351
 65 AATCTCTGTAATCAAGCGAAGATCCAAACTAAATGCTATGCAATGCTAC 124
 352 ATGATCTTCTGAATGAAGCGAAGATCCAACTTTAAATGCTATGCAATGCTAC 411
 125 CTGATCTAATTCGACCCCTAAGTCTTATGTTAGCTCCAAAGTCAAACTTAAA 184
 412 CCATTAACAATAACAATCCAAAGTACGTTGTTAGCTCCAAAGTCAAACTTAAA 471
 185 CCATTAACAATAACAATCCAAAGTACGTTGTTAGCTCCAAAGTCAAACTTAAA 244
 472 CCATTAACAATAACAATCCAAAGTACGTTGTTAGCTCCAAAGTCAAACTTAAA 531
 245 ATGCAATTAAGTCTGTAATCAATTAATTAATTAATTAATTAATTAATTAATTA 304
 532 AAACCAATTAATGCTGTAATCAATTAATTAATTAATTAATTAATTAATTAATTA 591
 305 TGAATTAATCTCTTCTGCTCAAGTTCTGCTGTTCAATGCTCAATTAATTAATTA 364
 592 TAGAGCTACTCTTCTGCTCAAGTTCTGCTGTTCAATGCTCAATTAATTAATTA 651
 365 GCTTAATTCGACCATGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 424
 652 GTGATATTCGAATCTGGAATCAAAAGCGAAGTAAATCAAAAGTCAAGTCAACTGG 711
 425 GAATTAATTAATCTGACGATGATGGAATTAATCTCT 462
 712 GAATTAATTAATCTGACGATGATGGAATTAATCTCT 749

RESULT 7
 US-08-501-253A-1
 Sequence 1, Application US/08501253A
 Patent No. 6146628

GENERAL INFORMATION:
 APPLICANT: Uckun, Patih
 APPLICANT: Tumer, Nilgun
 TITLE OF INVENTION: Biotherapeutic Agents Comprising
 TITLE OF INVENTION: Recombinant PAP and PAP Mutants
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merchant & Gould
 STREET: 90 South 7th Street, 3100 No. 6146628west Center
 CITY: Minneapolis
 STATE: MN
 COUNTRY: US
 ZIP: 55402

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/501.253A
 FILING DATE: 11-JUL-1995

CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Kettlerberger, Denise M.
 REGISTRATION NUMBER: 33,924
 REFERENCE/DOCKET NUMBER: 600.323US01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-332-5300
 TELEFAX: 612-332-9081
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1379 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 225..1163
 US-08-501-253A-1

Query Match 64.8%; Score 301.2; DB 3; Length 1379;
 Best Local Similarity 78.6%; Pred. No. 4.1e-78;
 Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

5 TAAATAGATCACTTGAATGCTGAATGCAACATTAACAATAATGCACTTTATG 64
 292 TGAATCAATCATCTACATATGTAAGTACACCATTAAGCAACCTTTCTGA 351
 65 AATCTCTGTAATCAAGCGAAGATCCAAACTAAATGCTATGCAATGCTAC 124
 352 ATGATCTTCTGAATGAAGCGAAGATCCAACTTTAAATGCTATGCAATGCTAC 411
 125 CTGATCTAATTCGACCCCTAAGTCTTATGTTAGCTCCAAAGTCAAACTTAAA 184
 412 CCATTAACAATAACAATCCAAAGTACGTTGTTAGCTCCAAAGTCAAACTTAAA 471
 185 CCATTAACAATAACAATCCAAAGTACGTTGTTAGCTCCAAAGTCAAACTTAAA 244
 472 CCATTAACAATAACAATCCAAAGTACGTTGTTAGCTCCAAAGTCAAACTTAAA 531
 245 ATGCAATTAAGTCTGTAATCAATTAATTAATTAATTAATTAATTAATTAATTA 304
 532 AAACCAATTAATGCTGTAATCAATTAATTAATTAATTAATTAATTAATTAATTA 591
 305 TGAATTAATCTCTTCTGCTCAAGTTCTGCTGTTCAATGCTCAATTAATTAATTA 364
 592 TAGAGCTACTCTTCTGCTCAAGTTCTGCTGTTCAATGCTCAATTAATTAATTA 651
 365 GCTTAATTCGACCATGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 424
 652 GTGATATTCGAATCTGGAATCAAAAGCGAAGTAAATCAAAAGTCAAGTCAACTGG 711
 425 GAATTAATTAATCTGACGATGATGGAATTAATCTCT 462
 712 GAATTAATTAATCTGACGATGATGGAATTAATCTCT 749

RESULT 8
 PCT-US96-11546-1
 Sequence 1, Application PC/TUS9611546

GENERAL INFORMATION:
 APPLICANT: Tumer, Nilgun E.
 APPLICANT: DNA Encoding Pokeweed Antiviral Protein
 TITLE OF INVENTION: Mutants
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
 STREET: 600 South Avenue West
 CITY: Westfield
 STATE: NJ
 COUNTRY: USA
 ZIP: 07090-1497

COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
PCT-US96-11546-1

Query Match          64.8%; Score 301.2; DB 6; Length 1379;
Best Local Similarity 78.6%; Pred. No. 4.1e-78;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 5 TAAATACGATCACCCTTGGATGCTGGAATGCGCACCATTTAAACAATATGCGCCTTTATGG 64
DB 292 TGAATACAAATCATCTACAAATGTTGGAAGTACACCATTAGCAATAGCCACTTTCTGGA 351
QY 65 AATCTCTGTAATCAAGCGAAAGATCCAAATCAATGCTATGAGCATCCATGCTAC 124
DB 352 ATGATCTTGTATGAAGCGAAAGATCCAAATGTTAAATGCTATGGAATACCAATGCTGC 411
QY 125 CTGATTAATTCGACCCCTAAGTACTTATGTTAGTCCAAAGTCCAAAGTCCAACTTAAA 184
DB 412 CCAATCAAAATTAACAATCCAAAGTACGTGTGAGTCCAAAGTCCAAATTAATAAAA 471
QY 185 CCAATTAACAATAGCTGAGAGCAAAATTAATTAATGATGAGGCTATTCGATCCCTTCA 244
DB 472 CCAATCAACAATAGCTGAGAGCAAAATTAATTAATGATGAGGCTATTCGATCCCTTGG 531
QY 245 ATGCAATTAAGTGTGCTTACCATATATTTAATGATTTAACAAGCAGCAAGCAGCATG 304
DB 532 AAACCAATTAATGTGCTTACCATATCTTTAATGATTTCTCGATTAAGCAGCAAGATG 591
QY 305 TGGAGAAATCTCTTGTGCTCAAGTCTAGTCTCGTGTGCAATGTCATTAACTTACATA 364
DB 592 TAGAGACTACTCTTTGGCCAAATGCGCAATTCGTGTGTAGTAAAAACATAAATCTTGATA 651
QY 365 GCTTAATTCGACGATGAGAAAGAAAGCAAGTAAACTCAAGAAATCAAGTCCAAATGG 424
DB 652 GTGCAATTCCAATAGGAATCAAAAGCGAGTAAATCAAGAAAGTCAAGTCCAACTGG 711
QY 425 GAATTCAAATATCTCAGGATGATGATTTGAAAAATCTCT 462
DB 712 GAATTCAAATATCTCAGAGTAAATTTGAAAAATTTCT 749
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RESULT 9
US-07-865-169-2
Sequence 2, Application US/07865169
Patent No. 6015940
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
APPLICANT: Lodge, Jennifer K.
APPLICANT: Kadlewski, Wojciech K.
TITLE OF INVENTION: Virus Resistant Potato Plants
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Dennis R. Hoerner, Jr., Monsanto Co. BB4P
STREET: 700 Chesterfield Parkway No. 6015940th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19920407
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10547)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-865-169-2

Query Match          64.1%; Score 298; DB 3; Length 1379;
Best Local Similarity 78.2%; Pred. No. 3.5e-77;
Matches 358; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 5 TAAATACGATCACCCTTGGATGCTGGAATGCGCACCATTTAAACAATATGCGCCTTTATGG 64
DB 292 TGAATACAAATCATCTACAAATGTTGGAAGTACACCATTAGCAATAGCCACTTTCTGGA 351
QY 65 AATCTCTGTAATCAAGCGAAAGATCCAAATCAATGCTATGAGCATCCATGCTAC 124
DB 352 ATGATCTTGTATGAAGCGAAAGATCCAAATGTTAAATGCTATGGAATACCAATGCTGC 411
QY 125 CTGATTAATTCGACCCCTAAGTACTTATGTTAGTCCAAAGTCCAAAGTCCAACTTAAA 184
DB 412 CCAATCAAAATTAACAATCCAAAGTACGTGTGAGTCCAAAGTCCAAATTAATAAAA 471
QY 185 CCAATTAACAATAGCTGAGAGCAAAATTAATTAATGATGAGGCTATTCGATCCCTTCA 244
DB 472 CCAATCAACAATAGCTGAGAGCAAAATTAATTAATGATGAGGCTATTCGATCCCTTGG 531
QY 245 ATGCAATTAAGTGTGCTTACCATATATTTAATGATTTAACAAGCAGCAAGCAGCATG 304
DB 532 AAACCAATTAATGTGCTTACCATATCTTTAATGATTTCTCGATTAAGCAGCAAGATG 591
QY 305 TGGAGAAATCTCTTGTGCTCAAGTCTAGTCTCGTGTGCAATGTCATTAACTTACATA 364
DB 592 TAGAGACTACTCTTTGGCCAAATGCGCAATTCGTGTGTAGTAAAAACATAAATCTTGATA 651
QY 365 GCTTAATTCGACGATGAGAAAGAAAGCAAGTAAATCTCAAGAAATCAAGTCCAAATGG 424
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Db	652	GTGCGATATCCAACTTGGAAATCAAAAGCGGAGTAAATCAAGAGTCAAGTCCAACTGG	711
Qy	425	GAATTCAAATACTCAGCAGTGCACATGGGAAAAATCTCT	462
Db	712	GAATTCAAATACTCAGCAGTAAATATGGGAAAAGATTTCT	749

RESULT 10

US-09-005-273-3
Sequence 3, Application US/09005273
Patent No. 6137030
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTEMBERG, KRUMHOLTZ &
ADDRESSEE: MENTILIK
STREET: 600 South, Avenue West
CITY: Westfield
STATE: New Jersey
COUNTRY: USA
ZIP: 07090

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,273
FILING DATE: 09-JAN-1998

? CLASSIFICATION: 800
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 08/500,611
 ? FILING DATE: 11-JUL-1995
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 08/500,694

? FILING DATE: 11-JUL-1995
 ?
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: PCT/US96/11546
 ? FILING DATE: 11-JUL-1996
 ? ATTORNEY/AGENT INFORMATION:
 ?

; NAME: Foley, Shawn P.
 ; REGISTRATION NUMBER: 33,071
 ; REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 3:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1379 base pairs

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TYPE: nucleic acid
STRANDEDNESS: single
FUNCTION: ...

! TOPOLOGY: linear
! MOLECULE TYPE: cDNA
! FEATURE:

NAME/KEY: CDS
LOCATION: 225-11

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NAME/KEY:  sig peptide
FEATURE:
;
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LOCATION: 225..29
US-09-005-273-3

Query Match

Best Local Similarity 78.2%; Pred. No. 3.5e-77;
Matches 358; Conservative 0; Mismatches 100; Indels 0; Gaps 0

[illegible]

QY 65 AATCTCTGCTAATCAAGCAAAAGATCCAAACTTAAATGCTATGCATACCAATGCTAC 124
Db 352 ATGATCTTCTGTAATCAAGCAAAAGATCCAAATTAAATGCTATGGAATATCCAAATGCTGC 411

[illegible]

Oy 185 CCATTACACTAATGCTGAGACGAAATTAATTACGTGATGGGCTATTCTGATCCCTTCA 244
 |||||
 Db 472 CCATACACTAATGCTGAGACGAAACAAATTTCATGTGATGGGTTATTCTGATCCCTTGG 531

DY 245 ATGGCAATPAGTGTCTTACCATATTATTAAATGATATTACAAGCACCGAAGCAGACTGATS 304
| | | | | | | | | | | | | | | | | | | | | |
Db 532 AAACCAATPAATNTGTCTTACCATATTCTTAATGATATTCAAGGTACTGAAGCCGAAGTS 591

OY	305	TGAGAAATACCTCTTTGGTCTCAAGATTAGTTCGTGGTGCAATGTCACATTAACTACAATA	364
Db	592	TAGAGACTACTCTTTGGCCCAATGCCAATTCCTCGGTAGTAGTAATAAACCATPAACCTTTGATA	651

Dy 365 GCTTATATCCGACCATGGAAAAAGAAAGCAATTACTCAAAGAATCAAGTCCAATTGG 424
| | | | | | | | | | | | | | | |
Db 652 GTTCGATATCCACATTGGAAATCGAAGGGGGAGTAATAATCAAGAAGTCAGGTCCAATTGG 711
| | | | | | | | | | | | | | | |

Oy	425	GAATTCAATACTCAGCAGTGCATGTGAAAAATCTCT	462
Db	712	GAATTCAAATACTGCACGTATATATTGAAACATTTCT	749

RESULT 11
US-08-138-636-1

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; Sequence 1, Application US/08138636
; Patent No. 5348865
; GENERAL INFORMATION:
; APPLICANT: Moon, Young-Ho
;

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APPLICANT: Jeon, Hong-Seoh
APPLICANT: Choi, Kyu-Mhan
APPLICANT: Lee, Kwan Ho
APPLICANT: Kim, Man Keun

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? STATE: MI
? COUNTRY: USA
? ZIP: 10022
? COMPUTER READABLE FORM:
? MENTING TYPE: PLANNING

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1 MEDIUM: 1155, Floppy disk
2
3 COMPUTER: IBM PC compatible
4
5 OPERATING SYSTEM: PC-DOS/MS-DOS
6
7 SOFTWARE: PatentIn Release #1.0, Version #1.25
8
9 COMPANY: Application Data.

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ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/08818

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687

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? INFORMATION FOR SEQ ID NO: 1:
?
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 918 base pairs
?
? TYPE: nucleic acid
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? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
?
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HYPOHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytoleuca insularis
IMMEDIATE SOURCE:
CLONE: antiviral protein (PIP)
US-08-138-636-1

Query Match 51.4%; Score 238.8; DB 2; Length 918;
Best Local Similarity 74.7%; Pred. No. 6e-60;
Matches 342; Conservative 0; Mismatches 107; Indels 9; Gaps 3;

QY 5 TAAATACGATCCTTTGATGCTGAAATGCCACATTACAAATATGCCACTTTATGG 64
DB TGAATACCATCATCTACCATGTTGAAATGACACCATTAAGAACTATGCACTTTGGAT 127
QY 65 AATCTCTGTAATCAAGCGAAAGATCCAAACTAAATGCTATGCACTTACCAATGCTAC 124
DB 128 A---CTTCGACTGAAGGCGAAGATCCAG--TTATGCTGTAATGAATACCAATGCTGC 181
QY 125 CTGATTAATTAATGACCCCTTAAGTACTTATTTGTTAAGCTCAAGTGCATAAATAA 184
DB 182 CCAATATGATCAAAATCCAAATATCATTTGGTTGAGCTCAAGGTTCAAAATGAAGAG 241
QY 185 CCATTACATTAATGCTGAGACGAAATTAATTAATGATGAGGCTATTTGATCCCTTCA 244
DB 242 GCATCACACTTAATGCTAAGACGAAACAATTAATATGATGAGGCTATTTGATCCCTTCA 301
QY 245 ATGSCAATTAATGCTGATCAATATTAATTAATTAATTAATTAATTAATTAATTAAT 304
DB 302 A---CAATTAAGTGTGCTTCAATCTTTAAGGCTATCTCGATCGAATGCGAAGATG 358
QY 305 TGGAGAACTCTTTGCTCAAGTCTAGTTCTCGTGTGCAATGCTCAATTAATACATA 364
DB 359 TAGAGACTACTCTTTGCGCAATATCCGATTTCTCGTGTGTTGTTAAATTAATTAATGATA 418
QY 365 GCTTATATCCGACCATGGAAGAAAGAGAGAAATTAATCAAGAAATCAAGTCAATGG 424
DB 419 GTGATATCCAACTTGAATCAAAAGCAGAGATTAATTAATTAATTAATTAATTAATTAAT 478
QY 425 GAATTCAAATCTCAGAGATGACATTTGAAATTAATCTCT 462
DB 479 GAATTCGAATCTCAGAGATGACATTTGAAATTAATCTCT 516

RESULT 12

US-08-319-622A-1
Sequence 1, Application US/08319622A
Patent No. 5656466

GENERAL INFORMATION:

APPLICANT: Moon, Young-Ho
APPLICANT: Choi, Kyu-Whan
APPLICANT: Jeon, Hong-Seob
APPLICANT: Kim, Chul-Hwan
APPLICANT: Kim, Man-Keun
TITLE OF INVENTION: Process for Preparing Virus-Resistant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,622A
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/00445
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: cDNA to mRNA
HYPOHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytoleuca insularis Nakai
TISSUE TYPE: leaf
IMMEDIATE SOURCE:
CLONE: PIP
US-08-319-622A-1

Query Match 51.4%; Score 238.8; DB 2; Length 918;
Best Local Similarity 74.7%; Pred. No. 6e-60;
Matches 342; Conservative 0; Mismatches 107; Indels 9; Gaps 3;

QY 5 TAAATACGATCCTTTGATGCTGAAATGCCACATTACAAATATGCCACTTTATGG 64
DB 68 TGAATACCATCATCTACCATGTTGAAATGACACCATTAAGAACTATGCACTTTGGAT 127
QY 65 AATCTCTGTAATCAAGCGAAAGATCCAAACTAAATGCTATGCACTTACCAATGCTAC 124
DB 128 A---CTTCGACTGAAGGCGAAGATCCAG--TTATGCTGTAATGAATACCAATGCTGC 181
QY 125 CTGATTAATTAATGACCCCTTAAGTACTTATTTGTTAAGCTCAAGTGCATAAATAA 184
DB 182 CCAATATGATCAAAATCCAAATATCATTTGGTTGAGCTCAAGGTTCAAAATGAAGAG 241
QY 185 CCATTACATTAATGCTGAGACGAAATTAATTAATGATGAGGCTATTTGATCCCTTCA 244
DB 242 GCATCACACTTAATGCTAAGACGAAACAATTAATATGATGAGGCTATTTGATCCCTTCA 301
QY 245 ATGSCAATTAATGCTGATCAATATTAATTAATTAATTAATTAATTAATTAATTAAT 304
DB 302 A---CAATTAAGTGTGCTTCAATCTTTAAGGCTATCTCGATCGAATGCGAAGATG 358
QY 305 TGGAGAACTCTTTGCTCAAGTCTAGTTCTCGTGTGCAATGCTCAATTAATACATA 364
DB 359 TAGAGACTACTCTTTGCGCAATATCCGATTTCTCGTGTGTTGTTAAATTAATTAATGATA 418
QY 365 GCTTATATCCGACCATGGAAGAAAGAGAGAAATTAATCAAGAAATCAAGTCAATGG 424
DB 419 GTGATATCCAACTTGAATCAAAAGCAGAGATTAATTAATTAATTAATTAATTAATTAAT 478
QY 425 GAATTCAAATCTCAGAGATGACATTTGAAATTAATCTCT 462
DB 479 GAATTCGAATCTCAGAGATGACATTTGAAATTAATCTCT 516

RESULT 13

US-08-471-564-1
Sequence 1, Application US/08471564
Patent No. 572326

GENERAL INFORMATION:

APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
APPLICANT: Choi, Kyu-Whan
APPLICANT: Lee, Kwan Ho
APPLICANT: Kim, Man Keun
TITLE OF INVENTION: No. 572326el Genome Coding Phytoleuca Antiviral

TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 THIRD AVE.
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,564
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/210,396
FILING DATE:
APPLICATION NUMBER: US 08/138,636
FILING DATE: 15-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/18818US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phycolacca leucolacca
IMMEDIATE SOURCE:
CLONE: antiviral protein (PIP)
US-08-471-564-1

Query Match 51.4%; Score 238.8; DB 2; Length 918;
Best Local Similarity 74.7%; Pred. No. 6e-60;
Matches 342; Conservative 0; Mismatches 107; Indels 9; Gaps 3;

QY 5 TAAATAGATGACCTTTGATGCTGGAATGCGACCATTAACCAAAATATGCCACTTTATG 64
DB 68 TGAATACCATATCTACCATGATGTAAGTACCAACCATTAAGAACTATCAACTTTGAT 127
QY 65 AATCTCTGTAATCAAGCAAGATCCAAATCAAAATGCTATGCGATACCAATGCTAC 124
DB 128 A-----CTTCGATCTGAAGCGCAAGATCCAG--TTATGCTGTAATGAAATACCAATGCTGC 181
QY 125 CTGATCTAATTCGACCCCTTAAGTACTTATGTTAGCTCCAAAGTCAAACTTAATA 184
DB 182 CCAATATGATCAAAATCAAAATGATATGTTAGCTCCAAAGTCCAAATGAAGAAG 241
QY 185 CCATTAAGCTAATGCTGAAGCAAAATCACTTAAGTATGAGGCTATCTGATCCCTTCA 244
DB 242 GCATCACTAATGCTGAAGCAAAATCACTTAAGTATGAGGCTATCTGATCCCTTCA 301
QY 245 ATGCAATAGTGTGCTACCATATATTAATGATATTAAGCAAGCAAGCAAGCTGATG 304
DB 302 A---CAATAGGTTGTTTTCATCTTTAAGGCTATCTGATGATGAAGCAAGATG 358
QY 305 TGAAGATCTCTTGTCTCAAGTTTGAAGTCTGCTGTTCAATGCTCAATTAAGTA 364
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DB 359 TAGAGACTACTCTTTGCCCAATGCGCATCTCGTGTGTAATTAACATTAATATGATA 418
QY 365 GCTTATATCCCATGGAAGAAAGCAAGTAACTCAAGAAATCAAGTCAATG 424
DB 419 GTGATATCCCAATGGAAGTAAATTAATTAAGTAAATGCAAGTCAAGTCAAGT 478
QY 425 GAATTCATTAATCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 462
DB 479 GAATTCATTAATCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 516
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RESULT 14
US-08-718-904-80
Sequence 80, Application US/08718904
Patent No. 6037329

GENERAL INFORMATION:
APPLICANT: Baird, J. Andrew
APPLICANT: Chandler, Lois Ann
APPLICANT: Sonowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPY
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESS: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6037329 Stenbury Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.415C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 1233 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURES:
NAME/KEY: CDS
LOCATION: 1..1230
OTHER INFORMATION: /product= "E. coli codon optimized"
OTHER INFORMATION: FGF-SAP"

US-08-718-904-80

Query Match 9.3%; Score 43.2; DB 3; Length 1233;
Best Local Similarity 48.7%; Pred. No. 0.0093;
Matches 148; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

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DB 529 GTGATTAATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 588
QY 121 CTACTGATTAATGATGACCTTTGATGCTGGAATGCGACCATTAACCAAAATATGCCACTTT 180
DB 589 GCAATGATGCTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGCTGC 648
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QY 181 AAAACATTACCTAATGCTGAGACGAATACTTATACGTATGGCTATTCTGATCCC 240
Db 649 GGCACTGTGCTCTGGGCTTAAACGCGATATTGTAGCTTGTAGCCTACCTGGCGATG 708
QY 241 TTCAATGGCAAT---AAGTGTGCTTACCATATTTATGATATTTACAGACCGAAGCC 297
Db 709 GATATATCCATGTAAACCGTCTTACTATTTCAAAACGAAATTAACCTGTGCTGAAGTG 768
QY 298 ACTG 301
Db 769 ACTG 772

RESULT 15

US-09-449-249-80
; Sequence 80, Application US/09449249
; Patent No. 6503886
; GENERAL INFORMATION:

APPLICANT: Baird, J. Andrew

Chandler, Lois Ann

Sosnowski, Barbara A.

TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERA

NUMBER OF SEQUENCES: 128

CORRESPONDENCE ADDRESSES:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/449,249

FILING DATE: 24-No. 6503886-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/718,904

FILING DATE: 24-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: No. 6503886tenburg Ph.D., Carol

REGISTRATION NUMBER: 39,317

REFERENCE/DOCKET NUMBER: 760100.415C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 80:

SEQUENCE CHARACTERISTICS:

LENGTH: 1233 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1230

OTHER INFORMATION: /product= "E. coli codon optimized

FCR-SAP"

SEQUENCE DESCRIPTION: SEQ ID NO: 80:

US-09-449-249-80

Query Match

Best Local Similarity 9.3%; Score 43.2; DB 3; Length 1233;

Matches 148; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

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Db 469 ATGTCACCTTCTATCAAGCTGATGTGTCAACCGACCGCTGTGATACAGCTCGTTT 528

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QY 181 AAAACATTACCTAATGCTGAGACGAATACTTATACGTATGGCTATTCTGATCCC 240
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QY 241 TTCAATGGCAAT---AAGTGTGCTTACCATATTTATGATATTTACAGACCGAAGCC 297
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QY 298 ACTG 301
Db 769 ACTG 772

Search completed: April 8, 2006, 09:48:54
Job time : 162.42 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:31:27 ; Search time 537.272 Seconds
(without alignments)
7157.007 Million cell updates/sec

Title: US-09-978-274A-5
Perfect score: 465
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	462	99.4	792	US-09-978-274A-3	Sequence 3, Appli
3	462	99.4	1092	US-09-978-274A-19	Sequence 19, Appli
4	459	98.7	945	US-09-978-274A-1	Sequence 1, Appli
5	301.2	64.8	1379	US-09-978-274A-30	Sequence 30, Appli
6	301.2	64.8	1379	US-11-106-187-1	Sequence 31, Appli
7	298	61.7	1368	US-09-978-274A-31	Sequence 31, Appli
8	286.8	64.1	1376	US-10-467-009-1	Sequence 1, Appli
9	54.6	11.7	855	US-11-106-187-20	Sequence 20, Appli
10	54.6	11.7	934	US-09-978-274A-32	Sequence 32, Appli
11	54.6	11.7	934	US-11-106-187-3	Sequence 3, Appli
12	46.6	10.0	765	US-09-792-793A-66	Sequence 66, Appli
13	46.6	10.0	765	US-10-375-209A-66	Sequence 66, Appli
14	46.6	10.0	984	US-09-792-793A-60	Sequence 60, Appli
15	46.6	10.0	984	US-10-375-209A-60	Sequence 60, Appli
16	46.6	10.0	993	US-09-792-793A-63	Sequence 63, Appli
17	46.6	10.0	993	US-10-375-209A-63	Sequence 63, Appli
18	46.6	10.0	999	US-09-792-793A-54	Sequence 54, Appli
19	46.6	10.0	999	US-09-792-793A-57	Sequence 57, Appli
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21	46.6	10.0	999	US-10-375-209A-57	Sequence 57, Appli
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	27	39.6	8.5	1251	6	US-10-189-360-74	Sequence 74, Appl
	28	39.6	8.5	1260	3	US-09-861-257-75	Sequence 75, Appl
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ALIGNMENTS

RESULT 1									
US-09-978-274A-5									
Sequence 5, Application US/09978274A									
Patent No. US20020116737A1									
GENERAL INFORMATION:									
APPLICANT: Thomas, Christopher									
APPLICANT: McPherson, Michael									
APPLICANT: Atkinson, Howard									
APPLICANT: Neelam, Anil									
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM									
FILE REFERENCE: 9341-028									
CURRENT APPLICATION NUMBER: US/09/978, 274A									
CURRENT FILING DATE: 2001-10-15									
PRIOR APPLICATION NUMBER: 0025225.4									
PRIOR FILING DATE: 2000-10-14									
NUMBER OF SEQ ID NOS: 32									
SOFTWARE: PatentIn version 3.1									
SEQ ID NO 5									
LENGTH: 465									
TYPE: DNA									
ORGANISM: Phylocacca americana									
US-09-978-274A-5									
Query Match									
Best Local Similarity 100.0%; Score 465; DB 3; Length 465;									
Best Local Similarity 100.0%; Pred. No. 1.7e-123;									
Matches 465; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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RESULT 2
US-09-978-274A-3
; Sequence 3, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Phylococca americana
US-09-978-274A-3
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Query Match 99.4%; Score 462; DB 3; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
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; Sequence 19, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PAP-S/Cytectin fusion
US-09-978-274A-19
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Query Match 99.4%; Score 462; DB 3; Length 1092;
Best Local Similarity 100.0%; Pred. No. 1.9e-122;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
US-09-978-274A-1
; Sequence 1, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
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FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978, 274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 945
TYPE: DNA
ORGANISM: *Phytolacca americana*
US-09-978-274A-1

Query Match 98.7%; Score 459; DB 3; Length 945;
Best Local Similarity 100.0%; Pred. No. 1,3e-121; Indels 0; Gaps 0;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-978-274A-30

Sequence 30, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978, 274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 1379
TYPE: DNA
ORGANISM: *Phytolacca americana*
US-09-978-274A-30

Query Match 64.8%; Score 301.2; DB 3; Length 1379;
Best Local Similarity 78.6%; Pred. No. 5e-76; Indels 98; Gaps 0;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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QY 185 CCATTAACAAATCAAAATCAAAATGATGCTGTTAGCTCCAAAGTCAAACTTAA 244
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QY 305 TGAAGAAATACCTTTGCTCAAGTTCTAGTTCTCGTGTGCAATGTCATTAACTACATA 364
DB 592 TGAAGAAATACCTTTGCTCAAGTTCTAGTTCTCGTGTGCAATGTCATTAACTACATA 651
QY 365 GCTTAATTCGACCGATGAGAAAGAAAGCAAGATTAATCTAAGAAATCAAGTCCAT 424
DB 652 GTCATATTCGACCGATGAGAAAGAAAGCAAGATTAATCTAAGAAATCAAGTCCAT 711
QY 425 GAATTCAAATATCTCAGAGAGTCACTTGGAAAAATCTCT 462
DB 712 GAATTCAAATATCTCAGAGAGTCACTTGGAAAAATCTCT 749
```

RESULT 6

US-11-106-187-1

Sequence 1, Application US/11106187
Publication No. US20050183162A1
GENERAL INFORMATION:
APPLICANT: TUMER, NILDUN B.
APPLICANT: WANG, PINGER
TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
FILE REFERENCE: ODIRS 3, 9-060 CONT
CURRENT APPLICATION NUMBER: US/11/106, 187
CURRENT FILING DATE: 2005-04-14
PRIOR APPLICATION NUMBER: US/09/721, 047
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: PCT/US99/11301
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/086, 374
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 1
LENGTH: 1379
TYPE: DNA
ORGANISM: *Phytolacca americana*
FEATURES:
NAME/KEY: CDS
LOCATION: (225)..(1163)
US-11-106-187-1

Query Match 64.8%; Score 301.2; DB 10; Length 1379;
Best Local Similarity 78.6%; Pred. No. 5e-76; Indels 98; Gaps 0;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

```
QY 5 TAAATACGATCAGCTTTGATGCTGGAATGCAACATTAACTAAATATGCCACTTTATG 64
DB 292 TGAATACATCATCTACATGATGGAAGTACCAACATTAGCAAAATATGCCACTTTCTGA 351
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OY	65	AATCTCTCGTATCAAGGAAAGATCCAAACTAAAAAGCTATGGCATACCAATGTAC	124
Db	352	ATGATCTTCTGTATGAGGAAAGATCCAACTTTAAAAAGCTATGGAATACCAATGTGC	411
OY	125	CTGATACTAATTCGACCCCTAAGTACTTATGGTATAGCTCCAAAGTGCAAACTAAAA	184
Db	412	CCAAATACAAATCAAAATCCAAAGTACGTGTGGTTGAGCTCCAAAGTTCAATATAAAAA	471
OY	185	CCATTACACTAATGCTGAGACGAAATTACTTATACGTATGGGCTATTTCTGATCCCTTCA	244
Db	472	CCATCACACTAATGCTGAGACGAAACAAATTTGATATGATAGGGTTATTCGATCCCTTTC	531
OY	245	ATGGCAATAGAGTGGTTACCACTATTTTAATCATTTTACAAACACCGAAGCACTGATG	304
Db	532	AAACCAATTAAGTGTGTATCCAAATCTTTTAATGATATCTCAAGTACTGAACGCGAAGATG	591
OY	305	TGGAATAATCTCTTTGGCTCAAGTTCTGTAGTTCTGCTGTGCAATAGTCCATTATCTACATA	364
Db	592	TAGAGACTACTCTTTTGCCCAATATGCCAATTTCTCTGTATAGTATAAAAATTAATCTTTGATA	651
OY	365	GCTTATATTCGACCAATGAAAAAGAAAGCAGAAAGTAACCTCAAGAAATCAAGTCCAAATGG	424
Db	652	GTCGATATTCCAATGTGAATCAAAAAGCGGAGTAAATCAAGAAAGTCAGGTCCAACTGG	711
OY	425	GAATTCAAATTAATCAGCACTGACATGTGAAAAATCTCT	462
Db	712	GAATTCAAATTAATCAGCACTGAAATATTTGTAAGATTTCT	749

```

RESULT 7
US-09-978-274A-31
Sequence 31, Application US/0978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978, 274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 1368
TYPE: DNA
ORGANISM: Phytolacca americana
US-09-978-274A-31

```

Query Match	64.1%	Score 298	DB 3	Length 1368
Best Local Similarity	78.2%	Pred. No. 4.1e-75		
Matches 358; Conservative		0; Mismatches 100;	Indels 0;	Gaps 0;

Qy	5	TAATAACATGCACCTTTGATGCTGGAAATGCCACCATTTAACAAATATGCCACCTTTATGG	64
Db	292	TGAATACATCATCTACATATGTTGGAAGTACCAACCATTTGCAAAATAGCGCATTTTTCGGA	351
Qy	65	AATCTCTCGTATATCAAGCGAAGAATCCAAACTAAATAGCTATGSCATACCAATGCTAC	124
Db	352	ATGATCTTCTGTATATGAAGGAAAGATCCAAAGTTTAAATATGCTATGSAATACCAATCTGC	411
Qy	125	CTGATACTAATTCGACCCCTTAAGTACTTATTTGGTTAAGCTCCAAAGTGCAAACCTTAAAA	184
Db	412	CCAAATACAAATCCAATCCAAAGACAGTGTGGTTGAGCTCCAAAGGTTCAAAATAAAAAAA	471
Qy	185	CCATTACACTATATGCTGAGACGAATATTAATTATACGTATATGGGCTATTTTCGATCCCTTCA	244
Db	472	CCATACACTAATATGCTGAGACGAACAAATTTGTAATGTATGAGGGTTATTTTCGATCCCTTTG	531
Qy	245	ATGGCAATAGTGTGCTTACCATATATTTATATGATATTTCAAAGCACGGAAGCACTGATG	304

[illegible]

```

RESULT 8
US-10-467-009-1
; Sequence 1, Application US/10467009
; Publication No. US20040241673A1
; GENERAL INFORMATION:
; APPLICANT: RUTGERS, THE STATE UNIVERSITY
; TITLE OF INVENTION: NON-CYTOTOXIC P4M MUTANTS
; FILE REFERENCE: OCIRS 3.4-076
; CURRENT APPLICATION NUMBER: US/10/467, 009
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: 60/266,396
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: Phytolacca americana
; PEPTIDE:
; NAME/KEY: CDS
; LOCATION: (225)..(1160)
US-10-467-009-1

```

Query Match	61.7%	Score 286.8	DB 8	Length 1376
Best Local Similarity	78.2%	Pred. No. 7.1e-72		
Matches 358	0	Mismatches 97	Indels 3	Gaps 1

QY	5	AAATATGACATCACTTTGATGCTGTGGAAATGGCACATTTAAACAAATATAGCCACTTTATGG	64
Db	292	TGAATACATATATCAATATGTTGGAAATGACACACATTAGCAAAATACGCCACTTTTCTGA	351
QY	65	AATCTCTTGGTAATCAAGCGAAAGATCCAAATCTAAATATGCTATGGCATCCAAATGCTAC	124
Db	352	ATGATCTTTCGTAAATGAAAGCGAAAGATCCAAAGTTTAAATATGCTATGGAAATACCAATGCTGC	411
QY	125	CTGATACTAATTTGACCCCTTAAGTACTATTTGGTTAAGCTCCAAAGTGCAAACCTTAATAA	184
Db	412	CCAAATACAAATACAAATCCAAAGTACGATGTTGGTTAGAGCTCCAAAGTTCAAAATATAAAAA	471
QY	185	CCATTACACTATGCTGAGACGAAATATACCTTATACGTATGAGGCTATTCTGATCCCTTCA	244
Db	472	CCATCACACTATGCTGAGACGAAACAAATTTGTATGATGGGTATATCTGATCCCTTTG	531
QY	245	ATGCGCAATAGTGTCTGTTACCATATATTTATGATATTTACAGCACCGAAGCACTGATG	304
Db	532	AAACCAATAAATGTCTGTTACCATATCTTTAATGATATCTCAGGTATCTGAAGCGCAAGATG	591
QY	305	TGGAAGATATCTTTGTCTCAAGTTCTAGTCTCGATGTGCAATGTCATTTAACTACATATA	364
Db	592	TAGAGACTACTCTTTTGCCCA--GCATATTTCTGTGTATGTAATAAACCTTAACCTTTGATA	648
QY	365	GCTTATATCCGACATGGAAAAAGAAAGACGAAGTAACTCAAGAAATCAAGTCCAAATGG	424
Db	649	GTCGATATCCAACTTGGAAATCAAAAGCGGAGTAAATCAAGAAAGTCAGGTCCAACTGG	708
QY	425	GAATTCAAATATCGACAGTGAACATTTGAAAAATCTCT	462

DB 709 GAATTCAAATACGACGATTAATTTGGAAGATTTC 746

RESULT 9

US-11-106-187-20
Sequence 20, Application US/11106187
Publication No. US20050183162A1
GENERAL INFORMATION:
APPLICANT: TUMER, NILGUN E.
APPLICANT: WANG, PINGER
TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
FILE REFERENCE: OCIRS 3.9-060 CONT
CURRENT APPLICATION NUMBER: US/11/106,187
CURRENT FILING DATE: 2005-04-14
PRIOR APPLICATION NUMBER: US/09/721,047
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: PCT/US99/11301
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/086,374
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 20
LENGTH: 855
TYPE: DNA
ORGANISM: Phytolacca americana
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(855)
US-11-106-187-20

Query Match 11.7%; Score 54.6; DB 10; Length 855;
Best Local Similarity 55.9%; Pred. No. 5.3e-05;
Matches 146; Conservative 0; Mismatches 109; Indels 6; Gaps 2;

QY 19 TTTGATGCTGGAATGCCACCTTAACAAATATGCACTTTATGGAATCTCTTGTAAT 78
DB 10 TTTGACGTTGGAAGAACCAACCAAGAACTTAATTTCTGACTAGTTGGAGAA 69
QY 79 CAAGGAAAGATCCAAACTAAATGCTATGCGATACCAATGCTACCTGATACCTAATTCG 138
DB 70 GCTGTGAAGACAGAAATTTGACATGCAATGGAATGATTAATGAGCAACCTCACTGAA 129
QY 139 ACCCTTAAGTACTTATTTGTTAGCTCCAGGTGCAAACTTAACCATTAACCTAATG 198
DB 130 CAACCAAGTATGTTGTTGTTGACCTCAATTCGATCTGGAACATTC---ACATTTAGCA 186
QY 199 CTGAGACGAATTAATTAATGATGATGCTATTTCTGATCCCTTCAATGCAATTAAGTGT 258
DB 187 ATCAGAAAGGGAACCTTAATTTGGAAGGCTATTTCTGACATTTCAATG---AAATGT 243
QY 259 CGTACCATTAATTTAATGAT 279
DB 244 CGTATCGGATCTTCAGAGAT 264

RESULT 10

US-09-978-274A-32
Sequence 32, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0052525.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1

SEQ ID NO 32
LENGTH: 934
TYPE: DNA
ORGANISM: Phytolacca americana
US-09-978-274A-32

Query Match 11.7%; Score 54.6; DB 3; Length 934;
Best Local Similarity 55.9%; Pred. No. 5.6e-05;
Matches 146; Conservative 0; Mismatches 109; Indels 6; Gaps 2;

QY 19 TTTGATGCTGGAATGCCACCTTAACAAATATGCACTTTATGGAATCTCTTGTAAT 78
DB 85 TTTGACGTTGGAAGAACCAACCAAGAACTTAATTTCTGACTAGTTGGAGAA 144
QY 79 CAAGGAAAGATCCAAACTAAATGCTATGCGATACCAATGCTACCTGATACCTAATTCG 138
DB 145 GCTGTGAAGACAGAAATTTGACATGCAATGGAATGATTAATGAGCAACCTCACTGAA 204
QY 139 ACCCTTAAGTACTTATTTGTTAGCTCCAGGTGCAAACTTAACCATTAACCTAATG 198
DB 205 CAACCAAGTATGTTGTTGTTGACCTCAATTCGATCTGGAACATTC---ACATTTAGCA 261
QY 199 CTGAGACGAATTAATTAATGATGATGCTATTTCTGATCCCTTCAATGCAATTAAGTGT 258
DB 262 ATCAGAAAGGGAACCTTAATTTGGAAGGCTATTTCTGACATTTCAATG---AAATGT 318
QY 259 CGTACCATTAATTTAATGAT 279
DB 319 CGTATCGGATCTTCAGAGAT 339

RESULT 11

US-11-106-187-3
Sequence 3, Application US/11106187
Publication No. US20050183162A1
GENERAL INFORMATION:
APPLICANT: TUMER, NILGUN E.
APPLICANT: WANG, PINGER
TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
FILE REFERENCE: OCIRS 3.9-060 CONT
CURRENT APPLICATION NUMBER: US/11/106,187
CURRENT FILING DATE: 2005-04-14
PRIOR APPLICATION NUMBER: US/09/721,047
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: PCT/US99/11301
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/086,374
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 3
LENGTH: 934
TYPE: DNA
ORGANISM: Phytolacca americana
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (1)..(75)
NAME/KEY: mat_peptide
LOCATION: (76)..(930)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(930)
US-11-106-187-3

Query Match 11.7%; Score 54.6; DB 10; Length 934;
Best Local Similarity 55.9%; Pred. No. 5.6e-05;
Matches 146; Conservative 0; Mismatches 109; Indels 6; Gaps 2;

QY 19 TTTGATGCTGGAATGCCACCTTAACAAATATGCACTTTATGGAATCTCTTGTAAT 78
DB 85 TTTGACGTTGGAAGAACCAACCAAGAACTTAATTTCTGACTAGTTGGAGAA 144

Qy	79	CAAGGGAAGATCCAAACTTAAATGCTATGGCATTCACCAATGGTACTGATACTATATGG	138
Db	145	GCTGGAAGACAGAGAAATTGCATGCGCATGGAGATGATATGGCCACAACCTCACTGAA	204
Qy	139	ACCCTTAAGTACTTATTGGTTAGCTCCAAAGGTGCMAACCTTAAACCAATTACATCATG	198
Db	205	CAACCGAAGTATGTGTGGTTGACCTCAAAATTGGATCTGGAAACATTC---ACATTAGCA	261
Qy	199	CTGAGACGAATACTTATACGTGATGGGCTATTCTGATCCCTTCATGGCAATTAAGTG	258
Db	262	ATCGAAGAGGGGAACTTATATTGGAGGGCTATTCTGCATTTACAATGG---AAATGT	318
Qy	259	CGTTACCATATATTAAATGAT	279
Db	319	CGTATCGAATCTTCAAGAT	339

```

RESULT 12
US-09-792-793A-66
Sequence 66, Application US/09792793A
Patent No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
APPLICANT: Cogging, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
FILE REFERENCE: 25020-601D
OTHER INFLAMMATORY CONDITIONS AND DISORDERS
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 66
LENGTH: 765
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Construct encoding
OTHER INFORMATION: Methionine-saporin fusion protein
NAME/KEY: CDS
LOCATION: (1)..(765)
US-09-792-793A-66

```

Query Match	10.0%;	Score 46.6;	DB 3;	Length 765;
Best Local Similarity	49.2%;	Pred. No. 0.01;		
Matches 152; Conservative	0;	Mismatches 154;	Indels 3;	Gaps 1;

OY		1	ATGATAAATACAGTACCCTTTGATGTGCTGGAAATGCACACTTAACAAAATTATGCCACCTT	60
Db		1	ATGTTACTACTATATTACCTCGTAGCCTGGTCAAATCCGACCGCGGCCAATTATAGCAGCTTC	60
OY		61	ATGGAATCTCTTCGTAATCAAGCGAAGAATCCAAACTAAAAATGCTATGGCATACCAATG	120
Db		61	GTCGATTAAGATTCGTAAACAAGTAAAGATCCGAATCGAAATACGGTGCTACTGATATT	120
OY		121	CTACCTGATATCAAATTTGACCCCTTAAGTACTTATATGTGTTAAGCTCCAAAGTGCAAACTTA	180
Db		121	GCGGTCAATCGGTCCGCGCGAACGAAAGAAAGTTCTCTGCGCATTAACCTTCCAAGCTCCCCGT	180
OY		181	AAAAACATTACACTAATGCTGAGACGAAATATACCTTAAACGTATGGCTATTTCTGATCCC	240
Db		181	GGCACTGTTTTCTCGGGCTGTGAAGCGCATTAACCTGTATGTTGTGCTTAATCTGGCGATG	240
OY		241	TTCAATGGCAATTAAGTGTGCT--TACCATATATTTAATGATATTAACAAGCACCGAAGCG	297
Db		241	GATATATACGAACGTGAACCGCGGCTACTACTTTCGTACGAGATTACAGCGCGGAATCC	300
OY		298	ACTGATGTG 306	
Db		301	ACTGCTCTG 309	

RESULT 13
US-10-375-209A-66

```

: Sequence 66 Application US/10375209A
: Publication No. US20030215421A1
:
: GENERAL INFORMATION:
: APPLICANT: McDonald, John R.
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AN
: TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
: FILE REFERENCE: 25020-601E
: CURRENT APPLICATION NUMBER: US/10/375, 209A
: CURRENT FILING DATE: 2003-02-24
: NUMBER OF SEQ ID NOS: 93
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 66
:
: LENGTH: 765
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Construct encoding
: FEATURE:
: OTHER INFORMATION: Methionine-Saporin fusion protein
: NAME/KEY: CDS
: LOCATION: (1)..(765)
:
: US-10-375-209A-66

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Query Match	10.0%	Score 46.6	DB 6	Length 765
Best Local Similarity	49.2%	Pred. NC. 0.01		
Matches 152; Conservative	0	Mismatches 154	Indels 3	Gaps 1

QY	1	TTGATAAATACGATACACCTTTGATGTCGAAATGCACACATTAACAATATATAGCCACCTT	60
Db	1	ATGGTACTACATATTAACCTTGACCTGTGCATTCGACCCGGCCAAATATAGACGCTTC	60
QY	61	ATGGAATCTCTTGGTATCAAGCGAAAGATCCAAATCTAAATATGCTATGCGATACCATG	120
Db	61	GTGATTAAGATTCGTATCAACGTAATAAGATCCGATCTGAAATACGGGTGACTGATATT	120
QY	121	CTACCTGATACATAATTCGACCCCTTAAGTACTTATTTGGTTAAGCTCAAGGTGCAAACCTA	180
Db	121	GCGGTACATCGGTCCGCGCGAAGAAAGTAAGTTCTGGGCACTTAATTCAAAAGCTCCGGT	180
QY	181	AAAAACATTAACCTTAATGCTGAGCGAAATTAACCTTAACGTGATGGGCTATTCTGATCCC	240
Db	181	GGCACGTGTTCTCGGGCGCTGAAACGGGAGTAACCTGATATGTTGGCTTAATCTGCGCATG	240
QY	241	TTTCATGGCATTAAGTGTGCT---TACCATATATTTAATGATATTAACAGACCGAAACGC	297
Db	241	GATATATACGAACGTGAACCGCGCCTACTACTTGTGTGACGAGATTACGAGCGCGGAATCC	300
QY	298	ACTGATGTG 306	
Db	301	ACTGCTCTG 309	

```

1 RESULT 14
2 US-09-792-793A-60
3 ; Sequence 60, Application US/09792793A
4 ; Patent No. US20020168370A1
5 ;
6 ; GENERAL INFORMATION:
7 ;
8 ; APPLICANT: McDonald, John R.
9 ;
10 ; APPLICANT: Coggin, Philip
11 ;
12 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AN
13 ; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
14 ;
15 ; FILE REFERENCE: 25020-601D
16 ;
17 ; CURRENT APPLICATION NUMBER: US/09/792,793A
18 ;
19 ; CURRENT FILING DATE: 2001-02-22
20 ;
21 ; NUMBER OF SEQ ID NOS: 93
22 ;
23 ; SOFTWARE: PatentIn Ver. 2.0
24 ;
25 ; SEQ ID NO 60
26 ;
27 ; LENGTH: 984
28 ;
29 ; TYPE: DNA
30 ;
31 ; ORGANISM: Artificial Sequence
32 ;
33 ; FEATURE:
34 ;
35 ; OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine

```

OTHER INFORMATION: toxin fusion protein SDF-1-Beta-AM-SAPORIN
NAME/KEY: CDS
LOCATION: (1)..(984)
US-09-792-793A-60

Query Match 10.0%; Score 46.6; DB 3; Length 984;
Best Local Similarity 49.2%; Pred. No. 0.012;
Matches 152; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 1 ATGATTAATACATGACCTTTGATGCTGAAATGCGACCATTAACAAATATGCGACCTTT 60
DB 220 ATGGTACTAGATTACCTGACCTGCTGCAATCGACCGCGCCAAATATGCGACCTTC 279
QY 61 ATGGAATCTCTGTAATCAAGCAAGATCCAAACTAAATGCTATGCGATACCAATG 120
DB 280 GTGGATTAAGATTCTGTAACAGCTAAAGATCCGAATTCGAATACGATGCTATGATTT 339
QY 121 CTACCTGACTAATTCGACCCCTTAAGTACTTATTTGTTAAGCTCCAAAGTCAAACTTA 180
DB 340 GCGGTATCGGTCCCGCGCAAGAAAGTTCTGCGCATTAACCTTCAAGCTCCGT 399
QY 181 AAAACATTACACTAATGCTAGAGCAAAATACTTAAGTATGCGCTATTTCTGATCCC 240
DB 400 GGCACTGTTCTCTGGGCTGAGCGGATTAACCTGATGTTGCTTATCTGCGCATG 459
QY 241 TTCATATGCAATTAAGTGTCT--TACCATATATTAAATGATTAATCAAGCAGCAAGCC 297
DB 460 GATAATACGAACGTAAACCGGCTACTACTTCTGTAAGGAGATTACAGCGCGGAATCC 519
QY 298 ACTGATGTG 306
DB 520 ACTGCTCTG 528

RESULT 15

US-10-375-209A-60
Sequence 60, Application US/10375209A
Publication No. US20030215421A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
FILE REFERENCE: 25020-601E
CURRENT APPLICATION NUMBER: US/10/375,209A
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 60
LENGTH: 984
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine-
OTHER INFORMATION: toxin fusion protein SDF-1-Beta-AM-SAPORIN
FEATURES:
NAME/KEY: CDS
LOCATION: (1)..(984)
US-10-375-209A-60

Query Match 10.0%; Score 46.6; DB 6; Length 984;
Best Local Similarity 49.2%; Pred. No. 0.012;
Matches 152; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 1 ATGATTAATACATGACCTTTGATGCTGAAATGCGACCATTAACAAATATGCGACCTTT 60
DB 220 ATGGTACTAGATTACCTGACCTGCTGCAATCGACCGCGCCAAATATGCGACCTTC 279
QY 61 ATGGAATCTCTGTAATCAAGCAAGATCCAAACTAAATGCTATGCGATACCAATG 120
DB 280 GTGGATTAAGATTCTGTAACAGCTAAAGATCCGAATTCGAATACGATGCTATGATTT 339
QY 121 CTACCTGACTAATTCGACCCCTTAAGTACTTATTTGTTAAGCTCCAAAGTCAAACTTA 180

DB 340 GCGGTATCGGTCCCGCGCAAGAAAGTTCTGCGCATTAACCTTCAAGCTCCGT 399
QY 181 AAAACATTACACTAATGCTAGAGCAAAATACTTAAGTATGCGCTATTTCTGATCCC 240
DB 400 GGCACTGTTCTCTGGGCTGAGCGGATTAACCTGATGTTGCTTATCTGCGCATG 459
QY 241 TTCATATGCAATTAAGTGTCT--TACCATATATTAAATGATTAATCAAGCAGCAAGCC 297
DB 460 GATAATACGAACGTAAACCGGCTACTACTTCTGTAAGGAGATTACAGCGCGGAATCC 519
QY 298 ACTGATGTG 306
DB 520 ACTGCTCTG 528

Search completed: April 9, 2006, 01:44:54
Job time : 539.272 secs

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OW nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:50:48 ; Search time 404.834 Seconds
(without alignments)
4595.111 Million cell updates/sec

Title: US-09-978-274a-5

Perfect score: 465
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Gapop 10.0 , Gapext 1.0

Searched: 9267905 seqs, 2000278028 residues

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Maximum Match 100%
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3: /SIDS5/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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10: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq2:*
11: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:*
12: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
13: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
14: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
15: /SIDS5/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	301.2	64.8	1360	US-11-010-795-19	Sequence 19, Appl
2	54.6	11.7	934	US-11-010-795-21	Sequence 21, Appl
3	41.6	8.9	1471	US-10-750-185-27060	Sequence 27060, A
4	41.6	8.9	1471	US-10-750-623-27060	Sequence 27060, A
5	38.2	8.2	588	US-09-925-065A-793732	Sequence 793732, A
6	37.8	8.1	588	US-09-925-065A-793731	Sequence 793731, A
7	35.6	7.7	994	US-10-301-480-611379	Sequence 611379, A
8	35.6	7.7	994	US-10-301-480-611378	Sequence 611378, A
9	35	7.5	647	US-09-925-065A-409152	Sequence 409152, A
10	35	7.5	650	US-10-301-480-475630	Sequence 475630, A
11	35	7.5	650	US-10-301-480-475630	Sequence 475630, A
12	35	7.5	18930	US-10-995-561-13213	Sequence 13213, A
13	34.6	7.4	650	US-10-301-480-219992	Sequence 219992, A
14	34.6	7.4	650	US-10-301-480-833401	Sequence 833401, A
15	34.6	7.4	655	US-09-925-065A-121758	Sequence 121758, A
16	34.4	7.4	700	US-09-925-065A-671817	Sequence 671817, A
17	34.4	7.4	1048	US-09-925-065A-64273	Sequence 64273, A
18	34.4	7.4	1048	US-10-301-480-165511	Sequence 165511, A

19	34.4	7.4	1048	US-10-301-480-778920	Sequence 778920, A
20	34.4	7.4	1708	US-10-750-185-44263	Sequence 44263, A
21	34.4	7.4	1708	US-10-750-623-44263	Sequence 44263, A
22	34	7.3	598	US-10-301-480-98532	Sequence 98532, A
23	34	7.3	598	US-10-301-480-711941	Sequence 711941, A
24	34	7.3	700	US-09-925-065A-671816	Sequence 671816, A
25	34	7.3	1341	US-10-750-185-57064	Sequence 57064, A
26	34	7.3	1341	US-10-750-623-57064	Sequence 57064, A
27	33.8	7.3	503	US-09-925-065A-214054	Sequence 214054, A
28	33.8	7.3	510	US-10-301-480-300908	Sequence 300908, A
29	33.8	7.3	510	US-10-301-480-914317	Sequence 914317, A
30	33.8	7.3	1951	US-10-750-185-45758	Sequence 45758, A
31	33.8	7.3	1951	US-10-750-623-45758	Sequence 45758, A
32	33.8	7.3	2784	US-11-129-741-2922	Sequence 2922, A
33	33.8	7.3	2784	US-11-129-741-2930	Sequence 2930, A
34	33.8	7.3	2784	US-11-129-741-4242	Sequence 4242, A
35	33.8	7.3	2900	US-10-750-185-50117	Sequence 50117, A
36	33.8	7.3	2900	US-10-750-623-50117	Sequence 50117, A
37	33.8	7.3	29942	US-10-895-064-3	Sequence 3, Appl
38	33.8	7.3	29942	US-10-895-064-34	Sequence 34, Appl
39	33.8	7.3	29942	US-10-895-064-457	Sequence 457, App
40	33.8	7.3	29942	US-10-895-064-724	Sequence 724, App
41	33.8	7.3	29942	US-10-895-064-1319	Sequence 1319, App
42	33.8	7.3	29942	US-10-895-064-1908	Sequence 1908, App
43	33.8	7.3	29942	US-10-895-064-2454	Sequence 2454, App
44	33.8	7.3	29942	US-11-129-741-3	Sequence 3, Appl
45	33.8	7.3	29942	US-11-129-741-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-11-010-795-19
Sequence 19, Application US/11010795
Publication No. US20060005271A1
GENERAL INFORMATION:
APPLICANT: TUMER, NILGUN B.
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
TITLE OF INVENTION: RESISTANT TO TRICHOPTERENE FUNGAL TOXINS
FILE REFERENCE: OCIRS 3.0-085
CURRENT APPLICATION NUMBER: US/11/010,795
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: 60/529,348
PRIOR FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 19
LENGTH: 1360
TYPE: DNA
ORGANISM: Phytolacca americana
FEATURE:
NAME/KEY: CDS
LOCATION: (207)..(1145)
US-11-010-795-19

Query Match 64.8%; Score 301.2; DB 14; Length 1360;
Best Local Similarity 78.6%; Pred. No. 1.3e-67;
Matches 360; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
DB 5 TAAATAGACACCTTGAGTCTGGAATGCAACATTAACAAATATGACCTTTATG 64
274 TGAATACATCATCTACAAATGTTGAAATGACCAATAGCAATATGACCACTTTTGA 333
65 AATCTCTGTAATCAAGCGAAGATCCAAACTTAATGCTATGATGCAATGCTATC 124
334 ATGATCTTCTGTAATGGAAGCGAAGATCAATGTTAAATGCTATGCAATGCTGC 393
125 CTGATCTAATTCGACCCCTTAAGTATTATGTTAAGTTCGAAGTGCATAAATA 184
394 CCAATACAAATATCAAAATCAAAAGTACGTTGTTGAGTCCAAAGTTCATAAATA 453

QY 185 CCATTACCTAATGCTGAGACGAATACTTATAGTGATGGCTATTCGATCCCTTCA 244
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Db 454 CACATCACATTAATCTGAGACGAACAATTGTATGTGATGGTATTCGATCCCTTGG 513
QY 245 ATGGCAATTAAGTGTGCTTACCATATATTTAATGATATTAACAAGCAGCACTGATG 304
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Db 514 AAACCAATTAATGTGCTTACCATATTCCTTATGATATCTCGATACGAAACGCAAGTGT 573
QY 305 TGGAGATTAATCTTGTGCTGCAAGTCTAGTTCGTTGTCGAATGCCATTAATCAATA 364
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Db 574 TAGAGACTACTCTTGTCCCAATGCCAATTCCTGTTAGTAAACATTAACCTTGTATA 633
QY 365 GCTTATATCCGACCATGGAAGAAAGAGAGAACTCAAGAAATCAAGTCCAAATGG 424
|||
Db 634 GTGATATTCGAACATTTGGAATCAAAAGCGGAGTAAATCAAGAAAGTCAAGTCCAACTGG 693
QY 425 GAATTCAATATCTGACGATGACATTTGAAAAATCTCT 462
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Db 694 GAATTCAATATCTGACGATGATATTTGAAAAAGATTTCT 731

RESULT 2

US-11-010-795-21
; Sequence 21, Application US/11010795
; Publication No. US2006005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NITGUN E.
; APPLICANT: DI, RONG
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; TITLE OF INVENTION: RESISTANT TO TRICHOECENE FUNGAL TOXINS
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010, 795
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 21
; LENGTH: 934
; TYPE: DNA
; ORGANISM: Phytolacca americana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(930)
US-11-010-795-21

Query Match 11.7%; Score 54.6; DB 14; Length 934;

Best Local Similarity 55.9%; Pred. No. 0.00034;
Matches 146; Conservative 0; Mismatches 109; Indels 6; Gaps 2;

QY 19 TTTGATGCTGGAATGCGACCATTAACAATATGCACTTTATGGAATCTCTCGTAT 78
|||
Db 85 TTTGACCTTGGAATGCGACCAACGAAACCTACTTATTTTCTGACTGATTTGGAGAA 144
QY 79 CAAGCGAAGATCCAAACTAAAATGCTATGCAATCAACATGCTACCTGATATCAATTCG 138
|||
Db 145 GCTGTGAAGAAGCAAGAAATGACATGCAATGAAATGAGCAACACCTCACTGAA 204
QY 139 ACCCTTAATTAATTTGTTAGCTCAAGGTGCAAACTTAAACCATTAACATAATG 198
|||
Db 205 CAACCCAAAGTATGTGTGTGACCTCAAAATTCGATCTGAAACATTC--ACATTTGCA 261
QY 199 CTGAGACGAATACTTATACGTATGAGGCTATTCGATCCCTCAATGCAATTAAGTGT 258
|||
Db 262 ATCGAAGGGGAAACCTTATATTTGAGGGCTATTTCTGACATTTACAAATG--AAATGT 318
QY 259 GCTTACCAATATATTTAATGAT 279
|||
Db 319 CGTTATGCGATCTTCAAGAT 339

RESULT 3
US-10-750-185-27060/c

; Sequence 27060, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27060
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Bovine 19866880349638
US-10-750-185-27060

Query Match 8.9%; Score 41.6; DB 8; Length 1471;
Best Local Similarity 59.2%; Pred. No. 0.88;
Matches 71; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 343 GCATGTCCATTAATCAATAGCTTATATCCAGCCATGAAAAAGCAAGATAAC 402
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Db 1377 GCATGTCTAAAGCATCTAAAGCTTGTGATCTTCCATGAGCAAGGCTATGTATAA 1318
QY 403 TCAGAAATCAAGTCATTTGGGAATCAATTAATCAATCACTGACGATGCAATTTCT 462
|||
Db 1317 GGTGAAATTAATGATTAAGGATTTTGAATCTCTTCAGTATTAATCAAAATTTCT 1258

RESULT 4

US-10-750-623-27060/c
; Sequence 27060, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27060
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Bovine 19866880349638
US-10-750-623-27060

Query Match 8.9%; Score 41.6; DB 8; Length 1471;

Best Local Similarity 59.2%; Pred. No. 0.88;
Matches 71; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 343 GCATGTCCATTAATCAATAGCTTATATCCAGCCATGAAAAAGCAAGATAAC 402
|||
Db 1377 GCATGTCTAAAGCATTAAGCTTGTGATCTTCCATGAGCAAGGCTATGTATAA 1318
QY 403 TCAGAAATCAAGTCATTTGGGAATCAATTAATCAATCACTGACGATGCAATTTCT 462
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; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21, 598
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1224788
; LENGTH: 994
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1224788

Query Match
Best Local Similarity 7.7%; Score 35.6; DB 10; Length 994;
Matches 50; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 342 TGCATGTCATTAACATACATATATCCGACCATGGAAGAAGCAAGTAA 401
Db 278 TGAAGGCTCATTAACATGAGCTTCATCAGAAAAAAGAAAGAAAGA 219
Qy 402 CTCAGAATCAAG 415
Db 218 AATAAGAAAGCCAG 205
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RESULT 9
US-09-925-065A-409152/c
; Sequence 409152, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 409152
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-409152

Query Match
Best Local Similarity 7.5%; Score 35; DB 6; Length 647;
Matches 92; Conservative 1; Mismatches 96; Indels 0; Gaps 0;

Qy 240 CTTCAATGCGAATAGTGTGCTTACCATATATTAATATTAACAACCGAAGCAG 299
Db 483 CTATCAGAAATTCAGATAGAACTAGATATTTGATATATTAAGAAATTAAGTAA 424
Qy 300 TGATGTGAGAAATCTTTGCTCAAGTTCTAGTTCGTGTGCAATGTCATTAACTA 359
Db 423 TTTAGTTAGTGAAGAAAGTATGAGTTTGGATCGAATTTTAAATTTATTACTA 364
Qy 360 CAATAGCTTATATCGACCATGAAAGAAAGCAAGTAACTCAAGAAATCAAGTCA 419
Db 363 GGCTCAATATATCTTTATTAATTAATGTAGAACCAATAAATCAACATTTTGGCA 304
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Qy 420 ATTGGAAAT 428
Db 303 ATGAGAAAT 295

RESULT 10
US-10-301-480-475630
; Sequence 475630, Application US/10301480
; Publication No. US2006005564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 475630
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-475630

Query Match
Best Local Similarity 7.5%; Score 35; DB 10; Length 650;
Matches 92; Conservative 1; Mismatches 96; Indels 0; Gaps 0;
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Qy 240 CTTCAATGCGAATAGTGTGCTTACCATATATTAATATTAACAACCGAAGCAG 299
Db 168 CTATCAGAAATTCAGATAGAACTAGATATTTGATATTAAGAAATTAAGTAA 227
Qy 300 TGATGTGAGAAATCTTTGCTCAAGTTCTAGTTCGTGTGCAATGTCATTAACTA 359
Db 228 TTTAGTTAGTGAAGAAAGTATGAGTTTGGATCGAATTTTAAATTTATTACTA 287
Qy 360 CAATAGCTTATATCGACCATGAAAGAAAGCAAGTAACTCAAGAAATCAAGTCA 419
Db 288 GGCTCAATATATCTTTATTAATTAATGTAGAACCAATAAATCAACATTTTGGCA 347
Qy 420 ATTGGAAAT 428
Db 348 ATGAGAAAT 356

RESULT 11
US-10-301-480-1089039
; Sequence 1089039, Application US/10301480
; Publication No. US2006005564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1089039
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1089039
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Query Match 7.5%; Score 35; DB 10; Length 650;
Best Local Similarity 48.7%; Pred. No. 34;
Matches 92; Conservative 1; Mismatches 96; Indels 0; Gaps 0;

QY 240 CTTCATGCGCAATGAGTGTCTTACCATATATTATATATACAGACCGAAGCAGC 299
DB 168 CTATCAGAGAAATTCAGATGAGAACTAGATATATATATATATATATATATAT 227

QY 300 TGATGTGAGAAATCTCTTGTCTCAATGTTCTGTGTGCAATGTCATATACATA 359
DB 228 TTTAGTTTATGCAAAAGTAATGCAATTTGATGCAATTTAAATTTATATATAC 287

QY 360 CAATAGCTTATATCCAGACAGAGAAAGAAAGCAAGTAATCTCAAGAAATCAATGCA 419
DB 288 GGTCTCAATATATATCTTATATATATATATATATATATATATATATATATAT 347

QY 420 ATGTGGAT 428
DB 348 ATGAGAAAT 356

RESULT 12

US-10-995-561-13213/C
; Sequence 13213, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13213
; LENGTH: 18930
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13213

Query Match 7.5%; Score 35; DB 8; Length 18930;
Best Local Similarity 49.7%; Pred. No. 96;
Matches 86; Conservative 1; Mismatches 86; Indels 0; Gaps 0;

QY 226 GGCTATCTGATCCCTTCAATGCAATGATGTCTTACCATATATTATATATATAC 285
DB 18147 GGCGCTTCTCAATCTCAATGCAATGATGCGCCCTGCAATCTGTATATATACCA 18088

QY 286 AGCACGCAACGCACTGATGTGAGAAATCTTGTCTCAAGTTCTGATGTTGCA 345
DB 18087 GATTCGATTCAGTGTGTGTGAGATCTTAAGACTTCATGTTTATATATGATTCGA 18028

QY 346 ATGTCATTAATCAATATGCTTATATCCAGCAATGAGAAAGAAAGCAAGAGT 398
DB 18027 ATTGCTATTTCTGACACCGCTATGTGAGCAAGGAGAAAGCAAGAGTGT 17975

RESULT 13

US-10-301-480-219992
; Sequence 219992, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 219992
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-219992

Query Match 7.4%; Score 34.6; DB 10; Length 650;
Best Local Similarity 67.1%; Pred. No. 43;
Matches 49; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 42 TAACAAATATGCGCACTTTATGGAATCTCTGTAATCAAGCGAAAGTCCAAACTTAA 101
DB 198 TAACAAATATCCATCTGATGCAAAATGTTATATATGCGGAGATGAGAAATATA 257

QY 102 ATGCTATGCATA 114
DB 258 ATGAGGGGGCATA 270

RESULT 14

US-10-301-480-833401
; Sequence 833401, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 833401
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-833401

Query Match 7.4%; Score 34.6; DB 10; Length 650;
Best Local Similarity 67.1%; Pred. No. 43;
Matches 49; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 42 TAACAAATATGCGCACTTTATGGAATCTCTGTAATCAAGCGAAAGTCCAAACTTAA 101
DB 198 TAACAAATATCCATCTGATGCAAAATGTTATATATGCGGAGATGAGAAATATA 257

QY 102 ATGCTATGCATA 114
DB 258 ATGAGGGGGCATA 270

RESULT 15

US-09-925-065A-121758/C
; Sequence 121758, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092

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; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121758
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-121758

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Query Match      7.4%; Score 34.6; DB 6; Length 655;
Best Local Similarity 67.1%; Pred. No. 43;
Matches 49; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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Qy 42 TAACAAATATGCCACTTTATGGAATCTCTGTAATCAAGCAAGATCCAAACTTAA 101
    |||||
Db 458 TAACAAATATGCCACTTACTGATGCAAAATGTTAATATGCGGGGATGAGAAAAATTAA 399
    |||||
Qy 102 ATGCTATGGCATA 114
    |||||
Db 398 ATGAGGGGGCATA 386
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Title: US-09-978-274A-6

Perfect score: 793
Sequence: 1 MINTTFDAGNATINKYATF.....SHNOVQLGIQLISDGIKIS 154

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODL=frame+ p2n.model -DEV=xlh
-O=/abs/ABSSMB.apool/US09978274/runat_07042006.173032.28388/app_query.fasta_1
-DB=genBml -QMT=fastcap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCMALIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=Pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=absg04
-USBR=US09978274 @CGN 1.1.5548 @runat 07042006.173032.28388 -NCPU=6 -ICPU=3
-NO_MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELTEXT=7

Database : GenBml:

1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	793	100.0	465	6	AX427706 Sequence
2	793	100.0	792	6	AX427704 Sequence
3	793	100.0	1092	6	AX427720 Sequence

4	788	99.4	945	6	AX427702
5	788	99.4	1249	15	PAPAPSRIP
6	773	97.5	786	15	AB071855
7	670.5	84.6	783	15	AB071854
8	613	77.3	882	6	A67183
9	608	76.7	714	15	AY603354
10	605	76.3	939	15	AY327475
11	598	75.4	711	15	AF338910
12	596	75.2	714	15	AY603352
13	596	75.2	942	15	AY547315
14	596	75.2	942	15	AY572976
15	596	75.2	1164	15	PAPAP
16	596	75.2	1195	6	A42103
17	596	75.2	14385	6	I4385
18	596	75.2	1195	6	I55866
19	596	75.2	1379	6	AR009535
20	596	75.2	1379	6	AR136704
21	596	75.2	1379	6	AR141172
22	596	75.2	1379	6	AX427731
23	595	75.0	1164	15	AY049785
24	594	74.9	714	15	AY603353
25	590	74.4	1195	6	A36639
26	589	74.3	1114	15	AF535515
27	588	74.1	1378	6	AX427732
28	588	74.1	1379	6	AR136705
29	559.5	70.6	2472	6	B05033
30	559.5	70.6	2472	15	FTCAPAP
31	554.5	69.9	1052	15	AY137202
32	542.5	68.4	951	6	A67185
33	542.5	68.4	2369	15	AF141331
34	527	66.5	1113	15	AY071928
35	463.5	58.4	918	6	A43003
36	463.5	58.4	918	6	A48150
37	463.5	58.4	918	6	I60482
38	463.5	58.4	918	6	I69987
39	399	50.3	1226	15	CAANTIPR
40	399	50.3	1226	15	CAAV
41	278.5	35.1	1180	15	MCU80072
42	274	34.6	902	15	AF535516
43	261	32.9	934	6	AX427733
44	261	32.9	1187	15	PAPAP11
45	247	31.1	1667	15	PAPAP1111

ALIGNMENTS

RESULT 1	AX427706	465 bp	DNA	linear	PAT 20-JUN-2002
LOCUS	Sequence 5 from Patent WO0233107.				
DEFINITION	AX427706				
ACCESSION	AX427706.1	GI:21537817			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	Phytolacca americana (American pokeweed)				
	Phytolacca americana				
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.				
REFERENCE	1				
AUTHORS	Neelam, A., Atkinson, H.J., Mcpherson, M.J. and Thomas, C.J.R.				
TITLE	Plant cell death system				
JOURNAL	Patent: WO 0233107-A 5 25-APR-2002;				
	CAMBRIDGE ADVANCED TECH (GB)				
FEATURES	Location/Qualifiers				
	1..465				
	/organism="Phytolacca americana"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:3527"				
	1..3				
	/note="Initiation codon added via PCR primer"				
	462..465				
	/note="Stop codon added via PCR primer"				
ORIGIN					

Alignment Scores:
Pred. No.: 3,38e-74 Length: 465
Score: 793.00 Matches: 154
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-6 (1-154) x AX427706 (1-465)

QY 1 MetIleAenThriLeThrPheAspAlaGlyAsnAlaThrIleAenLysTyraLathPhe 20
DB 1 ATGATTAATACGATCACTTGGATGCTGGAAATGCCACATTAAACAATATGCCACCTT 60
QY 21 MetGluSerLeuArgAnGlnAlaLysAspProLysLeuLysCysTyrglyIlePromet 40
DB 61 ATGGAACTCTTCTGTAATCAAGCAAGATCCAAATCAATATGCTATGCAATCAATG 120
QY 41 LeuProAspThrAsnSerThrProLysTyrlleuLeuValLysLeuGlnGlyAlaAsnLeu 60
DB 121 CTACCTTAATCAATATTCGACCCCTTAAGTACTTATGTTAGCTCCAAAGTGCAAACTTA 180
QY 61 LysThrIleThreuMetLeuArgArgAsnLeuTyraValMetGlyTyrsAspPro 80
DB 181 AAAACATTACATTAATCTGAGAGCAAAATTAATTATCGTAGGGCTATTGATGCC 240
QY 81 PheAnGlyAsnLysCysArgTyrsIlePheAsnAspIleThrsThrGluArgThr 100
DB 241 TTCAATGGCAATTAAGTGTGCTTACCATATTAATGATTAATACAGCAAGCAAGCACT 300
QY 101 AspValGluAenThriLeuCysSerSerSerSerArgValAlaMetSerIleAsnTy 120
DB 301 GATGTGGAAATACCTTTGCTCAAGTCTAGTTCTCGTGTGCAATGTCCATTAACTAC 360
QY 121 AsnSerLeuTyProThMetGluLysLysAlaGluValaAsnSerArgAsnGlnValGln 140
DB 361 AATAGCTTAATTCGACCATGAGAAAGAAACAGAAAGTAATCAAGAAATCAAGTCCA 420
QY 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
DB 421 TTGGGAATTCAAATTAATCTCAGCAGTGACATTGGAAAAATCTCT 462

RESULT 2
AX427704 792 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 3 from Patent WO0233107.
DEFINITION AX427704
ACCESSION AX427704.1 GI:21537816
VERSION
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
AUTHORS Neelam, A., Atkinson, H.J., McPherson, M.J. and Thomas, C.J.R.
TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A 3 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES
Source location/Qualifiers
1..792
/organism="Phytolacca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"
1..29
/note="Binding site for primer PS1BF"
1..3
/note="Initiation codon added via PCR primer"
misc_feature complement(436..462)
misc_feature /note="Binding site for primer PS1SR"
463..492
misc_feature /note="Binding site for primer PS2BF"

variation 612
/note="Nucleotide change from published sequence"
variation 681..686
/note="Sequence replacing removed XbaI site"
misc_feature complement(765..792)
/note="Binding site for primer PS2SR"
misc_feature 790..792
/note="Stop codon added via PCR primer"
ORIGIN

Alignment Scores:
Pred. No.: 6.03e-74 Length: 792
Score: 793.00 Matches: 154
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-6 (1-154) x AX427704 (1-792)

QY 1 MetIleAenThriLeThrPheAspAlaGlyAsnAlaThrIleAenLysTyraLathPhe 20
DB 1 ATGATTAATACGATCACTTGGATGCTGGAAATGCCACATTAAACAATATGCCACCTT 60
QY 21 MetGluSerLeuArgAnGlnAlaLysAspProLysLeuLysCysTyrglyIlePromet 40
DB 61 ATGGAACTCTTCTGTAATCAAGCAAGATCCAAATCAATATGCTATGCAATCAATG 120
QY 41 LeuProAspThrAsnSerThrProLysTyrlleuLeuValLysLeuGlnGlyAlaAsnLeu 60
DB 121 CTACCTTAATCAATATTCGACCCCTTAAGTACTTATGTTAGCTCCAAAGTGCAAACTTA 180
QY 61 LysThrIleThreuMetLeuArgArgAsnLeuTyraValMetGlyTyrsAspPro 80
DB 181 AAAACATTACATTAATCTGAGAGCAAAATTAATTATCGTAGGGCTATTGATGCC 240
QY 81 PheAnGlyAsnLysCysArgTyrsIlePheAsnAspIleThrsThrGluArgThr 100
DB 241 TTCAATGGCAATTAAGTGTGCTTACCATATTAATGATTAATACAGCAAGCAAGCACT 300
QY 101 AspValGluAenThriLeuCysSerSerSerSerArgValAlaMetSerIleAsnTy 120
DB 301 GATGTGGAAATACCTTTGCTCAAGTCTAGTTCTCGTGTGCAATGTCCATTAACTAC 360
QY 121 AsnSerLeuTyProThMetGluLysLysAlaGluValaAsnSerArgAsnGlnValGln 140
DB 361 AATAGCTTAATTCGACCATGAGAAAGAAACAGAAAGTAATCAAGAAATCAAGTCCA 420
QY 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
DB 421 TTGGGAATTCAAATTAATCTCAGCAGTGACATTGGAAAAATCTCT 462

RESULT 3
AX427720 1092 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 19 from Patent WO0233107.
DEFINITION AX427720
ACCESSION AX427720
VERSION AX427720.1 GI:21537829
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS Neelam, A., Atkinson, H.J., McPherson, M.J. and Thomas, C.J.R.
TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A 19 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES
Source location/Qualifiers
1..1092
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PAP-S/Cystatin fusion"

misc_feature 1..29
/note="Binding site for primer PS1BP"
variation 681..686
/note="Modified XbaI site"
misc_feature complement(742..786)
/note="Binding site for primer PCS-PAPS8"
misc_feature 766..806
/note="Binding site for primer PCS-Delta86P"
misc_feature 766..786
/note="REV NIA protease cleavage site"
misc_feature complement(1066..1092)
/note="Binding site for primer SYNPODelta86SR"

ORIGIN

Alignment Scores:

Pred. No.:	8,54e-74	Length:	1092
Score:	793.00	Matches:	154
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-09-978-274A-6 (1-154) x AX427720 (1-1092)

QY 1 MettIeaSnThrlEThrPheaSpAlaGlyAsnAlaThrlEaSnlyTyraLaThrPhe 20
DB 1 ATGATTAATACGATCACTTGTGATGCTGGAATGCAACATTAACAATATGCCACTTT 60
QY 21 MetGluSerLeuArgAnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMet 40
DB 61 ATGGAAATCTCTTGATATCAAGGAAAGATCCAAATGAATGCTATGCAATACCAATG 120
QY 41 LeuProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeu 60
DB 121 CTAAGTAACTAATTCGACCCCTAAGTACTTATGTTAGTCTCAAGGTCGAAACCTTA 180
QY 61 LysThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspPro 80
DB 181 AAAACATTAACAATAAGTGAAGCAAAATTAATTAAGTATGAGGCTATTCGATCCC 240
QY 81 PheAnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThr 100
DB 241 TTCAATGGCAATTAAGTGTGTTACCATATTAATTAATGATTAACAAGCAACGCACT 300
QY 101 AspValGluAsnThrLeuLysSerSerSerSerSerSerArgValAlaMetSerIleAsnTyr 120
DB 301 GATGGAGAAATACCTTGTCTCAAGTTCTAGTTCGATGTCATATGTCATTAATCTAC 360
QY 121 AsnSerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAnGlnValGln 140
DB 361 AATACCTATATCCGACCATGGAAGAAAGAAAGCAAGTAATCAAGAAATCAAGTCCAA 420
QY 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
DB 421 TTGGGAATTCAAATACTCAGCAGTGCATGTGAAAAAATCTCT 462

RESULT 4

AX427702 945 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 1 from Patent WO0233107.
DEFINITION AX427702
ACCESSION AX427702.1 GI:21537815
VERSION
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)

REFERENCE

AUTHORS Neelam, A., Atkinson, H.J., McPherson, M.J. and Thomas, C.J.R.
TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A 1 25-APR-2002;
CAMBRIDGE ADVANCBIO TECH (GB)

FEATURES

source

Location/Qualifiers

1..945
/organism="Phytolacca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"
1..24
/note="Binding site for primer PPS1BP"
complement(735..776)
/note="Binding site for primer PSXOR"
736..777
/note="Binding site for primer PSXDF"
750..759
/note="Sequence replacing removed XbaI site"
complement(922..945)
/note="Binding site for primer PPS2SR"

ORIGIN

Alignment Scores:

Pred. No.:	2,45e-73	Length:	945
Score:	768.00	Matches:	153
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	99.4%	Indels:	0
DB:	6	Gaps:	0

US-09-978-274A-6 (1-154) x AX427702 (1-945)

QY 2 11EaSnThrlEThrPheaSpAlaGlyAsnAlaThrlEaSnlyTyraLaThrPheMet 21
DB 73 ATTAATACGATCACTTGTGATGCTGGAATGCAACATTAACAATATGCCACTTTATG 132
QY 22 GluSerLeuArgAnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeu 41
DB 133 GAATCTCTTGATTAATCAAGGAAAGATCCAAATGAATGCTATGCAATACCAATGCTTA 192
QY 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
DB 193 CCTGATACCTAATTCGACCCCTTAAGTACTTATGTTAGTTCGAAAGTGCNAACCTTAA 252
QY 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
DB 253 ACCATTAACCTAATCTGAGCAAGAAATTAATTAATGATGAGGCTATTCGATCCCTTC 312
QY 82 AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
DB 313 AATGCAATTAAGTGTGTTACCATATTAATTAATGATTAACAAGCAACGCACTGAT 372
QY 102 ValGluAsnThrLeuLysSerSerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
DB 373 GTGGGAATACCTTGTCTCAAGTTCTAGTTCGATGTCATATGTCATTAATCAAT 432
QY 122 SerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAnGlnValGlnLeu 141
DB 433 AGCTTAATTCGACCATGGAAGAAAGCAAGTAATCAAGAAATCAAGTCCAAATG 492
QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
DB 493 GGAATTCAAATTAATCTCAGCAGTGCATGTGAAAAAATCTCT 531

RESULT 5

PAPASRIP 1249 bp mRNA linear PLN 18-APR-2005
LOCUS PAPASRIP
DEFINITION P.americana mRNA for pokeweed antiviral protein.
ACCESSION X98079
VERSION X98079.1 GI:1707648
KEYWORDS PAP-S gene; pokeweed antiviral protein (PAP); ribosome-inactivating protein.
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)

REFERENCE

AUTHORS Neelam, A., Atkinson, H.J., McPherson, M.J. and Thomas, C.J.R.
TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A 1 25-APR-2002;
CAMBRIDGE ADVANCBIO TECH (GB)

AUTHORS Poyet, J.L. and Hoeveler, A.
TITLE cDNA cloning and expression of pokeweed antiviral protein from seeds in *Escherichia coli* and its inhibition of protein synthesis in vitro
JOURNAL FEBS Lett. 406 (1-2), 97-100 (1997)
PUBMED 9109394
REFERENCE 2 (bases 1 to 1249)
AUTHORS Poyet, J.L.
TITLE Direct Submission
JOURNAL Submitted (22-MAY-1996) J.L. Poyet, Laboratoire de Biochimie-Biologie Moléculaire, UFR Sciences et Techniques, 16 route de Gray, 25030 Besancon Cedex, FRANCE
REMARK Revised by author 20-SEP-1996
FEATURES location/Qualifiers
SOURCE 1. 1249
 /organism="Phytolacca americana"
 /mol_type="mRNA"
 /db_xref="taxon:3527"
 /issue_type="seeds"
 1. 1249
 /gene="PAP-S"
 106. 1050
 /gene="PAP-S"
 /note="ribosome-inactivating protein type I"
 /codon_start=1
 /product="pokeweed antiviral protein"
 /protein_id="CAA6702.1"
 /db_xref="GI:1707649"
 /db_xref="GOA:P93444"
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 106. 177
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 178. 1047
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 1212. 1217
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ORIGIN
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 polyA_site
 polyA_site
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Alignment Scores:
 Pred. No.: 3.32e-73 Length: 1249
 Score: 788.00 Matches: 153
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 99.4% Indels: 0
 DB: 15 Gaps: 0
 US-09-978-274A-6 (1-154) x PAPAPSRIP (1-1249)
 Oy 2 IleaenThIleThPhaAaPAlaGlyAaenAlaThrIleaenLyTyAlaThrPhaMet 21
 Db 178 ATAAATACGATCACTTTGATGCTCGAAATGCGACCATTAACAAATATGCCCTTTATG 237
 Oy 22 GluSerLeuAaGAnGAlaIaAaAaPProLySLeuLySvCyTyGlyIleProMetLeu 41
 Db 238 GAATCTCTTCGTAATCAAGCGAAAGATCCAAATGCTAATAGCATACCAATGCTA 297
 Oy 42 ProAePThrAsnSerThrProLySlyLeuLeuValIySLeuGlnGlyAlaAaenLyS 61
 Db 298 CCTGATCTAATTCGACCCCTTAAGTACTTATGGTTAAGCTCCAAAGTCCAAACCTAAA 357
 Oy 62 ThrIleThrLeuMetLeuAaGAlaIaAaAaenLyTyValMetGlyTySerAaProPhe 81
 Db 358 ACCATTACACTAATGCTGAGACGAATATACTTATACGTATGGGCTATTCTGATCCCTTC 417

Oy 82 AaenLyAaenLySvCyAaGlyTyHleIlePhaAaAaPleThrSerThnGluAaGThaAaP 101
 Db 418 AATGCAATAGTGTCTGTTACCATATTTATATATTTACACACGAAAGCATGAT 477
 Oy 102 ValGluAaThrLeuCyAaSerSerSerSerSerAaGAlaAaMetSerIleaenTyAa 121
 Db 478 GTGAGAAATACTCTTTGCTCAAGTTAGTTCTCGTGTGCAATGTCATTAACAT 537
 Oy 122 SerLeuTyProThrMetGluLyAaGAlaGluValAaenSerAaAaenGlnValGlnLeu 141
 Db 538 AGCTTAATATCCAGCAAGAAAGAAAGCAAGATAAATCAAGAAATCAAGTCAATTG 597
 Oy 142 GlyIleGlnIleAaSerSerAaPleGlyTySer 154
 Db 598 GGAATTCAAATCTCAGCATGACATTCGAAATCTCT 636

RESULT 6
 AB071855 786 bp DNA linear PLN 19-MAR-2002
LOCUS Phytolacca americana paps2 gene for PAP-S2, partial cds.
DEFINITION AB071855
ACCESSION AB071855
VERSION AB071855.1 GI:19570839
KEYWORDS
SOURCE
ORGANISM
 Phytolacca americana (American pokeweed)
 Phytolacca americana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS Homjo, E. and Watanabe, K.
TITLE Cloning of genomic DNA encoding two types of pokeweed antiviral protein in seeds, PAP-S1 and PAP-S2, and functional comparison of their recombinant proteins with other PAP isoforms
JOURNAL 2 (bases 1 to 786)
AUTHORS Watanabe, K. and Homjo, E.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2001) Keiichi Watanabe, Saga University,
 Department of Applied Biological Sciences, Honjo-machi, Saga city,
 Saga 840-8502, Japan (E-mail: watakei@cc.saga-u.ac.jp,
 Tel: 81-952-28-8774, Fax: 81-952-28-8774)
FEATURES location/Qualifiers
SOURCE 1. 786
 /organism="Phytolacca americana"
 /mol_type="genomic DNA"
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 1. 786
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 /note="mature pokeweed antiviral protein-S2"
 /codon_start=1
 /product="PAP-S2"
 /protein_id="BAB86350.1"
 /db_xref="GI:19570840"
 /translation="INTFTPDAGNSTINKYATFMESLNOADPKLKCQYKPMIPDNT SPKYLVKLGQANLKITTLMLRRNNLYVWGYSDFPNKSKRYHFNIDITSTERTDVE NTUSSSSSRVAMISINSLYPTMEKAEVNSRQVQIGIQLSSDIGISGVDSFPV KTEAFLVLAIQWSEARFYIENQVKTENRAFYDPKVINLEBKWKISSEAIHNK NGALPELRLVDKGTWIVLRVDEINRDVALLKYVNGTCOAT"

ORIGIN

Alignment Scores:
 Pred. No.: 7.59e-72 Length: 786
 Score: 773.00 Matches: 149
 Percent Similarity: 99.3% Conservative: 3
 Best Local Similarity: 97.4% Mismatches: 1
 Query Match: 97.5% Indels: 0
 DB: 15 Gaps: 0

US-09-978-274A-6 (1-154) x AB071855 (1-786)

QY 2 11eaentThrleThrPheapAlaGlyAsnAlaThr11eaenlyTyra1aThrPheMet 21
DB 1 ATCAATACCTTCTGCTTTGATGCTGGAATATCCACCATTAACCAATATGCACTTTATG 60
QY 22 GUsertleuArgAnclnAlaLysaAppProlybLeuLybCyTyrcly11eProMetleu 41
DB 61 GAATCTCTTCGTATATACGGAAGATCCAAATCTAAATGCTATGCAATACCAATGCTTA 120
QY 42 ProAepThrAsnSerThrProlybTyraLeuVal1yLeuGlnGly1y1aAsnLeuLyb 61
DB 121 CCTGATACCTATATTCGACCCCTTAAGTACTTATGTTGCTTCAAGCTCAAGCTCACTTA 180
QY 62 Thr11eThrLeuMetleuArgaAsnLeuTyraValMetGlyTyraSerAppPrope 81
DB 181 ACCATTACACTATATGCTGAGACCAATATCTATACGTATGGCTATTCGATCCCTTC 240
QY 82 AaNGlyAsnLybCybaArgTyraHis11ePheAsnApp11eThrSerThrgluArgThraP 101
DB 241 AATGGCAATAGTGTGCTTACCAATATATTAATGATTAACAAGCACCAAGCTGAT 300
QY 102 ValGluAsnThrLeuCySerSerSerSerSerSerValAlaMetSer11eAsnTyraSn 121
DB 301 GTGGAGAAATCTCTTGTCTCAAGTTCTTACTTCGTGTGCAATGTCCATTAATCAAT 360
QY 122 SerLeuTyProThrMetGluLybAlaGluValaSnSerArgaAng1y1aGlnLeu 141
DB 361 AGCTATATATCCGACCTTGGAAAAGCAAGAAAGTAACTCAAGAAAGTCAAGTCCATTTG 420
QY 142 Gly11eGln11eLeuSerSerAsp11eGly1y11eSer 154
DB 421 GGAATTCAAATCTCAGCAGTGAATGGAATAATCTCT 459

RESULT 7
AB071854 783 bp DNA linear PLN 19-MAR-2002
LOCUS AB071854
DEFINITION Phytolacca americana papsi gene for PAP-S1, partial cds.
ACCESSION AB071854
VERSION AB071854.1 GI:19570837
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS
TITLE
1 Honjo, B. and Watanabe, K.
2 Cloning of genomic DNA encoding two types of pokeweed antiviral protein in seeds, PAP-S1 and PAP-S2, and functional comparison of their recombinant proteins with other PAP isoforms
Unpublished
2 (bases 1 to 783)
Watanabe, K. and Honjo, B.
JOURNAL
REFERENCE
AUTHORS
TITLE
Direct Submission
Submitted (19-SEP-2001) Keiichi Watanabe, Saga University,
Department of Applied Biological Sciences, Honjo-machi, Saga city,
Saga 840-5502, Japan (E-mail: watakeisc.saga-u.ac.jp,
Tel:81-952-28-8774, Fax:81-952-28-8774)

FEATURES
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/translation="INITPDAAGATNTINKVATPESGLRNEAKDLSLKYGIPLMLPNTN
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ORIGIN

Alignment Scores:
Pred. No.: 4,58e-61 Length: 783
Score: 670.50 Matches: 132
Percent Similarity: 91.5% Conservative: 8
Best Local Similarity: 86.3% Mismatches: 12
Query Match: 84.6% Indels: 1
DB: 15 Gaps: 1

US-09-978-274a-6 (1-154) x AB071854 (1-783)

TLCPSSNPVAKPINVNGLYPTLEBKAGVTSNNOYLGILISDGIKISGGSFTEK
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NCALPKPIELKRAADGTKMIVLAVDEIKEDVGLANTVNGTCQAT"

QY 2 11eaentThrleThrPheapAlaGlyAsnAlaThr11eaenlyTyra1aThrPheMet 21
DB 1 ATCAATACCTTCTGCTTTGATGCTGGAATATCCACCATTAACCAATATGCACTTTATG 60
QY 22 GUsertleuArgAnclnAlaLysaAppProlybLeuLybCyTyrcly11eProMetleu 41
DB 61 GAATCTCTTCGTATATACGGAAGATCCAAATCTAAATGCTATGCAATACCAATGCTTA 120
QY 42 ProAepThrAsnSerThrProlybTyraLeuVal1yLeuGlnGly1y1aAsnLeuLyb 61
DB 121 CCTGATACCTATATTCGACCCCTTAAGTACTTATGTTGCTTCAAGCTCAAGCTCACTTA 180
QY 62 Thr11eThrLeuMetleuArgaAsnLeuTyraValMetGlyTyraSerAppPrope 81
DB 181 ACCATTACACTATATGCTGAGACCAATATCTATACGTATGGCTATTCGATCCCTTC 240
QY 82 AaNGlyAsnLybCybaArgTyraHis11ePheAsnApp11eThrSerThrgluArgThraP 101
DB 241 GAC--AAATAGTGTGCTTACCAATATCTTATATGATTAAGGACATGAATACGTAT 297
QY 102 ValGluAsnThrLeuCySerSerSerSerSerValAlaMetSer11eAsnTyraSn 121
DB 298 GTGGAGAAATCTCTTGTCTCAAGTTCTTACTTCGTGTGCAATGTCCATTAATCAAT 357
QY 122 SerLeuTyProThrMetGluLybAlaGluValaSnSerArgaAng1y1aGlnLeu 141
DB 358 GGCCATATTCCTCACTTGTGAAAAGCAAGAGTAACTCAAGAAATCAAGTCCACTTA 417
QY 142 Gly11eGln11eLeuSerSerAsp11eGly1y11eSer 154
DB 418 GGAATTCAAATCTCAGCAGTGAATGGAATAATCTCT 456

RESULT 8
A67183 882 bp DNA linear PAT 05-MAY-1999
LOCUS A67183
DEFINITION Sequence 1 from Patent EP0808902.
ACCESSION A67183
VERSION A67183.1 GI:4756167
KEYWORDS
SOURCE
ORGANISM
Phytolacca insularis
Phytolacca insularis
Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
AUTHORS
TITLE
1 Moon, Y., Choi, J., Yun, Y., Jin, J., Hong, B., Lee, J., Choi, K., Lee, J.,
Song, S., Choi, Y., Kim, C. and Kim, M.
Novel genes encoding antiviral proteins of Phytolacca insularis
Nakai and recombinant microorganisms expressing the same proteins
Patent: EP 0808902-A 1 26-NOV-1997;
JINRO LTD (KR)
COMMENT
Other publication JP 9308489 19971202
Other publication CA 2186303 19971123
Other publication AU 6570696 19971127.
FEATURES
source
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/organism="Phytolacca insularis"
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SOURCE
ORGANISM Phytolacca heterotepala
Phytolacca heterotepala
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
AUTHORS Delll Bovl,P. and Corrado,G.
TITLE Direct Submission
JOURNAL Submitted (23-JUN-2003) Department of Soil, Plants and
Environmental Sciences, University of Naples 'Federico II', via
Universita' 100, Portici, Naples 80055, Italy
FEATURES
source
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OLGQIOLDSIDGKISGVSFSKRTAEFLVAIOISEARFKYIENQVKNRNFNP
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SGSCQTYNQNAMPQLIMSTYYNMANLGDLEFR"

ORIGIN

Alignment Scores:

Pred. No.: 4,33e-54 Length: 939
Score: 605.00 Matches: 112
Percent Similarity: 87.6% Conservative: 22
Best Local Similarity: 73.2% Mismatches: 19
Query Match: 76.3% Indels: 0
DB: 15 Gaps: 0

US-09-978-274a-6 (1-154) x AY327475 (1-939)

QY 2 Ileaanthrillethrrheaspaalaglyasnaalathrilleasnyetyralathrphemet 21
DB 67 GTGATATACATCATCTACCAATGTTGGAAGTACCAACATTAGCAATACGCCACTTTCTCG 126
QY 22 GluserleuarganginalalysaspProlyseuysCyTyTgYIlePrometleu 41
DB 127 GATGATCTTCGTAATGAAGCGAAGATCCAAATTAAATGCTATGGAATACCAATGCTG 186
QY 42 ProaphthraenseThrProlyetyrleuauVallylsleunginglyalaasleuys 61
DB 187 CCCAATCAAAATTCAAATCCAAAGTACGTTGGTGGCTCCAAAGGTTCAAAATAAAAA 246
QY 62 ThrillethreumelleuargargasnaasleuTyValMetGlyTySerAspProphe 81
DB 247 ACCATCAACATTAATCTGAGCGAAGCAATTTGATGATGATGCGGTATTCGATCCCTT 306
QY 82 AsnolyasnylyCyBargTyRHisIlePheasnaapIlethrSerThrgluargThrasp 101
DB 307 GATACCGAGTAGTGCCTTACCAATCTTAAATGATATCTCAGTACGAGCAAGCCAGAT 366
QY 102 ValgluabanthrleuCySerSerSerSerSerSerArgValAlaMetSerIleasnthrasn 121
DB 367 GTAGAGACTACTCTTGCCAAATTCCAATCTCTGTGTGTAAGAAAAACATTAACATATAT 426
QY 122 SerleuTyProthMetGluTyBalyalaagluValaasSerArgAsnGlnValGlnleu 141
DB 427 AGTCGATATCCAACTGGAATCAAAAGTGGAGATTAATCAAGAGTCAAGTCCAACTG 486
QY 142 GlylleaglnleuSerSerAspIleGlylyslleSer 154

DB 487 GGAAATTCAAATCTGACAGTGAATGAGTGAAGAAATTTCT 525
RESULT 11
AF338910
LOCUS AF338910 711 bp mRNA linear PLN 21-MAR-2001
Phytolacca americana antiviral protein (mpap) mRNA, partial cds.
ACCESSION AF338910
VERSION AF338910.1 GI:13398616
KEYWORDS
SOURCE Phytolacca americana (American pokeweed)
ORGANISM Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
AUTHORS Chen,D., Wang,X. and Zhou,G.
TITLE Pokeweed antiviral protein gene,partial cds
JOURNAL Unpublished
2 (bases 1 to 711)
Wang,X., Chen,D. and Zhou,G.
REFERENCE
AUTHORS Submitted (20-JAN-2001) Plant Pathology, Institute of Plant
Protection, Chinese Academy of Agriculture Sciences,
Yuanmingyuanxilu No.2, Beijing 100094, China
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NPKVIANRSTKSTAIHDAKNGVLPRLBLVDASGAKWIVLRDEKPKDVALNLY
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CDS

gene

QY 2 Ileaanthrillethrrheaspaalaglyasnaalathrilleasnyetyralathrphemet 21
DB 1 GTGATATACATCATCTACCAATGTTGGAAGTACCAACATTAGCAATACGCCACTTTCTCG 60
QY 22 GluserleuarganginalalysaspProlyseuysCyTyTgYIlePrometleu 41
DB 61 AATGATCTTCGTAATGAAGCGAAGATCCAAAGTAAATGCTATGGAATACCAATGCTG 120
QY 42 ProaphthraenseThrProlyetyrleuauVallylsleunginglyalaasleuys 61
DB 121 CCCAATCAAAATTCAAATCCAAAGTACGTTGGTGGCTCCAAAGGTTCAAAATAAAAA 180
QY 62 ThrillethreumelleuargargasnaasleuTyValMetGlyTySerAspProphe 81
DB 181 ACCATCAACATTAATCTGAGCGAAGCAATTTGATGATGATGCGGTATTCGATCCCTT 240
QY 82 AsnolyasnylyCyBargTyRHisIlePheasnaapIlethrSerThrgluargThrasp 101

ORIGIN

Alignment Scores:

Pred. No.: 1.75e-53 Length: 711
Score: 598.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.4% Indels: 0
DB: 15 Gaps: 0

US-09-978-274a-6 (1-154) x AF338910 (1-711)

Db 241 GAACCAATAAATGCTGTTACCATATCTTTATGATATCTCAGGTAAGCAAGCAAGAT 300
Qy 102 ValGluAnthrIleuCySerSerSerSerSerArgValAlaMetSerIleAsnTyraSn 121
Db 301 GTAAAGACTACTCTTTGCCAAATGCCAATCTCGTGTAGTAAACATTAACCTTGAT 360
Qy 122 SerLeuTyProThrMetGluLysLeuValAlaMetSerArgAsnGlnValGlnLeu 141
Db 361 AGTGATATTCACATTCGATTCGAAAGCGGAGTAAATCAAGAGTCAGTCCACTG 420
Qy 142 GlyIleGlnIleLeuSerSerSerSerSerSerSerSerSerSerSerSerSerSer 154
Db 421 GGAATTCATAATATCTGACAGTAATATTCGAAAGATTTCT 459
RESULT 12
AY603352 714 bp DNA linear PLN 17-MAY-2004
LOCUS Phytolacca americana antiviral protein PAP (pap) gene, pap-s
DEFINITION Phytolacca americana antiviral protein PAP (pap) gene, pap-s
ACCESSION AY603352
VERSION AY603352.1 GI:47175554
KEYWORDS
SOURCE Phytolacca americana (American pokeweed)
ORGANISM Phytolacca americana
Phytolacca americana; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE 1 (bases 1 to 714)
AUTHORS Chen, G., Lei, J., Cao, B. and Zeng, G.
TITLE Phytolacca americana antiviral protein (PAP) DNA
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 714)
AUTHORS Chen, G., Lei, J., Cao, B. and Zeng, G.
TITLE Phytolacca americana antiviral protein (PAP) DNA
JOURNAL Direct Submission
SUBMITTED (20-APR-2004) Horticultural College, South China
Agricultural University, Wushan, Guangzhou, Guangdong 510642, PR
China
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CDS <1..>714
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ORIGIN
Alignment Scores:
Pred. No.: 2.85e-53 Length: 714
Score: 596.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
Gaps: 0

US-09-978-274A-6 (1-154) x AY603352 (1-714)
Qy 2 IleAnthrIleThrPheAspAlaGlyAsnAlaThrIleAsnTyraAlaThrPheMet 21
Db 1 GTGAATCAATCATCTCAATGTTGAGATCCACATTAAGCAATAGCCACTTTCTG 60
Qy 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCyTYrGlyIleProMetLeu 41
Db 61 AATGATCTTGATATGAAGGAAAGATCCGAGTTAAATAGCTATGGAATACCAATGCTG 120
Qy 42 ProAnThrAsnSerThrProLysTyLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
Db 121 CCCAATCAATATCAATTCACAAAGTACGTGTGTTAGCTCCAAAGTTCCAAATTAATAA 180
Qy 62 ThrIleThrLeuMetLeuArgArgAsnAsnLeuTyraValMetGlyTySerAspProPhe 81
Db 181 ACCATCAACATTAATGCTGAGACGAAACAAATTTGATGTAGTGGTTATTCGATCCCTTT 240
Qy 82 AsnGlyAsnLysCyAspTyThrIleIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db 241 GAACCAATAAATGCTGTTACCATATCTTTATGATATCTCAGGTAAGCAAGCAAGAT 300
Qy 102 ValGluAnthrIleuCySerSerSerSerSerSerSerSerSerSerSerSerSer 121
Db 301 GTAAAGACTACTCTTTGCCAAATGCCAATCTCGTGTAGTAAACATTAACCTTGAT 360
Qy 122 SerLeuTyProThrMetGluLysLeuValAlaMetSerArgAsnGlnValGlnLeu 141
Db 361 AGTGATATTCACATTCGATTCGAAAGCGGAGTAAATCAAGAGTCAGTCCACTG 420
Qy 142 GlyIleGlnIleLeuSerSerSerSerSerSerSerSerSerSerSerSerSerSer 154
Db 421 GGAATTCATAATATCTGACAGTAATATTCGAAAGATTTCT 459
RESULT 13
AY547315 942 bp DNA linear PLN 13-JUL-2005
LOCUS Phytolacca americana antiviral protein gene, complete cds.
DEFINITION AY547315
ACCESSION AY547315
VERSION AY547315.1 GI:44889055
KEYWORDS
SOURCE Phytolacca americana (American pokeweed)
ORGANISM Phytolacca americana
Phytolacca americana; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE 1 (bases 1 to 942)
AUTHORS Zhao, Y., Wang, X., Zhou, G. and Li, H.
TITLE A pokeweed antiviral protein gene in roots of Phytolacca americana
JOURNAL Acta Virol. 48 (2), 131-132 (2004)
PUBMED 15462289
REFERENCE 2 (bases 1 to 942)
AUTHORS Zhao, Y., Wang, X. and Li, H.
TITLE Direct Submission
JOURNAL Submitted (11-FEB-2004) Plant Virology, Institute of Plant
Protection, CAAS, No.2 Yuanmingyuan Road West, Beijing 100094, P.R.
China
FEATURES
source location/Qualifiers
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CDS <1..>942
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VGIOILDSNIGKISGWSFTEKTEAREFLVLAIQWSEARFPIKINQVKTNNRAFPN

AUTHORS Lin, Q., Chen, Z.C., Antoniw, J.F. and White, R.F.
TITLE Isolation and characterization of a cDNA clone encoding the
JOURNAL anti-viral protein from Phytolacca americana
PUBMED Plant Mol. Biol. 17 (4), 609-614 (1991)
1912488
REFERENCE 2 (bases 1 to 1164)
AUTHORS Antoniw, J.F.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-1990) Antoniw, J.F., AFRC Inst of Arable Crops
Research, Dept. of Plant Pathology, Rothamsted Experimental
Station, Harpenden, Hert, AL5 2JQ, UK

FEATURES

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QLGIQILDSNIGISGVMSFTEKTEAEFLVAIQVSEARFKYIENQVKTNFRAFN
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CDS

gene

ORIGIN

Alignment Scores:

Pred. No.: 4,846-53 Length: 1164
Score: 596.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
DB: 15 Gaps: 0

US-09-978-274A-6 (1-154) x PAPAP (1-1164)

QY 2 ILeaenThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMet 21
DB :::::::::::::::::::::
68 GTGAATCAATCATCTCAATGTTGGAAGTACCAACATTAGCAATAACGCCCTTTCTG 127
QY 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeu 41
DB :::::::::::::::::::::
128 AATGATCTTCGTATGAAGCGAAGATCCAAAGTTTAAATGCTATGGAATACCAATGCTG 187
QY 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
DB :::::::::::::::::::::
188 CCATATCAAAATCAAAATCCAAAGTACGTTGTTGAGCTCCAAAGTTCAAAATAAAAA 247
QY 62 ThrIleThrLeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
DB :::::::::::::::::::::
248 ACCATCACTAAATGCTGAGCAAGAAACAATTTGTATGTGATGGTTATTCGATCCCTTT 307
QY 82 AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
DB :::::::::::::::::::::
308 GAACCAATTAATGTCGTTACCAATCTTAAATGATATCTCAGTTACTGAACGCCAAGAT 367
QY 102 ValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
DB :::::::::::::::::::::
368 GTAGAGACTACTCTTGGCCAAATGCCAATTCGCTGTTAGTAAACATAAATCTTGAT 427
QY 122 SerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAsnGlnValGlnLeu 141
DB :::::::::::::::::::::
428 AGTCATATCCAACTGTGAATCAAAAGCGGAGTAAATCAAGAAATCAAGTCCAACTG 487

QY 142 GlyIleGlnIleLeuSerSerSerAspIleGlyLysIleSer 154
DB :::::::::::::::::::::
488 GGAATTCAAATACTCGACAGTAATATTGAAAAGATTCT 526

Search completed: April 9, 2006, 07:31:32
Job time : 3518 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 9, 2006, 00:56:13 ; Search time 408.713 Seconds
(without alignments)
2511.204 Million cell updates/sec

Title: US-09-978-274A-6
Perfect score: 793
Sequence: 1 MINTTPDAGNATINKATP.....SRNOVGLQILSSDIGKIS 154

Scoring table:
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODL=frame+ p2n.model -DRV=xlh
-O=/abes/ABSWEB_spool/US09978274/runat_07042006_173031_28376/app.query.fasta.1
-Db=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes03h
-USER=US09978274 @CGN 1 1 144 @runat 07042006 173031 28376 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG -DRV-TIMEOUT=120
-MARK_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq 21: *
1: Geneseqn1980s: *
2: Geneseqn1990s: *
3: Geneseqn2000s: *
4: Geneseqn2001as: *
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6: Geneseqn2002as: *
7: Geneseqn2002bs: *
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9: Geneseqn2003bs: *
10: Geneseqn2003cs: *
11: Geneseqn2003ds: *
12: Geneseqn2004as: *
13: Geneseqn2004bs: *
14: Geneseqn2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	793	100.0	465	6	AAD42717 Pokeweed
2	793	100.0	792	6	AAD42716 Pokeweed
3	793	100.0	1092	6	AAD42729 Pokeweed
4	788	99.4	945	6	AAD42715 Pokeweed

5	613	77.3	882	2	AAT99556
6	596	75.2	1378	12	ADG76061
7	596	75.2	1379	3	AAZ45197
8	596	75.2	1379	3	AAZ59220
9	596	75.2	1379	4	AAZ87929
10	596	75.2	1379	6	AAD42738
11	596	75.2	1379	10	ADIO5787
12	595	75.0	1164	11	ADM74765
13	592	74.7	1164	11	ADM74751
14	590	74.4	1195	2	AAQ56672
15	588	74.1	1378	6	AAD42739
16	588	74.1	1379	3	AAZ59221
17	580	73.1	1195	2	AAQ81457
18	559.5	70.6	2472	2	AAQ43967
19	542.5	68.4	2369	2	AAZ99557
20	542.5	68.4	2369	2	ABA96543
21	463.5	58.4	918	2	AAQ64893
22	463.5	58.4	918	2	AAQ64782
23	344.5	43.4	603	2	ABA96547
24	301.5	38.0	600	2	ABA96716
25	261	32.9	934	3	AAZ45198
26	261	32.9	934	6	AAD42740
27	196.5	24.8	765	3	AAZ61131
28	196.5	24.8	984	3	AAZ61125
29	196.5	24.8	993	3	AAZ61128
30	196.5	24.8	999	3	AAZ61122
31	196.5	24.8	999	3	AAZ61119
32	191.5	24.1	864	1	AAW91504
33	190.5	24.0	804	2	AAQ53896
34	190.5	24.0	804	2	AAQ85385
35	190.5	24.0	804	2	AAQ99042
36	190.5	24.0	804	2	AAT17964
37	190.5	24.0	804	3	AAA12862
38	190.5	24.0	804	9	ACD67205
39	190.5	24.0	804	10	ADC34589
40	190.5	24.0	804	10	ADH92013
41	188.5	23.8	765	3	AAA12895
42	188.5	23.8	765	9	ACD27612
43	188.5	23.8	765	10	ADC34645
44	188.5	23.8	765	10	ADH92069
45	188.5	23.8	783	2	AAT18231

ALIGNMENTS

RESULT 1	
AAD42717	
ID	AAD42717 standard; DNA; 465 BP.
XX	
AC	AAD42717;
XX	
DT	15-NOV-2002 (first entry)
XX	
DE	Pokeweed PAP-Salpa protein encoding DNA.
XX	
KW	Neurotic effect; transgenic plant; antiviral protein; pokeweed; gene;
KW	PAP-Salpa; ds.
XX	
OS	Phytolacca americana.
XX	
FH	Key
FT	Location/Qualifiers
FT	1..465
FT	/*tag= a
FT	/product= "PAP-Salpa protein"
XX	
PN	WO200233107-A2.
XX	
PD	25-APR-2002.
XX	
PF	15-OCT-2001; 2001WO-GB004593.
XX	
PR	14-OCT-2000; 2000GB-00025217.
XX	

Aat99556	Phytolacc
Adg76061	American
Aaz45197	Wild-type
Aaz59220	Pokeweed
Aaz87929	P. americ
Aad42738	Pokeweed
Adio5787	DNA encod
Adm74765	HIV-1 inh
Adm74751	HIV-1 inh
Aag56672	Sequence
Aad42739	Pokeweed
Aaz59221	Variant p
AAQ81457	Phytolacc
AAQ43967	Pokeweed
AAZ99557	Pokeweed
ABA96543	Phytolacc
AAQ64893	Antiviral
AAQ64782	DNA pLMC2
ABA96547	Cloning v
ABA96716	Cloning v
Aaz45198	Wild-type
Aad42740	Pokeweed
AAZ61131	DNA encod
AAZ61125	DNA encod
AAZ61128	DNA encod
AAZ61122	DNA encod
AAZ61119	DNA encod
AAW91504	DNA of ri
AAQ53896	Saporin c
AAQ85385	Saporin c
AAQ99042	M13mp18-G
Aat17964	Saporin c
Aaa12862	Saporin D
Adc67205	Common so
Adc34589	Common so
ADH92013	DNA encod
AAA12895	Mammalian
Adc34645	Common so
Adh92069	Mammalian
Aat18231	Amplified

XX	PA	(ADRE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX	PI	Thomas CJR, Mcpherson MJ, Atkinson HU, Neelam A;
XX	DR	WPI; 2002-489891/52.
XX	DR	P-PsDB; AA25920.
XX	PT	Inducing necrotic effect in specific cells of plant by transforming plant
XX	PT	with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX	PT	which acts in response to application of specific stimulus to plant.
XX	ES	Claim 3, Page 77; 87pp; English.
XX	CC	The invention relates to a method of inducing a necrotic effect in
XX	CC	specific cells of a plant. The method involves transforming the plant
XX	CC	with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX	CC	PAP, PAPIT and PAP-S, where the gene(s) comprises a promoter which acts
XX	CC	in response to the application of a specific stimulus to the plant so as
XX	CC	to facilitate expression of the pokeweed antiviral protein in specific
XX	CC	cells of the plant. The method is useful for inducing a necrotic effect
XX	CC	in specific cells of a plant. The present sequence is pokeweed PAP-Salpa
XX	CC	protein encoding DNA
XX	SQ	Sequence 465 BP; 165 A; 97 C; 76 G; 127 T; 0 U; 0 Other;
XX	Alignment Scores:	
XX	Pred. No.:	1,42e-91
XX	Score:	793.00
XX	Percent Similarity:	100.08
XX	Best Local Similarity:	100.08
XX	Query Match:	100.08
XX	DB:	6
XX		Gaps:
XX		0
XX	US-09-978-274A-6 (1-154) x AAD42717 (1-465)	
QY	1	MetIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnIleSTyTAlaThrPhe 20
DB	1	ATGATATAAATACATCATCCCTTTGATGCTGGAAAGCCACCACTTAACAATATGACACCTTT 60
QY	21	MetGluSerLeuArgAsnGlnAlaIleAspProIleLeuIleCysTyTgIlePProMet 40
DB	61	ATGGAAATCTCTTCGTATATCAAGGAAGAATCCAAACTAATAAGTCATATGCCAATG 120
QY	41	LeuProAspThrAsnSerThrProIleSTyTLeuLeuValIleLeuGlnIleAlaAsnLeu 60
DB	121	CTACCTGATACATTAATTCGACCCCTTAAGTCTTATTTGGTTAAAGTCCCAAGGTGCAAACTTA 180
QY	61	LysThrIleThrLeuMetLeuArgAsnAsnLeuTyTAlaMetGlyTyrSerAspPro 80
DB	181	AAAAACATTAACATTAATGCTGAGACGCAAAATTAATTAACGTAAAGGGCTATTTGATCCC 240
QY	81	PheAsnGlyAsnIleCysArgTyrAlaIlePheAsnAspIleThrSerThrGluArgThr 100
DB	241	TTCAATATGCAATTAAGTGTGCTTACCATATATTTAATGATATTTCAGACCAAGGCACT 300
QY	101	AspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTyr 120
DB	301	GATGGAGAAATTAATCTTTGCTCAAGTTCTAGATTCCTCGGTTCGAATGTCCATTAATCTAC 360
QY	121	AsnSerLeuTyrProThrMetGluIleValAlaGluValAsnSerArgAsnGlnValGln 140
DB	361	AAATGCTTATATCCGACCAATGAGAAAGCAAGAGTAATCAAGTAATCAAGTCCAA 420
QY	141	IleuGlyIleGlnIleLeuSerSerAspIleGlyIleSer 154
DB	421	TTGGGAATTCGAATATCTCAGACAGTGCATTTGAAAAATCTCT 462
XX	RESULT 2	
XX	AAD42716	
XX	ID	AAD42716 standard; DNA; 792 BP.
XX	AC	AAD42716;
XX	XX	

DT	15-NOV-2002 (first entry)
XX	Pokeweed mature PAP-S protein encoding DNA.
DE	Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KW	gene; ds.
KX	Phytolacca americana.
OS	
XX	
FH	Key Location/Qualifiers
FT	CDS 1..792
FT	/tag= a
FT	/product= "Mature PAP-S protein"
FT	primer_bind 1..29
FT	/tag= b
FT	/bound_moiety= "Primer PS1BP"
FT	primer_bind complement(436..462)
FT	/tag= c
FT	/bound_moiety= "Primer PS1SR"
FT	primer_bind 463..492
FT	/tag= d
FT	/bound_moiety= "Primer PS2BP"
FT	misc_feature 681..686
FT	/tag= e
FT	/note= "Sequence replacing removed XbaI site"
FT	primer_bind complement(765..792)
FT	/tag= f
FT	/bound_moiety= "Primer PS2SR"
PN	MO20023107-AZ.
PD	25-APR-2002.
PF	15-OCT-2001; 2001WO-GB004593.
PR	14-OCT-2000; 2000GB-00025217.
XX	(ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
PA	Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;
PI	WPI; 2002-489891/52.
DR	P-PSDB; AA625919.
XX	
PT	Inducing necrotic effect in specific cells of plant by transforming plant
PT	with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT	which acts in response to application of specific stimulus to plant.
XX	
PS	Claim 2; Page 76; 87pp; English.
XX	
CC	The invention relates to a method of inducing a necrotic effect in
CC	specific cells of a plant. The method involves transforming the plant
CC	with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC	PAP ¹ , PAP ^{II} and PAP-S, where the gene(s) comprises a promoter which acts
CC	in response to the application of a specific stimulus to the plant so as
CC	to facilitate expression of the pokeweed antiviral protein in specific
CC	cells of the plant. The method is useful for inducing a necrotic effect
CC	in specific cells of a plant. The present sequence is pokeweed mature PAP-
CC	S protein encoding DNA
SQ	Sequence 792 BP; 268 A; 161 C; 151 G; 212 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	3,06e-91 Length: 792
Score:	793.00 Matches: 154
Percent Similarity:	100.0% Conservative: 0
Best Local Similarity:	100.0% Mismatches: 0
Query Match:	100.0% Indels: 0
DB:	Gaps: 0
US-09-978-274A-6 (1-154) x AAB42716 (1-792)	
QY	1 NecTleantnrltThPheasaplaaglyaaMaJaThrlleaenlystYzralatnrPhe 20

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Db 1 ATGATTAATAATACATCACTTTGATGCTGGAAATGACCACTTAACAAATATGCGACCTTT
Qy 21 MetGluSerLeuArgAsnGlnAlaIysAspProIyLeuIysCysErgIylLeuProMet 40
Db 61 ATGGAAATCTCTTGATATACAGGAAAGATCCAAAATCAAATGATGATGCGATACCAATG 120
Qy 41 LeuProAspThrAsnSerThrProIySylYrLeuLeuValIysLeuGlnGlnIylAlaAsnLeu 60
Db 121 CTACCTGATACCTAAATTGACCCCTTAAGTACTTATGTTAGCTCCAAAGTCCAAACCTA 180
Qy 61 LysThrIleThrLeuMetLeuArgArgAsnAsnLeuYrValMetGlyYrSerAspPro 80
Db 181 AAACCATTAACATATGCTAGAGACGAATTAACCTTAATAGTATGCGATATCTGATCCC 240
Qy 81 PheAsnGlyAsnIySylCysArgYrHisIlePheAsnAspIleThrSerThrGluArgThr 100
Db 241 TTCAATGGCAATTAAGTGTGCTTACCAATATTAATTAATTAACAGCACCAAGCGCACT 300
Qy 101 AspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnYr 120
Db 301 GATGTGGAATTAATCTTTGCTCAAGTTCTAGTTCTCGGTGCAATGCTCAATTAACCTAC 360
Qy 121 AsnSerLeuYrProThrMetGluIySylValIysIleValAsnSerArgAsnGlnValGln 140
Db 361 AATAGCTTAATATCCAGCATGAGAAAGAAAGCAAGAACTCAAGAAATCAAGTCCAA 420
Qy 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyIylSer 154
Db 421 TTGGGAATTCAAATATCTCAGCAGTACATGGAAATAATCTCT 462
```

```
RESULT 3
AAD42729
ID AAD42729 standard; DNA; 1092 BP.
```

```
AC AAD42729;
XX 29-AUG-2003 (revised)
DT 15-NOV-2002 (first entry)
XX
XX Pokeweed PAP-S/rice cystatin delta D86 fusion DNA.
XX
XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
XX Km chimeric; rice; cystatin delta D86; NIA protease cleavage site; PCS; de.
XX
XX Phytolacca americana.
XX OS Oryza sativa.
XX OS Tobacco; Etch virus.
XX OS Chimeric.
XX
XX Key
XX FT primer_bind
XX FT 1..29
XX FT /tag= a
XX FT /bound_moiety= "Primer PS1BP"
XX FT misc_feature
XX FT 681..686
XX FT /tag= b
XX FT /note= "Modified XbaI site"
XX FT primer_bind
XX FT complement(742..786)
XX FT /tag= c
XX FT /bound_moiety= "Primer PCS-PAPSR"
XX FT 766..806
XX FT /tag= d
XX FT /bound_moiety= "Primer PCS-Delta86P"
XX FT 766..786
XX FT /tag= e
XX FT /note= "TEV NIA protease cleavage site"
XX FT primer_bind
XX FT complement(1066..1092)
XX FT /tag= f
XX FT /bound_moiety= "Primer SYNPOTDelta86P"
XX
XX WO200233107-A2.
XX
XX 25-APR-2002.
```

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XX
PF 15-OCT-2001; 2001WO-GB004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX WPI, 2002-489891/52.
```

```
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
XX PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX PT which acts in response to application of specific stimulus to plant.
```

```
XX
XX Disclosure; Page 83; 87pp; English.
```

```
XX
XX The invention relates to a method of inducing a necrotic effect in
XX CC specific cells of a plant. The method involves transforming the plant
XX CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX CC PAP', PAPRI and PAP-S, where the gene(s) comprises a promoter which acts
XX CC in response to the application of a specific stimulus to the plant so as
XX CC to facilitate expression of the pokeweed antiviral protein in specific
XX CC cells of the plant. The method is useful for inducing a necrotic effect
XX CC in specific cells of a plant. The present sequence is a fusion DNA. This
XX CC sequence comprises pokeweed pro-PAP-S DNA, rice cystatin delta D86 DNA
XX CC on 29-AUG-2003 to standardise OS field)
```

```
XX
XX SQ Sequence 1092 BP; 369 A; 195 C; 222 G; 306 T; 0 U; 0 Other;
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Alignment Scores:

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Pred. No.: 4.87e-91 Length: 1092
Score: 793.00 Matches: 154
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0
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US-09-978-274a-6 (1-154) x AAD42729 (1-1092)
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Qy 1 MetIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnIylYrAlaThrPhe 20
Db 1 ATGATTAATAATACATCACTTTGATGCTGGAAATGACCACTTAACAAATATGCGACCTTT 60
Qy 21 MetGluSerLeuArgAsnGlnAlaIysAspProIyLeuIysCysErgIylLeuProMet 40
Db 61 ATGGAAATCTCTTGATATACAGGAAAGATCCAAAATCAAATGATGATGCGATACCAATG 120
Qy 41 LeuProAspThrAsnSerThrProIySylYrLeuLeuValIysLeuGlnGlnIylAlaAsnLeu 60
Db 121 CTACCTGATACCTAAATTGACCCCTTAAGTACTTATGTTAGCTCCAAAGTCCAAACCTA 180
Qy 61 LysThrIleThrLeuMetLeuArgArgAsnAsnLeuYrValMetGlyYrSerAspPro 80
Db 181 AAACCATTAACATATGCTAGAGACGAATTAACCTTAATAGTATGCGATATCTGATCCC 240
Qy 81 PheAsnGlyAsnIySylCysArgYrHisIlePheAsnAspIleThrSerThrGluArgThr 100
Db 241 TTCAATGGCAATTAAGTGTGCTTACCAATATTAATTAATTAACAGCACCAAGCGCACT 300
Qy 101 AspValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnYr 120
Db 301 GATGTGGAATTAATCTTTGCTCAAGTTCTAGTTCTCGGTGCAATGCTCAATTAACCTAC 360
Qy 121 AsnSerLeuYrProThrMetGluIySylValIysIleValAsnSerArgAsnGlnValGln 140
Db 361 AATAGCTTAATATCCAGCATGAGAAAGAAAGCAAGAACTCAAGAAATCAAGTCCAA 420
Qy 141 LeuGlyIleGlnIleLeuSerSerAspIleGlyIylSer 154
Db 421 TTGGGAATTCAAATATCTCAGCAGTACATGGAAATAATCTCT 462
```

```
RESULT 4
AAd42715
ID AAd42715 standard; DNA; 945 BP.
XX
XX AAd42715;
AC
XX 15-NOV-2002 (first entry)
DT
XX
DE Pokeweed pro-PAP-S protein encoding DNA.
XX
XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KM gene; ds.
XX
XX Phytoacca americana.
OS
XX
XX Key Location/Qualifiers
FH 1..945
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FT /product= "Pro-PAP-S protein"
FT primer_bind 1..24
FT /*tag= b
FT /bound_molecly= "Primer PPS1BF"
FT complement(735..776)
FT primer_bind /*tag= c
FT /bound_molecly= "Primer PSXDR"
FT 736..777
FT /*tag= d
FT /bound_molecly= "Primer PSXDP"
FT 750..759
FT /*tag= e
FT /note= "Sequence replacing removed XbaI site"
FT primer_bind complement(922..945)
FT /*tag= f
FT /bound_molecly= "Primer PPS2BR"
XX
XX WO200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-GB004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;
PI
XX WPI; 2002-489891/52.
DR
XX P-PSDB; AAE25918.
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT which acts in response to application of specific stimulus to plant.
XX
XX Claim 24; Page 73-74; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
CC specific cells of a plant. The method involves transforming the plant
CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
CC in response to the application of a specific stimulus to the plant so as
CC to facilitate expression of the pokeweed antiviral protein in specific
CC cells of the plant. The method is useful for inducing a necrotic effect
CC in specific cells of a plant. The present sequence is pokeweed pro-PAP-S
CC protein encoding DNA
XX
XX SQ Sequence 945 BP; 307 A; 187 C; 180 G; 271 T; 0 U; 0 Other;
XX
Alignment Scores: 1.72e-90 Length: 945
Pred. No.: 788.00 Matches: 153
Score: 100.0% Conservative: 0
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 100.0%
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Query Match: 99.4% Indels: 0
DB: 6 Gaps: 0
US-09-978-274A-6 (1-154) x AAd42715 (1-945)
OY 2 ILeaAnthrilleThrePheAaPaIaGlyAaNaIaThrIleAaNYTYraIaThrPheMet 21
Db 73 ATAAATACGATCACTTGTGATGCGAAATGCCACCTTAACAAATATGCGACCTTATG 132
OY 22 GluSerLeuArgAngIaIaIyAaAPProLyLeuLeuCySTYrGIyIleProMetLeu 41
Db 133 GAATCTCTGTAATCAAGGAAAGATCAAAACTAAATGCTATGCGATACCAATGCTA 192
OY 42 ProAeThraAaSerThrProLyTYrLeuLeuValIySbeuGInGIyAlaAaNYLeuLyS 61
Db 193 CCGATATCAATTCAGACCCCTTAAGTACTTATGTTAAGCTCCAGGTGCAAACTTAAA 252
OY 62 ThrIleThreLeuMetLeuAArgAaAaNYLeuTYrValMetGIYTYrSerAaPProPhe 81
Db 253 ACCATTACACTAAATGCTGAGACGAAATTAACCTTAACGTATGCGCTATTCGATCCCTTC 312
OY 82 AaNGIyAaNYLySCyAaGTyTHaIlePheAaAaPPIleThraSerThrGuaArgThraSP 101
Db 313 AATGGCAATAGAGTGTCTTACCATATTAATGAATATTCAGACACGAAAGCACTGAT 372
OY 102 ValGIuAaNYThreLeuCySbeSerSerSerSerArgValAlaMetSerIleAaNYThraSN 121
Db 373 GTGAGAAATACCTCTTCTCAAGTTCTAGTTCTGCTTGTGCAAGTGCATTAACTACAT 432
OY 122 SerLeuTYrProThrMetGIuLyGIyAlaGIuValAaSerArgAngIaIaGIuLeu 141
Db 433 AGCTTATATCCGACCATGAAAGAAAGAAAGTAACATCAAGAAATCAAGTCCAATTG 492
OY 142 GlyIleGIuIleLeuSerSerAaPPIleGIyIySerIleSer 154
Db 493 GGAATCAAAATACCTACGACAGTGAATGAGAAAATCTCT 531
RESULT 5
AAT99556
ID AAT99556 standard; DNA; 882 BP.
XX
XX AAT99556;
AC
XX 17-OCT-2003 (revised)
DT 08-JUN-1998 (first entry)
XX
XX Phytoacca insularis antiviral protein gPIP2 gene.
DE
XX
XX Antiviral protein; gPIP2 gene; virucide; transgenic plant;
KW virus resistance; immunocjugate; AIDS; cancer; therapy; ss.
XX
XX OS
XX Phytoacca insularis; Nakai.
XX
XX Key Location/Qualifiers
FH 1..882
FT /*tag= a
FT CDS /transl_except= (pos:715..717, aa:Ile)
XX
XX BP808902-A2.
XX
XX 26-NOV-1997.
XX
XX 30-SBP-1996; 96EP-00307159.
XX
XX 22-MAY-1996; 96KR-00017404.
XX
XX (JINR-) JIN RO LTD.
XX
XX Moon Y, Choi J, Yun Y, Jin J, Hong E, Lee J, Choi K, Lee J;
PI Song S, Choi Y, Kim C, Kim M;
XX
XX WPI; 1998-001788/01.
DR P-PSDB; AAW26773.
```


XX Antiviral proteins of Phytoecia insularis Nakai and their genes - useful
PT in plant antiviral agents and immunocoujugates for the treatment of AIDS
PR and cancer.

PS Claim 2; Page 10-12; 26pp; English.

XX This polynucleotide comprises the coding region of the Phytoecia
CC insularis Nakai gene coding for a 32.8 kDa novel antiviral protein
CC designated GP12 (see AAM26773). The GP12 gene was isolated from leaf
CC genomic DNA by PCR amplification (see AAT99558-59). Another gene (see
CC AAT99557), encoding a 35.7 kDa protein (see AAM26774) designated GP150,
CC has also been isolated from P. insularis Nakai. Also claimed are vectors
CC encoding these antiviral proteins and host cells transformed or
CC transfected with these vectors. R. coli XL1-Blue MRP, GP12 (KCCM-10080)
CC host cells are claimed, as is a process for preparing antiviral protein
CC bodies. The antiviral proteins and recombinant proteins inhibit protein
CC synthesis. They can be used as active ingredients of antiviral agents of
CC plant viruses, and employed in the manufacture of immunocoujugates for
CC the treatment of AIDS and cancer. The isolated genes can be used in the
CC breeding of transgenic plants having viral resistance. (Updated on 17-OCT
CC -2003 to standardise OS field)

SQ Sequence 882 BP; 301 A; 164 C; 174 G; 243 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,678-68 Length: 882
Score: 613.00 Matches: 114
Percent Similarity: 87.7% Conservative: 21
Best Local Similarity: 74.0% Mismatches: 19
Query Match: 77.3% Indels: 0
DB: 2 Gaps: 0

US-09-978-274a-6 (1-154) x AAT99556 (1-882)

QY 1 MetLeaenhrilrlethPheAspAlaGlyAsnAlarhrileAsnlyeTyraLarhrPhe 20
DB 1 ATGGGATATCCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 60
QY 21 MetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrglyLePromet 40
DB 61 CTGATATATCTTCGTAATGAAGCAAAACATCCAGCTTAAATGCTAATGAAATACCAATG 120
QY 41 LeuProAspThrAsnSerThrProLysTyrlleuValLysLeuGlnGlyAlaAsnLeu 60
DB 121 TTGCCCATATCAAAATCCAAATCCAAAGTACGTTGTTAGCTCCAAAGTTCAATATA 180
QY 61 LysThrilethrleuMetleuArgAsnAsnLeuTyraLmetGlyTyrSerAspPro 80
DB 181 AAAACCATCACATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 240
QY 81 PheAsnGlyAsnLysCysArgTyrllePheAsnAspillethrSerThrGluArgThr 100
DB 241 TTTGATACCAATATGATGTTACCATATCTTAAATGATATCTCAAGTACGAAGCCAA 300
QY 101 AspValGluAsnThrleuCysSerSerSerSerSerArgValAlaMetSerilleAsnTy 120
DB 301 GATGTAGACCTACTCTTTCGCAATCCCAATCTTCGTTGTAATAAATCAATAACTAT 360
QY 121 AsnSerLeuTyrrProthMetGluLysLysAlaGluValAsnSerArgAsnGlnValGln 140
DB 361 GATGTGATATCCAAATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 420
QY 141 LeuGlyilleGlnilleuSerSerAspilleGlyLysilleSer 154
DB 421 CTGGGAATTCAAATATCTGACAGTGAATGGAAGATTCT 462

RESULT 6
ADG76061
ID ADG76061 standard; DNA; 1378 BP.
XX
AC ADG76061;

XX 11-MAR-2004 (first entry)
DT American pokeweed antiviral protein (PAP) DNA Segid 1.
XX

XX gene; ds; pokeweed antiviral protein; PAP; HIV-1; anti-HIV; antiviral;
KW nucleoside analogue inhibitor; viral protease inhibitor; viral infection;
XX american pokeweed; retroviral.

OS Phytoecia americana.

XX WO2003106479-A2.

XX 24-DEC-2003.

XX 17-JUN-2003; 2003WO-US019141.

XX 17-JUN-2002; 2002US-0389649P.

XX (PARK-) PARKER HUGHES INST.

XX Uckun FM;

XX WPI; 2004-082156/08.

XX P-PSDB; ADG76064.

PT Novel modified pokeweed antiviral protein useful for inhibiting viral
PT replication, for inducing depurination of viral RNA, or for treating
PT viral infection in subject.

XX Example 2; SEQ ID NO 1; 62pp; English.

CC This invention relates to novel modified pokeweed antiviral proteins
CC (PAPs). Specifically, it refers to modifications relative to wild-type
CC PAP that confer increased activity towards viral RNA, particularly
CC retroviral RNA such as HIV-1 and drug resistant HIV-1. Furthermore,
CC modified PAP also exhibits decreased activity towards ribosomal RNA
CC relative to wild-type PAP. The present invention describes a molecular
CC model of PAP-HIV RNA interactions that have been used for the rational
CC redesign of PAP mutants with potent anti-HIV activity, where
CC modifications have been introduced in regions other than the active site.
CC Accordingly, these mutants represent antiviral agents that can work as
CC nucleoside analogue inhibitors of reverse transcriptase, as well as viral
CC protease inhibitors that can be used for treating viral infections. As
CC such, they are useful for inhibiting viral replication and for
CC depriving viral RNA. This polynucleotide sequence is of the DNA encoding
CC the wild type american pokeweed antiviral protein (PAP) of the invention.

SQ Sequence 1378 BP; 487 A; 234 C; 268 G; 389 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,046-65 Length: 1378
Score: 596.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
DB: 12 Gaps: 0

US-09-978-274a-6 (1-154) x ADG76061 (1-1378)

QY 2 IleAsnhrilrlethPheAspAlaGlyAsnAlarhrileAsnlyeTyraLarhrPheMet 21
DB 290 GTGAATTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 349
QY 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrglyLePrometLeu 41
DB 350 AATGATCTTCGTAATGAAGCAAAAGTATCAAGTTAAATGCTAATGAAATCAATCTG 409
QY 42 ProAspThrAsnSerThrProLysTyrlleuValLysLeuGlnGlyAlaAsnLeuLys 61
DB 410 CCAATACCAATATCAAAATGATGTTGTTGAGCTCCAAAGTTCAATAAATAAAA 469
QY 62 ThrilethrleuMetleuArgAsnAsnLeuTyraLmetGlyTyrSerAspProPhe 81

```

D 470 ACCATCAACATTAAGCTGAGAGCGAACAATTGTATGATGGGTATTATTCGATCCCTTT 529
Q 82 AenGlyanLysCybaGTYrHieIlePheAenAapIleHrSerThnGluArqThnAsp 101
D 530 GAAACCAATTAATATCGTTACCATATCTTTATGATATCTCAGGACTGAAACGCGCAAGAT 589
Q 102 ValGluAenThrLeuCySerSerSerSerSerArgValAlaMetSerIleAenTyraSn 121
D 590 GTAGAGACTACTCTTTGCCCCAATGCGCAATTCGCTGTAGTAAACATTAACCTTGAT 649
Q 122 SerLeuTyProThrMetGluLysAlaGluValAenSerArgAenGlnValGlnLeu 141
D 650 AGTCGATATCCAACTTGGAATCAAAAGCGGAGATAAATCAAGAACTCAGTCCAACTG 709
Q 142 GlyIleGlnIleLeuSerSerAapIleGlyLysIleSer 154
D 710 GGAATTCAAATATCTGACAGTAATATTCGAAAGATTCT 748

RESULT 7
AAZ45197
ID AAZ45197 standard; DNA; 1379 BP.
AC AAZ45197;
DT 29-FEB-2000 (first entry)
XX
XX
XX wild-type pokeweed antiviral protein (PAP) nucleotide sequence.
XX
XX
XX Pokeweed antiviral protein; PAP; PAP II; antifungal; transgenic plant;
XX ribosome inhibiting protein; RIP; cereal crop; viral resistance; PVX;
XX potato virus X; cucumber mosaic virus; CMV; ss;
XX tomato yellow leaf curl virus.
XX
XX Phytolacca americana.
XX
XX
XX Key Location/Qualifiers
XX CDS 225..1166
XX /tag= a
XX /product= "PAP"
XX /note= "Pokeweed antiviral protein"
XX
XX
XX MO9960843-A1.
XX
XX
XX 02-DEC-1999.
XX
XX 21-MAY-1999; 99WO-US011301.
XX
XX 22-MAY-1998; 98US-0086374P.
XX
XX (RUTP ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX
XX Turner NE, Wang P;
XX
XX WPI; 2000-062555/05.
XX P-PSDB; AAY58025.
XX
XX New antiviral DNA useful for generating transgenic plants resistant to
XX viruses and/or fungi.
XX
XX Example; Page 4-5; 43pp; English.
XX
XX This is the Pokeweed antiviral protein (PAP) nucleotide sequence. PAP is
XX a type I ribosome-inhibiting protein (RIP) found in the cell walls of
XX Phytolacca americana (pokeweed). It is a single polypeptide chain that
XX catalytically removes a specific adenine residue from a highly conserved
XX stem-loop structure in the 28S rRNA of eukaryotic ribosomes. The pokeweed
XX antiviral protein II (PAP II) protein confers antiviral and or antifungal
XX activities to plants. A DNA molecule encoding a PAP II protein with an
XX intact catalytic active site amino acid residue (E172) is useful for
XX generating transgenic plants. PAP II DNA is useful for generating a
XX transgenic plants (especially cereal crops) through transforming a
XX protoplast or introducing the DNA directly into a plant part prior to
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CC regeneration. Cells and seeds which exhibit anti-viral and/or anti-fungal
CC activity thus have increased resistance to viruses and/or fungi. Viruses
CC include potato virus X (PVX), cucumber mosaic virus (CMV), and tomato
CC yellow leaf curl virus, and fungi include Pythium, Phytophthora,
CC Sclerotinia and Aspergillus. PAP II proteins also confer resistance to
CC other plants pests including insects, bacteria and nematodes. PAP II DNA
CC is also useful for identifying a PAP II protein having reduced
CC cytotoxicity. PAP II has a reduced cytotoxicity compared to PAP, so
CC unlike PAP transgenic plants which are stunted and sterile, PAP II
CC transgenic plants have a normal and fertile phenotype
XX
XX
XX Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 1,04e-65 Length: 1379
XX Score: 596.00 Matches: 110
XX Percent Similarity: 86.9% Conservative: 23
XX Best Local Similarity: 71.9% Mismatches: 20
XX Query Match: 75.2% Indels: 0
XX DB: 3 Gaps: 0
XX
XX US-09-978-274a-6 (1-154) x AAZ45197 (1-1379)
Q 2 IleAenThrIleThrPheAenAlaGlyAenAlaThrIleAenLysTyraIeThrPheMet 21
D 291 GTGAATCAATCAATCAATCAATGTTGGAAGTACCAACCATTAAGCAATGCTTCTG 350
Q 22 GluSerLeuArgAenGlnAlaLysAenProLysLeuLysCybTYrGlyIleProMetLeu 41
D 351 AATGATCTTCGTAATGGAAGCGAAGATCCAAAGTTTAAATGCTAATGGAATTCATGCTG 410
Q 42 ProAenThrAenSerThrProLysTyLeuLeuValLysLeuGlnGlyAlaAenLys 61
D 411 CCCAATCAATCAATCAATCCAAAGTACGTGTGTTAGCTCCAAAGTCCAAATTAATAA 470
Q 62 ThrIleThrLeuMetLeuArgAenAenLysLeuTyraIeGlyTySerAenProPhe 81
D 471 ACCATCAACATTAAGCTGAGAGCGAACAATTGTATGATGGGTATTATTCGATCCCTTT 530
Q 82 AenGlyanLysCybaGTYrHieIlePheAenAapIleHrSerThnGluArqThnAsp 101
D 531 GAAACCAATTAATATCGTTACCATATCTTTATGATATCTCAGGACTGAAACGCGCAAGAT 590
Q 102 ValGluAenThrLeuCySerSerSerSerSerArgValAlaMetSerIleAenTyraSn 121
D 591 GTAGAGACTACTCTTTGCCCCAATGCGCAATTCGCTGTAGTAAACATTAACCTTGAT 650
Q 122 SerLeuTyProThrMetGluLysAlaGluValAenSerArgAenGlnValGlnLeu 141
D 651 AGTCGATATCCAACTTGGAATCAAAAGCGGAGATAAATCAAGAACTCAGTCCAACTG 710
Q 142 GlyIleGlnIleLeuSerSerAapIleGlyLysIleSer 154
D 711 GGAATTCAAATATCTGACAGTAATATTCGAAAGATTCT 749

RESULT 8
AAZ59220
ID AAZ59220 standard; cDNA; 1379 BP.
AC AAZ59220;
DT 20-APR-2000 (first entry)
XX
XX
XX Pokeweed antiviral protein coding sequence spring leaf form.
XX
XX
XX Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
XX resistance; potato virus X; potato virus Y; potato leaf roll virus;
XX tuber; ss.
XX
XX Phytolacca americana.
XX
XX US6015940-A.
```

PD 18-JAN-2000.
 XX
 PF 07-APR-1992; 92US-00865169.
 XX
 PR 07-APR-1992; 92US-00865169.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Kaniewski WK, Turner NE, Lodge JK,
 XX
 DR WPI; 2000-126326/11.
 XX
 PT Production of transgenic potato plants or tubers expressing pokeweed
 PT antiviral protein which are resistant to potato virus X or Y.
 XX
 PS Claim 6; Fig 4; 30pp; English.
 XX
 CC This is the coding sequence for the spring leaf form of the pokeweed
 CC antiviral protein (PAP) which is used to generate transgenic potato
 CC plants. PAP is able to confer resistance to infection by potato virus X
 CC (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in the
 CC potato plant or tuber expressing PAP
 XX
 SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.04e-65 Length: 1379
 Score: 596.00 Matches: 110
 Percent Similarity: 86.9% Conservative: 23
 Best Local Similarity: 71.9% Mismatches: 20
 Query Match: 75.2% Indels: 0
 DB: Gaps: 0
 US-09-978-274A-6 (1-154) x AAC59220 (1-1379)
 QY 2 ILeaAntHrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMet 21
 DB 291 GTGAATCAATCATCTACATGTTGGAAGTACCACTTACCAATACGCGCACTTTCTG 350
 QY 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIlePrometLeu 41
 DB 351 AATGATCTTCGTAATGAAGCGAAGATCCAGTTAAATGCTATGGAATACCAATGCTG 410
 QY 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
 DB 411 CCCAATCAATACCAATCCAAAGTACCTGTTGGTGAAGCTCCAGGTTCAATTAATAA 470
 QY 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
 DB 471 ACCATCACTAATAGCTGAGAGCAAAACAATTGTATGTAGAGGGTTATTCGATCCCTT 530
 QY 82 AsnGlyAsnLysCysAspGlyThrIlePheAsnAspIleThrSerThrGluArgThrAsp 101
 DB 531 GAAACCAATTAATGCTGTTACCATATCTTATATGATATCAAGGTACGAAGCCCAAGAT 590
 QY 102 ValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
 DB 591 GTAGAGACTACTCTTGGCCAAATGCCAATCTCGTGTAGTAAATAACAATAACTTGTAT 650
 QY 122 SerLeuTyrProThrMetGlnLysLysAlaGluValAsnSerArgAsnGlnValGlnLeu 141
 DB 651 AGTGAATATCCAAATTCGAATGCAAAAGCGGAAGTAAATCAAGAAGTCAGTCCAACTG 710
 QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
 DB 711 GGAATTCAAATATCTGACAGTAATATGTGAAGAATTTCT 749
 RESULT 9
 AAC87929 standard; DNA; 1379 BP.
 ID AAC87929
 XX AAC87929;
 AC AAC87929;
 XX

DT 06-MAR-2001 (first entry)
 XX
 DE P. americana pokeweed antiviral protein encoding DNA SEQ ID NO:1.
 XX
 KW Phytolecta americana; pokeweed; pokeweed antiviral protein; PAP; cancer;
 KW biotherapeutic; fusion protein; immunocjugate; mutant; cytostatic;
 KW anti-HIV; human immunodeficiency virus; AIDS; leukemia; lymphoma;
 KW brain tumour; neuroblastoma; soft tissue sarcoma; osteosarcoma; ss.
 XX
 OS Phytolecta americana.
 XX
 FH Key Location/Qualifiers
 FT CDS 225..1166
 FT /tag=a
 FT /product="pokeweed antiviral protein (PAP)"
 XX
 XX US6146628-A.
 XX
 XX 14-NOV-2000.
 XX
 XX 11-JUL-1995; 95US-00501253.
 XX
 XX 11-JUL-1995; 95US-00501253.
 XX
 XX (MINU) UNIV MINNESOTA & RUTGERS.
 XX (UNNE-) UNIV STATE NEW JERSEY.
 XX
 XX Uckun FM, Turner NE;
 XX
 XX WPI; 2001-040422/05.
 XX P-PSDB; AAB36500.
 XX
 XX Immunocjugates useful for treating cancer and acquired immunodeficiency
 PT syndrome, comprises mutant pokeweed anti-viral protein and a targeting
 PT moiety that binds a cell surface receptor.
 XX
 PS Disclosure; Col 47-50; 32pp; English.
 XX
 CC The present invention describes a fusion protein or an immunocjugate
 CC (1), comprising mutant Pokeweed Anti-viral protein (PAP) having an amino
 CC acid substitution at residue 75, 97 or 176 of native PAP and a targeting
 CC moiety that binds a cell surface receptor. (1) can have cytostatic and
 CC anti-HIV activities, and is an inhibitor of cellular RNA or protein
 CC synthesis. (1) is useful for treating AIDS and cancers including
 CC leukemia, lymphoma, a brain tumour, neuroblastoma, osteosarcoma, soft
 CC tissue sarcoma, breast, prostate, ovarian, testicular, melanoma, lung, or
 CC colon cancer. Immunocjugates prepared using PAP mutants exhibit an
 CC improved therapeutic index over immunocjugates containing either wild-
 CC type PAP or variant PAP. The present sequence encodes the wild-type PAP,
 CC which is given in the exemplification of the present invention
 XX
 SQ Sequence 1379 BP; 488 A; 234 C; 268 G; 389 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.04e-65 Length: 1379
 Score: 596.00 Matches: 110
 Percent Similarity: 86.9% Conservative: 23
 Best Local Similarity: 71.9% Mismatches: 20
 Query Match: 75.2% Indels: 0
 DB: Gaps: 0
 US-09-978-274A-6 (1-154) x AAC87929 (1-1379)
 QY 2 ILeaAntHrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMet 21
 DB 291 GTGAATCAATCATCTACATGTTGGAAGTACCACTTACCAATACGCGCACTTTCTG 350
 QY 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIlePrometLeu 41
 DB 351 AATGATCTTCGTAATGAAGCGAAGATCCAGTTAAATGCTATGGAATACCAATGCTG 410
 QY 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
 DB 411 CCCAATCAATACCAATCCAAAGTACCTGTTGGTGAAGCTCCAGGTTCAATTAATAA 470

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Db 411 CCCAATACAAATACAAATCCAAAGTAGCTGTTGGTTGAGCTCAAGGTTCAATATAAAAA 470
Qy 62 ThrIleThrlleuMetLeuAArgAAsnLeuTyValMetGlyTyrSerAspProPhe 81
Db 471 ACCATTCACACTAAATGCTGAGACGAAACAAATTTGATGTGANGGGTTATTCGATCCCTTT 530
Qy 82 AAsnGlyAsnTySerCyAsArgTyrH1sIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db 531 GAAACCAATATAATTCCTTACCAATCTTTATATCATCTCAGGTACTGAACGCCAAGAT 590
Qy 102 ValGluAsnThrlleuCySerSerSerSerSerArgValAlaMetSerIleAsnTyAsn 121
Db 591 GTAGAGACTACTCTTTGCCCAATTCGCCAATTCCTGTTAGTATAAAAACATTAACCTTGAT 650
Qy 122 SerLeuTyTrProThrMetGluValylsValagluValAsnSerArgAsnGlnValGlnLeu 141
Db 651 AGTCGATATCCAAATTCGAATCAAAAAGCGAGTAAATCAAAAGACAGTCCAACTG 710
Qy 142 GlyIleGlnIleLeuSerSerAspIleGlyIleSer 154
Db 711 GGAATTCGAATCTCGACAGTAATATTGGAAAGATTCT 749

RESULT 10
AAd42738
ID AAd42738 standard; DNA; 1379 BP.
XX
AC AAd42738;
XX
DT 15-NOV-2002 (first entry)
XX
DE Pokeweed PAP' DNA #1.
XX
KM Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds.
XX
OS Phytolacca americana.
XX
FH Key Location/Qualifiers
FT misc_feature 290..1076
FT /*tag= a
FT /note= "Mature PAP' sequence"
XX
XX WO200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-GB004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX PA Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX
XX WPI; 2002-489891/52.
XX
XX DR WPI; 2002-489891/52.
XX
XX PT Inducing necrotic effect in specific cells of plant by transforming plant
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX PT which acts in response to application of specific stimulus to plant.
XX
XX PS Claim 5; Page 86; 87p; English.
XX
XX CC The invention relates to a method of inducing a necrotic effect in
XX specific cells of a plant. The method involves transforming the plant
XX with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
XX in response to the application of a specific stimulus to the plant so as
XX to facilitate expression of the pokeweed antiviral protein in specific
XX cells of the plant. The method is useful for inducing a necrotic effect
XX in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX
XX SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
Alignment Scores:
```

```
Pred. No.: 1,04e-65 Length: 1379
Score: 596.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
Gaps: 6
US-09-978-274A-6 (1-154) x AAd42738 (1-1379)
Qy 2 IleAsnThrlleThrllePheAspAlaGlyAsnAlaThrIleAsnTyTrIleAsnThrllePheMet 21
Db 291 GTGAATACAAATCAATCTCAATGTTGGAAGTACCAACATTAAGCAATACGACCTTTCTG 350
Qy 22 GluSerLeuArgAsnGlnAlaTyAspProTyLeuTySerTyArgIleProMetLeu 41
Db 351 AATGATCTTGTATATGAGAGCAAGATCCAACTTAAAGCTATGGAATACCAATCTG 410
Qy 42 ProAspThrAsnSerThrProTyTrLeuLeuValylsLeuGlnGlyAlaAsnLeuTy 61
Db 411 CCCAATACAAATACAAATCCAAAGTAGCTGTTGGTTGAGCTCAAGGTTCAATATAAAAA 470
Qy 62 ThrIleThrlleuMetLeuAArgAAsnLeuTyValMetGlyTyrSerAspProPhe 81
Db 471 ACCATTCACACTAAATGCTGAGACGAAACAAATTTGATGTGANGGGTTATTCGATCCCTTT 530
Qy 82 AAsnGlyAsnTySerCyAsArgTyrH1sIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db 531 GAAACCAATATAATTCCTTACCAATCTTTATATCATCTCAGGTACTGAACGCCAAGAT 590
Qy 102 ValGluAsnThrlleuCySerSerSerSerSerArgValAlaMetSerIleAsnTyAsn 121
Db 591 GTAGAGACTACTCTTTGCCCAATTCGCCAATTCCTGTTAGTATAAAAACATTAACCTTGAT 650
Qy 122 SerLeuTyTrProThrMetGluValylsValagluValAsnSerArgAsnGlnValGlnLeu 141
Db 651 AGTCGATATCCAAATTCGAATCAAAAAGCGAGTAAATCAAAAGACAGTCCAACTG 710
Qy 142 GlyIleGlnIleLeuSerSerAspIleGlyIleSer 154
Db 711 GGAATTCGAATCTCGACAGTAATATTGGAAAGATTCT 749

RESULT 11
AD105787
ID AD105787 standard; DNA; 1379 BP.
XX
XX AD105787;
XX
XX 15-APR-2004 (first entry)
XX
XX DE DNA encoding the wild-type pokeweed antiviral protein.
XX
XX KM ribosome depurination; antifungal; antiviral; virucide; anti-HIV;
XX cytoskeletal; immunosuppressive; agricultural biotechnology; pharmaceuticals;
XX medicine; cancer; AIDS; viral infection; autoimmune disease; T-cell;
XX B-cell; transgenic; plant; wild-type; pokeweed antiviral protein; gene;
XX ds.
XX
XX OS Phytolacca americana.
XX
XX FH Key Location/Qualifiers
FT CDS 225..1166
FT /*tag= a
FT /product= "wild-type pokeweed antiviral protein"
XX
XX WO200262952-A2.
XX
XX 15-AUG-2002.
XX
XX PD 01-FEB-2002; 2002WO-US002792.
XX
XX PE 02-FEB-2001; 2001US-0266396P.
XX
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
PA
```

XX Tumor NE, Hudak KA, Parikh B;
 XX WPI: 2003-156656/15.
 DR P-PSDB; ADI05788.
 XX
 PT New Pokeweed Antiviral Protein (PAP) mutant that is less toxic than wild-
 PT type PAP, useful in agricultural biotechnology or in the fields of
 PT pharmaceuticals and medicine, e.g. treating cancer, AIDS, viral infection
 PT or autoimmune disease.
 XX
 PS Disclosure; SEQ ID NO 1, SIPP; English.
 XX
 CC The invention relates to a novel Pokeweed Antiviral Protein (PAP) mutant
 CC that is less toxic than wild-type PAP and exhibits ribosome depurination
 CC activity, where the mutant is a central domain mutant or N-terminal
 CC domain mutant. The PAP mutants have the following activities: antifungal,
 CC antiviral, virucide, anti-HIV, cytostatic and immunosuppressive. The PAP
 CC mutants are useful in agricultural biotechnology as well as in the fields
 CC of pharmaceuticals and medicine. The PAP mutants and methods are useful in
 CC treating mammals with cancer, AIDS, viral infection or autoimmune
 CC diseases associated with cancer, AIDS, viral infection or autoimmune
 CC The transgenic plants are useful in exhibiting resistance to a broad
 CC spectrum of plant pests e.g. viruses and fungi. This polynucleotide
 CC sequence represents the DNA encoding the wild-type pokeweed antiviral
 CC protein of the invention.
 XX
 SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,04e-65 Length: 1379
 Score: 596.00 Matches: 110
 Percent Similarity: 86.9% Conservative: 23
 Best Local Similarity: 71.9% Mismatches: 20
 Query Match: 75.2% Indels: 0
 DB: 10 Gaps: 0

US-09-978-274A-6 (1-154) x ADI05787 (1-1379)

QY 2 ILeaNTTrlIeThPhaSpAlaGlyAenAlaThrlIeAenLyTyraLaThrPhemC 21
 DB 291 GGAATACCAATCATCTACCAATGTTGGAAATCCACCATTAAGAAATCCCACTTTTCG 350
 QY 22 GluSerLeuAAGSnglAlaLySaPProLySLeuLyCySTYGLYIleProMetLeu 41
 DB 351 AATGATCTTCGTAATGAAGCGAAAGATCCAACTTTAAATGCTAATGCAATACCAATGCTG 410
 QY 42 ProAspThrAenSerThrProLySTyLeuLeuValLySLeuGlnGlyAlaAenLeuLyS 61
 DB 411 CCCAATACCAATACCAATCCAAATCGTGTGTTGAGCTCCAAAGTTCAATATMAAAA 470
 QY 62 ThrIleThrLeuMetLeuAAGSnglAlaLySaPProLySLeuLyCySTYGLYIleProMetLeu 81
 DB 471 ACCATACCAATCATCTACCAATGTTGGAAATCCACCATTAAGAAATCCCACTTTTCG 530
 QY 82 AenGlyAenLyCyAArgTyHisIlePhaAenAplIeThSerThGluArgThraP 101
 DB 531 GAAACCAATTAATGCTTACCAATCTTTAATGATATCTGAGTATCGAAGCCCAAGAT 590
 QY 102 ValGluAenThrLeuCySerSerSerSerSerSerSerValAlaMetSerIleAenTyraP 121
 DB 591 GTAGAGACTACTCTTGGCCCAATGCAATCTCGGTGTAGTAAACATAAATTGAT 650
 QY 122 SerLeuTyrrProThrMetGluLySAlaGluValAenSerThraGlnGlnLeu 141
 DB 651 AGTCATATCCAAATCAATGAAATCAAAAGCGGAGTAAATCAAGATCGAGTCCAACTG 710
 QY 142 GlyIleGlnIleLeuSerSerAplIeGlyLySLeuSer 154
 DB 711 GGAATTCAAATCTCGACAGTAAATATGGAAGATTTC 749

RESULT 12
 ADM74765

ID ADM74765 standard; cDNA; 1164 BP.
 XX
 AC ADM74765;
 XX
 AC 03-JUN-2004 (first entry)
 DT
 XX
 DT
 XX
 DE HIV-1 inhibition activity related Tat cDNA.
 XX
 XX human immunodeficiency virus; HIV-1; tumour; plant;
 KW Chinese phytoactin leaf; trans-acting activation factor; Tat; mutant;
 KW gene; ss.
 XX
 OS Human immunodeficiency virus 1.

XX
 FH Key Location/Qualifiers
 FT CDS 2..943
 FT /tag= a
 FT /product= "Tat HIV-1 protein"

XX CN1400220-A.
 XX
 PD 05-MAR-2003.
 XX
 XX 02-AUG-2001; 2001CN-00123911.
 PF
 XX 02-AUG-2001; 2001CN-00123911.
 PF
 XX 02-AUG-2001; 2001CN-00123911.
 PR
 XX (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
 PA
 XX Peng X, Bai L, Yin B;
 PI
 XX WPI: 2003-469263/45.
 DR P-PSDB; ADM74766.
 XX

Two kinds of cDNA with activity capable of extensively inhibiting HIV and its expression, separation and purification method in protokaryon.

Example 9; Page 11-12; 17pp: Chinese.

CC The present invention relates to two kinds of cDNA which can inhibit
 CC human immunodeficiency virus (HIV-1) activity, including separation clone
 CC of two kinds of cDNA, external mutation, fusion expression in prokaryons
 CC and application of the cDNA in preparation of preparation for curing the
 CC virus and tumours. One of the described cDNAs is obtained by separation
 CC and cloned from a plant Chinese phytoactin leaf, and one from the trans-
 CC acting activation factor (Tat) mutant coded by human immunodeficiency
 CC virus HIV-1 gene. This polynucleotide sequence represents the Tat cDNA
 CC used in the HIV-1 inhibition activity of the invention.

Sequence 1164 BP; 403 A; 203 C; 218 G; 340 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.09e-65 Length: 1164
 Score: 595.00 Matches: 110
 Percent Similarity: 87.6% Conservative: 24
 Best Local Similarity: 71.9% Mismatches: 19
 Query Match: 75.0% Indels: 0
 DB: 11 Gaps: 0

US-09-978-274A-6 (1-154) x ADM74765 (1-1164)

QY 2 ILeaNTTrlIeThPhaSpAlaGlyAenAlaThrlIeAenLyTyraLaThrPhemC 21
 DB 68 GGAATACCAATCATCTACCAATGTTGGAAATCCACCATTAAGAAATCCCACTTTTCG 127
 QY 22 GluSerLeuAAGSnglAlaLySaPProLySLeuLyCySTYGLYIleProMetLeu 41
 DB 128 GATATATCTTCGTAATGAAGCGAAAGATCCAACTTTAAATGCTAATGCAATACCAATGCTG 187
 QY 42 ProAspThrAenSerThrProLySTyLeuLeuValLySLeuGlnGlyAlaAenLeuLyS 61
 DB 188 CCCAATACCAATACCAATCCAAATCGTGTGTTGAGCTCCAAAGTTCAATATMAAAA 247

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QY 62 ThrllThrlleuMetleuAargAgsnAnleuTyValMetGlyTYrSerAspProPhe 81
DB 248 ACCATTCACATTAAGCTGAGACGAACAATTGTATGATGGGTATTCGATCCCTT 307
QY 82 AsnGlyAnlySvAargTYrHisllePheAnspIleThrSerThGluArgThrasp 101
DB 308 GATACCAATTAAGTGTCTGATACCAATCTTGTATCTCAGGACTGAAGCCCAAGAT 367
QY 102 ValGluAnThrlleuSvSerSerSerSerArgValAlaMetSerlleAsnThrasp 121
DB 368 GTAAAGACTACTCTTTGCCCAATCCCAATTCCTGTTAGTAAACATTAACATATAT 427
QY 122 SerleuTYrProThrMetGluLysAlaGluValAensSerArgAsnGlnValGlnleu 141
DB 428 AGTCGATATCCAACTGGAATCAAAAGCGGAGTAAATCAAGAACTCAAGTTCACTG 487
QY 142 GlylleGlnlleuSerSerAspIleGlyLysIleSer 154
DB 488 GGAATTCAAATATCTGACGATATATGGAAGATTCT 526

RESULT 13
ADM74751
ID ADM74751 standard; cDNA; 1164 BP.
XX
AC ADM74751;
XX
DT 03-JUN-2004 (first entry)
XX
DE HIV-1 inhibition activity related cDNA.
XX
KW human immunodeficiency virus; HIV-1; tumour; plant;
KM Chinese phytoacca leaf; trans-acting activation factor; Tat; mutant;
KM gene; ss.
XX
OS Human immunodeficiency virus 1.
XX
FH Key Location/Qualifiers
FT CDS 1..1164
FT /tag= a
FT /product= "HIV-1 related protein"
XX
FN CN1400220-A.
XX
PD 05-MAR-2003.
XX
PF 02-AUG-2001; 2001CN-00123911.
XX
PR 02-AUG-2001; 2001CN-00123911.
XX
PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
XX
PI Peng X, Bai L, Yan B;
XX
PI WPI; 2003-469263/45.
XX
PI P-PSDB; ADM74752.
XX
PT Two kinds of cDNA with activity capable of extensively inhibiting HIV and
PT its expression, separation and purification method in protokaryon.
XX
XX Example 8; Page 9-10; 17pp; Chinese.
XX
CC The present invention relates to two kinds of cDNA which can inhibit
CC human immunodeficiency virus (HIV-1) activity, including separation clone
CC of two kinds of cDNA, external mutation, fusion expression in prokaryons
CC and application of the cDNA in preparation of preparation of curing the
CC virus and tumours. One of the described cDNAs is obtained by separating
CC and cloned from a plant Chinese phytoacca leaf, and one from the trans-
CC acting activation factor (Tat) mutant coded by human immunodeficiency
CC virus HIV-1 gene. This polynucleotide sequence represents a cDNA used in
CC the HIV-1 inhibition activity of the invention.
XX
SQ Sequence 1164 BP; 379 A; 239 C; 248 G; 298 T; 0 U; 0 Other;
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Alignment Scores:
Pred. No.: 2,65e-65 Length: 1164
Score: 592.00 Matches: 109
Percent Similarity: 87.6% Conservative: 25
Best Local Similarity: 71.2% Mismatches: 19
Query Match: 74.7% Indels: 0
DB: 11 Gaps: 0

US-09-978-274A-6 (1-154) x ADM74751 (1-1164)
QY 2 lleaAnThrlleThrPheApeAlaGlyAsnAlaThrlleAnlyTYrValAlaThrPheMet 21
DB 289 GTGAATCAATCAATCAATCAATGTTGGAAGTCCCACTTACCAATCGCCACTTTCTGT 348
QY 22 GluSerleuAargAnGlnAlaLysAspProLysleuSvTYrGlylleProMetleu 41
DB 349 GATATCTCTGTAATGAAAGCCAAAGATCCAGTTTAAATGCTAATGAAATCAAGTTTG 408
QY 42 ProAspThrasenSerThrProLysTYrleuValLysleuGlnGlyAlaAsnleuSv 61
DB 409 CCCAATCAATCAATCAATCCAAAGTACGTTGTTGAGCTCCAAAGTTCAATTAATAA 468
QY 62 ThrllThrlleuMetleuAargAgsnAnleuTyValMetGlyTYrSerAspProPhe 81
DB 469 ACCATTCACATTAAGCTGAGACGAACAATTGTATGATGGGTATTCGATCCCTT 528
QY 82 AsnGlyAnlySvAargTYrHisllePheAnspIleThrSerThGluArgThrasp 101
DB 529 GATACCAATTAAGTGTCTGATACCAATCTTGTATGATCTCAGGACTGAAGCCCAAGAT 588
QY 102 ValGluAnThrlleuSvSerSerSerSerArgValAlaMetSerlleAsnThrasp 121
DB 589 GTAAAGACTACTCTTTGCCCAATCCCAATTCCTGTTAGTAAACATTAACATATATAT 648
QY 122 SerleuTYrProThrMetGluLysAlaGluValAensSerArgAsnGlnValGlnleu 141
DB 649 AGTCGATATCCAACTGGAATCAAAAGCGGAGTAAATCAAGAACTCAAGTTCACTG 708
QY 142 GlylleGlnlleuSerSerAspIleGlyLysIleSer 154
DB 709 GGAATTCAAATATCTGACGATATATGGAAGATTCT 747

RESULT 14
AA056672
ID AA056672 standard; cDNA; 1195 BP.
XX
AC AA056672;
XX
DT 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 04-SEP-1994 (first entry)
XX
DE Sequence of Phytoacca antiviral protein (PAP) cDNA.
XX
KW Antiviral protein; PAP; virus-resistance; transgenic plant; ss.
XX
OS Phytoacca americana; L.
XX
FH Key Location/Qualifiers
FT CDS 33..974
FT /tag= a
XX
PN BP585554-A1.
XX
PD 09-MAR-1994.
XX
PF 30-JUN-1993; 93BP-00110445.
XX
PR 16-AUG-1992; 92KR-00014895.
XX
PA (JINR-) JIN RO LTD.
XX
PI Kim M, Lee K, Na B, Jeong H, Choi K, Moon Y, Jeon H;
```

XX WPI; 1994-076002/10.
DR P-PSDB; AAR46548.
XX
PT Expression vector for Phytoelacca antiviral protein - used for producing
PT transgenic virus-resistant plants and for producing the antiviral agent.
XX
PS Disclosure; Fig 1; 15pp; English.
XX
CC To isolate PAP gene, total cellular mRNA was purified from leaves of
CC Phytoelacca americana L. obdd. in Korea. A cDNA library was constructed.
CC The PAP gene was selected by immunoscreening employing anti-PAP antibody.
CC A deletion mutant was prepd. from the isolated PAP gene, and the DNA
CC sequence of the PAP genome was determined. (Updated on 25-MAR-2003 to
CC correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 1195 BP, 420 A, 201 C, 230 G, 344 T, 0 U, 0 Other;
SQ
Alignment Scores:
Pred. No.: 4.95e-65 Length: 1195
Score: 590.00 Matches: 109
Percent Similarity: 86.3% Conservative: 23
Best Local Similarity: 71.2% Mismatches: 21
Query Match: 74.4% Indels: 0
DB: Gaps: 0
US-09-978-274A-6 (1-154) x AAO56672 (1-1195)
QY 2 1leanthr11ethrphespa1aglyasna1athr1leasnlysytyralathrphemet 21
DB 99 GTGAATACATCATCTACATCAATGTTGGAAGTACCAATAGCAATATGCAATGCTG 158
QY 22 GluserleuarganglinalyaspProlysleuysCytyrgly11eprometleu 41
DB 159 AATGATCTTGTAATGAAAGCAAGATCCAGTTAAATGCTATGGAATCCAAATGCTG 218
QY 42 ProasphThraanserThrProlysytyrleuValysleuGlnGlyalaasnleuys 61
DB 219 CCCATACAAATACAAATCCAAAGTACGTTGTTGTTGAGCTCCAAAGTTCAAATTAATAA 278
QY 62 ThirlethleuMetleuarganglinalyasnleuysValMetGlytyrSeraspProphe 81
DB 279 ACCATCACATTAATGCTGAGACGAAGCAATTTGTTATGATGAGTTATTCGATCCCTTT 338
QY 82 Asnglyasnlysytyrthiethleasnaap11ethrserThrgluargthrasp 101
DB 339 GAAACCACTAAATGCTGTTACCATATCTTTAATGATATCTCGAGTACGAAGCCAAAT 398
QY 102 ValglubanThrleuCyserSerSerSerSerSerArgValAlametSer1leasnTyraen 121
DB 399 GTAGAGACTACTCTTTGCCCAATGCCAATCTCTGTTGAGTGAATTAACATTTTGAT 458
QY 122 SerleuTyProthMetGluylsValagluValaasnSerArganglinalyasnleu 141
DB 459 AGTCGATATCCAAATGCTGAATCAAAACGGGAGTAAATCAAGAAAGTCAAGTCCAACTG 518
QY 142 GlytleGlnleleuSerSerasp11eGlyys11eSer 154
DB 519 GGAATTCAAATATCTGACAGTAATATTTGAAAGATTCT 557
RESULT 15
AAD42739
ID AAD42739 standard; DNA; 1378 BP.
XX
AC AAD42739;
XX
DT 15-NOV-2002 (first entry)
XX
XX Pokeweed PAP' DNA #2.
DB Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds.
XX
XX Phytoelacca americana.
OS

XX
FH Key Location/Qualifiers
FT misc_feature 290..1076
FT /*tag= a
FT /note= "Mature PAP' sequence"
XX
XX WO200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-GB004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX
XX WPI; 2002-489891/52.
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX which acts in response to application of specific stimulus to plant.
XX
XX Claim 5; Page 86-87; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
XX specific cells of a plant. The method involves transforming the plant
XX with a chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
XX in response to the application of a specific stimulus to the plant so as
XX to facilitate expression of the pokeweed antiviral protein in specific
XX cells of the plant. The method is useful for inducing a necrotic effect
XX in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX
SQ Sequence 1378 BP; 488 A; 234 C; 269 G; 387 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.1e-64 Length: 1378
Score: 588.00 Matches: 109
Percent Similarity: 86.3% Conservative: 23
Best Local Similarity: 71.2% Mismatches: 21
Query Match: 74.1% Indels: 0
DB: Gaps: 0
US-09-978-274A-6 (1-154) x AAD42739 (1-1378)
QY 2 1leanthr11ethrphespa1aglyasna1athr1leasnlysytyralathrphemet 21
DB 291 GTGAATACATCATCTACATCAATGTTGGAAGTACCAATAGCAATATGCAATGCTG 350
QY 22 GluserleuarganglinalyaspProlysleuysCytyrgly11eprometleu 41
DB 351 AATGATCTTGTAATGAAAGCAAGATCCAAAGTTAAATGCTATGGAATCCAAATGCTG 410
QY 42 ProasphThraanserThrProlysytyrleuValysleuGlnGlyalaasnleuys 61
DB 411 CCCAATCAAAATACAAATCCAAAGCAGTGTGTTGAGTCCCAAGGTTCAAAATTAATAA 470
QY 62 ThirlethleuMetleuarganglinalyasnleuysValMetGlytyrSeraspProphe 81
DB 471 ACCATCACATTAATGCTGAGACGAAGCAATTTGATGTATGAGTTATTCGATCCCTTT 530
QY 82 Asnglyasnlysytyrthiethleasnaap11ethrserThrgluargthrasp 101
DB 531 GAAACCACTAAATGCTGTTACCATATCTTTAATGATATCTCGAGTACGAAGCCAAAT 590
QY 102 ValglubanThrleuCyserSerSerSerSerSerArgValAlametSer1leasnTyraen 121
DB 591 GTAGAGACTACTCTTTGCCCAATGCCAATCTCTGTTGAGTGAATTAACATTTTGAT 650
QY 122 SerleuTyProthMetGluylsValagluValaasnSerArganglinalyasnleu 141

Db	651	AGTCGATATCCACACATTGGAATCAAAAGCGGAGTAAATCAAGAGTCAGTCCAACTG	710
Qy	142	GlyIleGlnIleLeuSerSerAspIleGlyIleSer	154
		::	
Db	711	GGAATCAAACTCGACAGTAATTTGAAAGATTCT	749

Search completed: April 9, 2006, 02:22:26
Job time : 411.713 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 9, 2006, 01:41:02 ; Search time 2798.92 seconds
(without alignments)
2574.284 Million cell updates/sec

Title: US-09-978-274A-6

Perfect score: 793
Sequence: 1 MINTTTPDAGNATINKYATP.....SRNQVGLGIQLSDIGKIS 154

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gse1:*
10: gb_gse2:*
11: gb_gse3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	187	23.6	498	5	B0588134 B012337-0
2	184	23.2	829	5	B0588134 B012337-0
3	171.5	21.6	489	2	CN782289 EST00385
4	151.5	19.1	841	7	BE130330 L48-484T3
5	151.5	19.1	903	7	CO121195 GR_EB028
6	150	18.9	1021	2	CO103587 GR_EB003
7	149	18.8	639	2	BE036639 MP03B03 M
					BE037217 MP18B02 M

8	138.5	17.5	603	5	B0590856
9	138	17.4	811	2	BE034055
10	136	17.2	837	1	AM053634
11	125	15.8	661	6	CF227046
12	125	15.8	662	6	CF227047
13	124	15.6	546	5	B0588856
14	121	15.3	621	7	CV052755
15	120	15.1	644	6	CA838401
16	120	15.1	667	6	CA838446
17	120	15.1	678	6	CA840373
18	118.5	14.9	346	5	B0584811
19	113.5	14.3	659	5	BQ488214
20	112.5	14.2	497	5	BQ488214
21	112.5	13.9	494	7	CN600715
22	104.5	13.2	1310	1	AJ922191
23	104.5	12.9	422	6	CF227044
24	102.5	12.8	419	6	CF226983
25	101.5	12.8	949	1	AJ927358
26	100.5	12.7	658	5	B0583480
27	99	12.5	671	7	CN846973
28	98.5	12.4	671	7	CN846973
29	98	12.4	672	10	CG167941
30	98	12.4	636	1	AM053585
31	97	12.2	472	8	DN953953
32	97	12.2	504	5	B0594182
33	97	12.2	665	6	CF227084
34	95.5	12.0	669	7	CN848288
35	92.5	11.7	491	8	DN142823
36	92.5	11.7	611	5	BQ490182
37	92	11.6	503	8	DN142727
38	91.5	11.5	317	8	CX110999
39	91	11.5	573	6	CD930847
40	91	11.5	632	7	CN010200
41	90.5	11.4	1038	2	BE033546
42	89.5	11.3	463	2	BE605223
43	89.5	11.3	813	10	CL957625
44	88.5	11.2	665	10	CE458462
45	88.5	11.2	875	2	BG369793

ALIGNMENTS

RESULT 1
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LOCUS B0588134 498 bp mRNA linear EST 06-DEC-2002
DEFINITION B012337-024-009-G14-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone
024-009-G14 5-PRIME, mRNA sequence.
ACCESSION B0588134
VERSION B0588134.1 GI:26117717
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
AUTHORS Herwig,R., Schultz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wuck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radloff,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpi-bp.koeln.mpg.de
Insert Length: 498 Std Error: 0.00
Plate: 9 row: G column: 14
Seq primer: SP6; CATACGATTACGTGACACTATAG.
Location/Qualifiers

FEATURES

SOURCE

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/mol_type="mRNA"
/cultivar="KMS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:184726"
/db_xref="taxon:161934"
/clone="024-009-G14"
/issue_type="leaf"
/lab_host="EMDH108"
/clone_id="MP12-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinzelleneber Saatgut AG Bindeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACCGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

ORIGIN

Alignment Scores:
Pred. No.: 1.18e-13 Length: 498
Score: 187.00 Matches: 43
Percent Similarity: 62.1% Conservative: 16
Best Local Similarity: 45.3% Mismatches: 30
Query Match: 23.6% Indels: 6
Gaps: 3

US-09-978-274A-6 (1-154) x BQ588134 (1-498)
QY 5 TTTTTPheAspAlaGlyAsnAlaThrIleAsnLeuTyrAlaThrPheMetGluSerLeu 24
DB 168 GTTACTTTTGGACCTTGAACAGCTTCAAAAGACAAATATGGACCTTTCTAGCAATCTA 227
QY 25 ATGAAGNAlaIleAspProIleuLeuIleAsnLeuTyrAlaThrPheMetGluSerLeu 44
DB 228 CCGACAAATGTGAAGATTCMAAGCTAGTATCGAAGAAATTCATGCTCCCTGCACCA 287
QY 45 AAsnSerThrProIleuLeuValIleAsnLeuTyrAlaThrPheMetGluSerLeu 60
DB 288 TCAAAACAGCAAAATATCTTTAGCCGAGCTTAAAGCTTAAAGCCGCTACTGACATA 347
QY 61 TGTATTTTleuMetLeuArgArgAsnLeuTyrValMetGlyTyrSerAspPro 80
DB 348 ---ACCATCACACTTCTGTAGCAAAATGACTTATATGATGAGCTTTACTGATCAA 404
QY 81 PheAsnGlyAsnLeuCySarGlyTyrHisIlePheAsnAspIleThr 95
DB 405 GTTAGCAAGGT---AAATTACAGAGCTCACTTCTCCGATATTAGT 446

RESULT 2
CN782289 829 bp mRNA linear EST 21-MAY-2004
LOCUS CN782289 EST00385 cgsed Chenopodium quinoa cDNA clone S02J22 5' similar to
DEFINITION anti-tetral ribosome-inactivating protein CAP30B [Chenopodium album],
mRNA sequence.

ACCESSION
VERSION CN782289.1 GI:47561753

KEYWORDS
SOURCE EST.
ORGANISM Chenopodium quinoa (quinoa)

Chenopodium quinoa (quinoa)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Chenopodium.

1 (bases 1 to 829)
Coles, N.D., Coleman, C.B., Christensen, S.A., Jøllsen, E.N.,
Stevens, M.R., Bonifacio, A., Rojas-Beltran, J.A., Fairbanks, D.J. and

REFERENCES

Maughan, P.J.
Development and use of an expressed sequenced tag library in quinoa
(Chenopodium quinoa Willd.) for the discovery of single nucleotide

JOURNAL
COMMENT polymorphisms
Plant Sci. 168 (2), 439-447 (2005)
Contact: Coleman, Craig B.
Department of Plant and Animal Sciences
Brigham Young University
275 WIDB, Brigham Young University, Provo, UT 84602, USA
Tel: (801) 422-5145
Fax: (801) 422-0008
Email: craig-coleman@byu.edu
Plate: 02 Row: J Column: 22
Seq primer: M13 Forward
High quality sequence stop: 829.

FEATURES

SOURCE

1. .829
/organism="Chenopodium quinoa"
/mol_type="mRNA"
/cultivar="Real"
/db_xref="taxon:63459"
/clone="S02J22"
/issue_type="Developing Seed"
/lab_host="XL-1 Blue"
/clone_id="cgsed"
/note="Vector: pTribX2; Site 1: SfiI; Site 2: SfiI;
Developing Seed cDNA library from Chenopodium quinoa"

ORIGIN

Alignment Scores:
Pred. No.: 6e-13 Length: 829
Score: 184.00 Matches: 50
Percent Similarity: 50.7% Conservative: 23
Best Local Similarity: 34.7% Mismatches: 63
Query Match: 23.2% Indels: 8
Gaps: 4

US-09-978-274A-6 (1-154) x CN782289 (1-829)
QY 13 ThrIleAsnLeuTyrAlaThrPheMetGluSerLeuArgAsnAlaIleAspProIle 32
DB 122 ACACGAATCTTATTAACCTTTCTGCAAGTATACGAGCAAACTAAGATCCAAAC 181
QY 33 LeuIleAsnLeuTyrAlaThrPheMetGluSerLeuAsnSerThrProIleuLeu 52
DB 182 TTAGGTATGAAGGAATCCCAATGATCCGACCAACCAACCAAGATACATATCTTTG 241
QY 53 ValIleAsnLeuTyrAlaThrPheMetGluSerLeuAsnSerThrProIleuLeu 69
DB 242 GTTGAACCTTGAATCAAAAGATGAATGATATTCATTAAGCTTTTAACTAATA 301
QY 70 AAsnAsnLeuTyrValMetGlyTyrSerAspProPheAsnGlyAsnLeuCySarGlyTyrHis 89
DB 302 AACGACTTGTATGTAGTGGCTTGTCTGATTAATT---GAGGCAAAAGTTCGGCCAT 358
QY 90 TTTTTCATCTTAACATT-----GACACCATTTGATTAAGCAAAAGTTT 409
DB 359 TTTTTCATCTTAACATT-----GACACCATTTGATTAAGCAAAAGTTT 409
QY 110 SerSerSerArgValAlaMetSerIleAsnLeuTyrProThrMetGluLeu 129
DB 410 CCAGAAATTCAGGTTTCAATTAATATATGATGAGGAAAGTTTACAGTCAATACGAAGC 469
QY 130 TGAAGAGTValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAsp 149
DB 470 AATGCTGTCAAAAC---CAATTAGTTTCCGTGGGTTTATTAACCTTAACCTTAA 526
QY 150 TleGlyLeuIle 153
DB 527 ATGGAAGAGTTC 538

RESULT 3

BE130330 489 bp mRNA linear EST 20-FEB-2001
LOCUS BE130330 L48-484T3 Ice plant Lambda Uni-Zap XR expression library, 48 hours
DEFINITION NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-484 5',

RNA sequence.
ACCESSION BE130330
VERSION BE130330.1 GI:8577693
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Bukariyola; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Astroceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 489)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T7
BACKWARD: T3
Plate: L48-5 row: G column: 12
Seq primer: T3
High quality sequence stop: 350
POLY-A=NO.
FEATURES
source
location/Qualifiers
1..489
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="L48-484"
/tissue_type="leaf, 48 h 0.4M NaCl"
/dev_stage="Six week old"
/clone_lib="ice plant lambda Uni-Zap XR expression library, 48 hours NaCl treatment"
/note="Vector: lambda Uni-Zap XR, Bluescript SK-, Site_1: EcoRI, Site_2: XhoI"
ORIGIN
Alignment Scores:
Pred. No.: 1,21e-11 Length: 489
Score: 171.50 Matches: 43
Percent Similarity: 56.4% Conservative: 14
Best Local Similarity: 42.6% Mismatches: 35
Query Match: 21.6% Indels: 9
Gaps: 4
DB: 2
US-09-978-274A-6 (1-154) x BE130330 (1-489)
QY 2 l|e|a|n|t|h|r|i|e|t|h|r|p|h|e|a|p|a|g|l|y|a|s|n|a|l|a|t|h|r|-----|l|e|a|n|l|y|t|r|a|l|a|t|h|r| 19
Db 150 A|T|A|C|A|C|T|A|T|A|C|C|T|G|G|A|C|A|T|C|T|G|G|A|G|A|G|C|T|A|C|T|G|C|G|A|T|A|C|A|T|A|C|A|T|A|C|A| 209
QY 20 P|h|e|m|e|t|G|U|S|e|r|L|e|u|A|g|n|l|a|l|y|a|s|p|p|o|l|y|s|l|e|u|y|s|y|t|r|g|l|y|l|e|t|r|o| 39
Db 210 T|T|C|T|G|A|A|T|C|T|A|G|C|A|T|G|A|A|C|T|G|A|G|A|T|C|C|A|T|G|A|G|A|A|C|C|C|A|T|A|G|T|A|T|A|C|A| 269
QY 40 M|e|t|L|e|u|-----|P|r|o|a|s|P|h|r|A|s|n|-----|S|e|r|T|h|r|P|o|l|y|s|T|r|L|e|u|L|e|u|V|a|l|l|e|u| 55
Db 270 G|T|A|T|G|G|A|A|A|A|C|T|A|G|A|C|T|T|C|C|A|G|A|T|G|A|C|A|G|A|C|A|T|A|T|C|T|T|G|T|A|G|A|G|C|T|G| 329
QY 56 G|l|n|g|l|A|a|s|n|l|e|u|L|e|u|t|h|r|i|l|e|t|h|r|L|e|u|L|e|u|A|g|A|s|n|l|e|u|T|r|V|a|l|l|e|u| 75
Db 330 C|A|G|C|G|A|G|C|A|C|C|A|A|G|T|C|A|T|A|T|A|T|C|T|A|G|C|A|G|A|G|A|C|A|A|T|T|A|T|A|T|T|C|A|T|G| 389
QY 76 G|l|y|t|r|S|e|r|A|s|p|-----|P|r|o|P|h|e|a|s|n|l|y|a|n|l|y|s|y|a|g|t|r|y|H|i|s|t|l|e|P|h|e|a|s|n| 92
Db 390 G|G|C|T|A|C|A|G|T|G|A|C|A|T|T|G|A|T|T|A|A|A|A|T|A|A|A|A|A|T|A|A|A|A|T|G|C|G|C|A|C|A|T|G|T|T|C|A|G| 449
QY 93 A|s|p| 93

Db 450 G|A|T| 452
RESULT 4
LOCUS CO121195 841 bp mRNA linear EST 16-JUN-2004
DEFINITION GR_EB02B11.f GR_EB Gossypium raimondii cDNA clone GR_EB02B11 5', mRNA sequence.
ACCESSION CO121195
VERSION CO121195.1 GI:48819882
KEYWORDS EST.
SOURCE Gossypium raimondii
ORGANISM Gossypium raimondii
Bukariyola; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae; eustoside II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE 1 (bases 1 to 841)
AUTHORS Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C., Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and Wing,R.A.
TITLE Global assembly of Cotton ESTs
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
Plate: 02 row: B column: 11.
FEATURES
source
location/Qualifiers
1..841
/organism="Gossypium raimondii"
/mol_type="mRNA"
/db_xref="taxon:29730"
/clone="GR_EB02B11"
/tissue_type="floral"
/dev_stage="3 to +3 DPA"
/lab_host="DH10B"
/clone_lib="GR_EB"
/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2: EcoRV; library made by Invitrogen with RNA supplied by Wendle lab. Directional cloned into NotI-EV. Colonies plated/picked by AGI. More glycerol clones held in -80."
ORIGIN
Alignment Scores:
Pred. No.: 1.08e-08 Length: 841
Score: 151.50 Matches: 43
Percent Similarity: 46.5% Conservative: 30
Best Local Similarity: 27.4% Mismatches: 65
Query Match: 19.1% Indels: 19
Gaps: 5
DB: 7
US-09-978-274A-6 (1-154) x CO121195 (1-841)
QY 2 l|e|a|n|t|h|r|i|e|t|h|r|p|h|e|a|p|a|g|l|y|a|s|n|a|l|a|t|h|r|l|e|a|n|l|y|t|r|a|l|a|t|h|r|p|h|e|m|e|t| 21
Db 34 A|T|T|A|C|A|C|A|G|A|G|A|T|C|A|C|A|C|T|G|A|A|G|C|C|A|G|A|C|T|C|T|A|T|C|T|G|A|T|T|A|T|G| 93
QY 22 G|U|S|e|r|L|e|u|A|g|n|l|a|l|y|a|s|p|p|o|l|y|s|l|e|u|y|s|y|t|r|g|l|y|l|e|t|r|o|P|r|o|M|e|L|e|u| 41
Db 94 A|A|G|A|T|C|T|G|A|C|A|T|T|G|A|C|A|G|C|G|T|G|A|G|A|G|C|G|G|A|G|A|C|A|T|G|C|C|A|T|A|T|T|G| 153
QY 42 P|r|o|a|s|P|h|r|A|s|e|r|T|h|r|P|r|o|-----|L|y|t|r|L|e|u|L|e|u|V|a|l|l|e|u|G|l|n|g|l|y| 57
Db 154 C|T|T|C|C|G|A|T|C|T|G|A|C|A|G|C|C|T|A|G|A|T|C|T|C|G|G|A|A|A|T|G|T|T|C|G|T|A|G|A|G|C|T|T|C|A|A|T| 213
QY 58 A|l|a|s|n|l|e|u|y|t|h|r|i|l|e|t|h|r|L|e|u|L|e|u|A|g|A|s|n|l|e|u|T|r|V|a|l|l|e|u|G|l|y|l|e|t|r|o| 77
Db 214 -|-G|T|T|A|C|A|A|C|T|G|C|A|T|T|A|G|C|C|T|C|A|T|G|C|A|T|G|T|A|T|G|T|A|T|C|T|T|G|G|T|T|A|T| 270
QY 78 S|e|r|A|s|p|P|r|o|P|h|e|a|s|n|l|y|a|n|l|y|s|y|a|g|t|r|y|H|i|s|t|l|e|P|h|e|a|s|n|A|s|p|l|e|t|h|S|e|r|T|h|r| 97

Db	271	CGGCAAGTCGGGGCTCC-----TATTCTTACGAGATGCCAGAC---	312
Qy	98	GluaGrThraApValGluAenThrLeuCySerSerSerSerSerAraGValAlaMetSer	117
Db	313	-----GATGACGTAATGCTTTGTCTCCAGCGAGTACT-----GGC	348
Qy	118	IlleaSnThrAenSerLeuTyrProThrMetGluValuSyluSaIaGluValaIaSerAraGsn	137
Db	349	CTACCCCTTTACAGGACAGATATGGGGCACCTTAAGCGGTGCTGGCGGAGTGAAGACAGAAAG	408
Qy	138	GlnValGlnLeuGluGlyIleGlnIleLeuSerSerAapIleGlyValIleSer	154
Db	409	GAATCCCTCTGGGAATGATGAACTAACGCCAACATATTGATTAACCTGAAT	459
RESULT 5			
LOCUS	COL03587		
DEFINITION	GR_EB0032E01.r GR_Eb Gossypium raimondii cDNA clone GR_EB0032E01	903 bp mRNA linear EST 16-JUN-2004	
ACCESSION	COI03587		
VERSION	COI03587.1	GI:48802273	
KEYWORDS	EST.		
SOURCE	Gossypium raimondii		
ORGANISM	Gossypium raimondii		
REFERENCE	Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosidae; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.		
AUTHORS	1 (bases 1 to 903) Klim,H.,Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C., Udall,J.A., Rapp,R.A., Mendel,J.F., Rao,K., Soderlund,C. and Wing,R.A.		
TITLE	Global assembly of Cotton ESTs		
JOURNAL	Unpublished (2004)		
COMMENT	Contact: Rod A. Wing Arizona Genomics Institute The University of Arizona Forbes Building Room 303, Tucson, AZ, 85721-0036, USA Tel: 520 626 9595 Fax: 520 621 1259 Email: rwing@genome.arizona.edu Plate: 0032 row: E column: 01.		
FEATURES			
source	1..903 /organism="Gossypium raimondii" /mol_type="mRNA" /db_xref="taxon:29730" /clone="GR_EB0032E01" /rname_type="floral" /dev_stage="3 to +3 DPA" /lab_host="DH10B" /clone_lib="GR_Eb" /note="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2: EcoRV; library made by Invitrogen with RNA supplied by Wendle lab. Directional cloned into NotI-EV. Clones plated/picked by AGI. More glycerol clones held in -80."		
ORIGIN			
Alignment Scores:			
Prod. No.:	1.19e-08	Length:	903
Score:	151.50	Matches:	43
Percent Similarity:	46.5%	Conservative:	30
Best Local Similarity:	27.4%	Mismatches:	65
Query Match:	19.1%	Indels:	19
DB:	7	Gaps:	5
US-09-978-274A-6 (1-154) x COI03587 (1-903)			
Qy	2	IlleaSnThrLeThrPheApAlaGlyAaSnAlaThrIleAenSyluSaIaThrPheMet	21
Db	172	ATTTACACAGTGAATTCACCACTGAAGAAGCCACCGAAGACTTTATCTGATGATTATG	233
Qy	22	GluSerLeuAraGsnGlnAlaIaAapProLeuSyluSyluGlyIleProMetLeu	41

[illegible]

Score:	149.00	Matches:	38
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/lab_host="EMDH10B"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 837)

Cushman, J.C.
An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum

Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
Poly(A) tail, 10 nt: 838..847
PCR Primers
FORWARD: T7
BACKWARD: T3
Insert Length: 847 Std Error: 5.00
Plate: L30-15 row: A column: 5
Seq primer: T3
High quality sequence stop: 450.
Location/Qualifiers
1..837

FEATURES
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/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="L30-1401"
/cissue_type="Leaf, 30 h 0.4M NaCl"
/dev_stage="Six week old"
/clone_lib="Ice plant lambda Uni-Zap XR expression
library, 30 hours NaCl treatment"
/note="Vector: lambda Uni-Zap XR, Bluescript SK-; Site_1:
BcoRI; Site_2: XhoI"

ORIGIN

Alignment Scores:

Pred. No.: 1,13e-06 Length: 837
Score: 136.00 Matches: 45
Percent Similarity: 48.3% Conservative: 24
Best Local Similarity: 31.5% Mismatches: 56
Query Match: 17.2% Indels: 18
DB: 1 Gaps: 7

US-09-978-274A-6 (1-154) x AM053634 (1-837)

QY 15 AaunlyTYrAlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLeuLys 34
DB 5 AACACATATTCACATTCATGACATCTCCGAGCTCAACTCTCGGC--ACAACCGCA 61
QY 35 CysTYrGlyIleProMetLeuProAspThrAsnSerThr-----ProLysTYr 50
DB 62 TGT-----CAATCCCGGTGACACCGTCAACCGACCGATCTCCAAAGATTTC 109
QY 51 LeuLeuValLysLeuGlnGlyAlaLeuLeuLysThrIleThrLeuMetLeuArgArgAsn 70
DB 110 GTTCCTCGTGCAGCTCAAAACAACCTCGCAAAAGACCATACACTCGCAATCAAGCTGACA 169
QY 71 AaunlyTYrValMetGlyTYrSerAspProPheAsnGlyAsnLysCysArgTYrHisIle 90
DB 170 AGCGCTATGTCGTGGCTACCGCGACAAGCTT---GGCGAAAGAACCGTCCCAACTTC 226
QY 91 PheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSerSerSer 110
DB 227 CTTACCGAGTCTCCACGCTCGCTAGG-----AACCACTCTTCAAGGCGCG 274
QY 111 SerSerArgValAlaMetSerIleAsnTYrAsnSerLeuTYrProThrMetGlnLysLys 130
DB 275 ACGGTTCCG-----AACHTTCGTTCCGAGGAGGAGTACATGACCTTAAGAGAGGCT 325
QY 131 AlaGluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAspIle 150

DB 326 GCAAG---CAAGCGCCGAATGCAATAGACTTAGGGGTGAATTAAGATTGGATC 382
QY 151 GlyLysIle 153
DB 383 GAGTCGGGT 391

RESULT 11

CP227046

LOCUS CP227046 661 bp mRNA linear EST 04-AUG-2003
DEFINITION IH202 subtracted Iris tepal cDNA library Iris hollandica cDNA clone
IH202, mRNA sequence.

ACCESSION CP227046
VERSION CP227046.1 GI:33438082
KEYWORDS EST.

SOURCE
ORGANISM

Iris hollandica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
Iris.

1 (bases 1 to 661)

REFERENCE
AUTHORS Van Doorn, W.G., Balk, P.A., van Houwelingen, A.M., Hoeberichts, F.A.,
Hall, R.D., Vorse, O., van der Schoot, C. and van Woudagen, M.F.
TITLE Gene expression during anthesis and senescence in Iris flowers
JOURNAL Plant Mol. Biol. 53 (6), 845-863 (2003)
PUBMED 15082930

COMMENT
Contact: Wouter G. van Doorn
Institute for Agro technological Research (ARO)
Wageningen University and Research Centre
P.O. Box 17, 6700 AA, Wageningen, The Netherlands
Tel: 0031 317 475105
Fax: 0031 317 475347
Email: wouter.vandoorn@wur.nl.
Location/Qualifiers
1..661

FEATURES

source

/organism="Iris hollandica"
/mol_type="mRNA"
/cultivar="Blue Magic"
/db_xref="taxon:35876"
/clone="IH202"
/cissue_type="sepal"
/clone_lib="subtracted Iris tepal cDNA library"
/note="Vector: pGEMT-Basy; mRNA isolated from Iris sepals
was substracted using pedicel material as the driver. Equal
amounts of mRNA from each developmental stage were pooled
for cDNA synthesis. The pGEM-T Basy Vector System
(Promega) was used to construct the cDNA library."

ORIGIN

Alignment Scores:

Pred. No.: 2,21e-05 Length: 661
Score: 125.00 Matches: 42
Percent Similarity: 46.0% Conservative: 27
Best Local Similarity: 28.0% Mismatches: 63
Query Match: 15.8% Indels: 18
DB: 6 Gaps: 5

US-09-978-274A-6 (1-154) x CP227046 (1-661)

QY 2 IleaenThrIleThrPheAspAlaGlyAsnAlaThrIleAaunlyTYrAlaThrPheMet 21
DB 76 ATTGAACAGTGCAGTTCGCTGCTACCTGGACACACAGCAAACTATAGCTTCTCTTA 135
QY 22 GluSerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTYrGlyIleProMetLeu 41
DB 136 CAGACCTTACCAACGCGCTTAAGCAGTGAAGT--ACGTCGATGATATCTTGTGCTG 192
QY 42 Pro---AspThrAsnSerThrProLysTYrLeuLeuValLysLeuGlnGlyAlaAsnLeu 60
DB 193 CCGGGCAATCGGTTCCACAGAGATTGCTCTTGTCACACTCTTGAATTGGACAC 252
QY 61 LysThrIleThrLeuMetLeuArgArgAsnAaunlyTYrValMetGlyTYrSerAspPro 80
DB 253 ACGCGATACGCTGCTGCTTAATCGGCTCAATCGCTTATCGTAGACTTACAA----- 306

QY 81 Pheannglyanlyscysargtyrhielpheanapliethserthgluargthr 100
 DB 307 -----GCTAAATACTGTTACTCTGCTCCGAC-----ACT 339
 QY 101 AspyalgluamthrlleuCyserSerSerSerSerargvalalmetserilleasntyr 120
 DB 340 CCGGCATCTCAGCTTATGAGCAACCGCACCGCTTAGTTTACAGGAGCTAC 399
 QY 121 AmserleutyrrprothmetglulylalyalgluValaanserargxasnglnvalgln 140
 DB 400 ATTGCCTT-----CAAAATGTCGCAAAACAGTAGAGAAATTTGAT 444
 QY 141 LeuglyileglnlleuSerSeraspile 150
 DB 445 CTGGATCATCCACTTCGCAACGCGCATC 474

RESULT 12
 CF227047 662 bp mRNA linear EST 04-AUG-2003
 LOCUS IH215 subcloned Iris tepal cDNA library Iris hollandica cDNA clone
 DEFINITION IH215, mRNA sequence.
 ACCESSION CF227047.1 GI:33438083
 VERSION CF227047.1
 KEYWORDS EST.
 SOURCE Iris hollandica
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae; Iris.

REFERENCE 1 (bases 1 to 662)
 Van Doorn, W.G., Balk, P.A., van Houweijngen, A.M., Hoeberichts, F.A., Hall, R.D., Vorst, O., van der Schoot, C. and van Woudagen, M.F.
 Gene expression during anthesis and senescence in Iris flowers
 Plant Mol. Biol. 53 (6), 845-863 (2003)
 PUBMED 15082930
 CONTACT: Wouter G. van Doorn
 Institute for Agro technological Research (ATO)
 Wageningen University and Research Centre
 P.O. Box 17, 6700 AA, Wageningen, The Netherlands
 Tel: 0031 317 475105
 Fax: 0031 317 475347
 Email: wouter.vandoorn@wur.nl.
 Location/Qualifiers
 FEATURES
 source 1..662
 /organism="Iris hollandica"
 /mol_type="mRNA"
 /cultivar="Blue Magic"
 /db_xref="taxon:35876"
 /clone="IH215"
 /issue_type="sepal"
 /clone_lib="subcloned Iris tepal cDNA library"
 /note="Vector: pGEMT-Easy; mRNA isolated from Iris sepals was subcloned using pedicel material as the driver. Equal amounts of mRNA from each developmental stage were pooled for cDNA synthesis. The pGEMT-Easy Vector System (Promega) was used to construct the cDNA library."

ORIGIN
 Alignment Scores: 2.21e-05 Length: 662
 Pred. No.: 125.00 Matches: 42
 Score: 125.00 Conservative: 27
 Percent Similarity: 46.0% Mismatches: 63
 Bees Local Similarity: 28.0% Indels: 18
 Query Match: 15.8% Gaps: 5
 DB: 6
 US-09-978-274A-6 (1-154) x CF227047 (1-662)

QY 2 ILeasanthrllethrlpheanapliaglyasnlalrhlleasnllytyrAlatrPhemet 21
 DB 109 ATTGAACAGTGCAGTTCCTGCTGCACTGGAGCACCGCAACCTATAGCTTTCTTA 168

QY 22 GluserleuargannglnlalysAspprolyleuLyCystrglyilePrometleu 41
 DB 169 CAGACCTACGACGCCCTTAAGCAGTGAAGT---AGCGTGAATGATATCTTCTGCTG 225
 QY 42 Pro---AspThranserthrrprolyertyrleuValylleuglnlyalAasnlleu 60
 DB 226 CTCTGGCAATCCGGGTCTCCAGACAGATTTGCTCTCTGTGCAACTTGTGATGGAGCAAC 285
 QY 61 LythrlllethrlleuMetleuArgargAasnlleutyrrValmetglytyrSerAspPro 80
 DB 286 ACGCGCATCGCGTGGCTTAATGCGTCATACCTTATCTGTAGCTTACAA----- 339
 QY 81 Pheannglyanlyscysargtyrhielpheanapliethserthgluargthr 100
 DB 340 -----GCTAAATACTGTTACTCTGCTCCGAC-----ACT 372
 QY 101 AspyalgluamthrlleuCyserSerSerSerSerargvalalmetserilleasntyr 120
 DB 373 CCGGCATCTCAGCTTATGAGCAACCGCACCGCTTAGTTTACAGGAGCTAC 432
 QY 121 AmserleutyrrprothmetglulylalyalgluValaanserargxasnglnvalgln 140
 DB 433 ATTGCCTT-----CAAAATGTCGCAAAACAGTAGAGAAATTTGAT 477
 QY 141 LeuglyileglnlleuSerSeraspile 150
 DB 478 CTGGATCATCCACTTCGCAACGCGCATC 507

RESULT 13
 B0588856 546 bp mRNA linear EST 06-DEC-2002
 LOCUS B0588856
 DEFINITION B012534-024-014-P10-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
 cDNA clone 024-014-P10 5-PRIME, mRNA sequence.
 ACCESSION B0588856
 VERSION B0588856.1 GI:26118439
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 546)
 Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., and Radelof, U.
 and Radelof, U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 PUBMED 12472698
 CONTACT: Weisshaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mp1z-koeln.mpg.de
 Insert length: 546 Std Error: 0.00
 Plate: 14 row: P column: 10
 Seq primer: Sp6; CATACGATTTAGGTGACACTATAG.
 Location/Qualifiers
 FEATURES
 source 1..546
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:187113"
 /db_xref="taxon:161934"
 /clone="024-014-P10"
 /issue_type="storage root"
 /adb_note="EMDH10B"
 /clone_lib="MP1Z-ADIS-024-storage root"
 /note="Vector: pCMVSPORT6; Site 1: SalI, Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinfanzleben Saatzucht AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites SalI-NciI, primer sites and orientation:
SP6-Sali-CCAGCGCTCCG-Sprine-cDNA-polYA-CC-NciI-T7; Note:
Sequencing granted in the context of the GABI-Best
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

ORIGIN

Alignment Scores:

Pred. No.:	2, 27e-05	Length:	546
Score:	124.00	Matches:	41
Percent Similarity:	46.9%	Conservative:	19
Best Local Similarity:	32.0%	Mismatches:	52
Query Match:	15.6%	Indels:	16
DB:	5	Gaps:	6

US-09-978-274A-6 (1-154) x BQ58856 (1-546)

QY 3 AenThrlleThrPheAspAlaGly--AenAlaThrlleAsnlyeTyraLathrPheMet 21

Db 186 AACACTGTGTCAATGGAGCTTTCACCTTCCTGATCCGTAAATGCTATCCAAATTCCTG 245

QY 22 GluSerLeuArgAsnGlnAlaIysAspProlyleuLysCytyrGlylleProMetLeu 41

Db 246 AGGAGACTGGCAATCAATGAGAGCTCCGATCAGGATCTGC-----GGCTTA 293

QY 42 ProAspThrAsnSerThrPro-----LysTyrlleuVallyleuGlnGly 57

Db 294 CCATCCAGCGCAGCATGCTCTCGTTAGAGGCCAAGATATATATACAGTGAACCTTAAGANT 353

QY 58 AlaAsnLeuLysThrlleThrMetLeuArgAsnAsnLeuTyraLathrMetGlyTy 77

Db 354 AGCAACAGAAATGTGGTATCCATAGGAATAGATGATGATTTGATGATGATGATGAT 413

QY 78 SerAspProPheAsnGlyAsnLysCytyrGlyllePheAsnAspThrSerThr 97

Db 414 CAAGCAAGATTTCACGGG---ATACTTCGGTCCACTTCCTTAATGACGTTCCCGAGCT 470

QY 98 GluValThrAspValGluAsnThrlleuCytyrSerSerSerSerSerArgValAlaMetSer 117

Db 471 GCACGG-----AACACCCCTTTTCCAAAGATGCGGCAATTAGAAACAACATAT 518

QY 118 Ile-----AsnTyraAsnSerLeu 123

Db 519 TTTCGAGGCAACTACGACAGTCTT 542

RESULT 14

CV052755

LOCUS

DEFINITION EST 12203 Half-Ripe Apricot Fruit Lambda Zap II Library Prunus

armeniaca cDNA clone bse017c17g 5', mRNA sequence.

CV052755

VERSION

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

TITLE

High Throughput Detection of Isoenes among 5724 3' EST from

Apricot Fruit (Prunus armeniaca)

Unpublished (2003)

Contact: Audergon JM

Unité de génétique et amélioration des fruits et légumes

Institut National de la Recherche Agronomique

Domaine Saint-Maurice BP 94 84143 Montfavet cedex

Tel: 00-33-(0)4-32-72-26-68

Fax: 00-33-(0)4-32-72-26-62

Email: audergon@aviignon.inra.fr

Seq primer: T3.

FEATURES Location/Qualifiers

source

1..621

/organism="Prunus armeniaca"

/mol_type="mRNA"

/cultivar="Bergeron"

/db_xref="taxon:36596"

/clone="bse017c17g"

/dev_stage="Half-Ripe stage"

/clone_lib="Half-Ripe Apricot Fruit Lambda Zap II Library"

/note="Organ: Fruit; Vector: Lambda Zap II; Site: 1: Eco

RI; Site: 2: XhoI; Oriented library, construction described

in Molecular cloning and expression of a cDNA encoding

1-aminocyclopropane-1-carboxylate (ACC) oxidase from

apricot fruit (Prunus armeniaca cv. Bergeron) by

Mbeguie-Mbeguie D, Chahine H, Gomez RW, Gouble B, Audergon

JM, Soucy M, Albagnac G, File-Lycaon B in Physiol Plant

105:294-303 1999"

ORIGIN

Alignment Scores:

Pred. No.:	6, 73e-05	Length:	621
Score:	121.00	Matches:	42
Percent Similarity:	41.4%	Conservative:	21
Best Local Similarity:	27.6%	Mismatches:	67
Query Match:	15.3%	Indels:	22
DB:	7	Gaps:	5

US-09-978-274A-6 (1-154) x CV052755 (1-621)

QY 5 lIethrPheAspAlaGlyAsnAlaThrlleAsnlyeTyraLathrPheMetGluSerLeu 24

Db 62 CTATCTTCACACCTAAGAACACACACCCCGCAAAATACCGGACTCATATGAACTCTT 121

QY 25 ArgAsnGlnAlaIysAspProlyleuLysCytyrGlylleProMetLeuProAspThr 44

Db 122 CGACAGCAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 181

QY 45 AsnSerThrPro-----LysTyrlleuVallyleuGlnGlyAlaAsnLeuLys 61

Db 182 GAAGATGTGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 241

QY 62 ThrIleThrMetLeuArgAsnAsnLeuTyraLathrMetGlyTyrSer----- 78

Db 242 ACCATCAGCTCTGCAATGATGTGTGAACGCTTACGTGTGTGTATGCTGACAGATGC 301

QY 79 ---AspProPheAsnGlyAsnLysCytyrGlylleProMetLeuProAspThr 91

Db 302 CGATCTCTCTTCTTAAGAAATGCTGTAGATCCGCTCCATCCACACTTGTTC 361

QY 92 AsnAspIleThrSerThrGluArgThrAspValGluAsnThrlleuCytyrSerSerSer 111

Db 362 CGCGACACACTCGGATGCTCTCTGCACTTCGACGCGACACTAC-----ACCGGCTT 415

QY 112 SerArgValAlaMetSerIleAsnTyraAsnSerLeuTyraLathrMetGlyLysAla 131

Db 416 TCGGAGCTGTGCGCAAGAACAGCTGAACCGAATTA-----GCA 454

QY 132 GluValAsnSerArgAsnGlnValGlnLeuGlylle 143

Db 455 CGTATGTGTCTCGTAACCCAGCAGTGCAGAGTCTG 490

RESULT 15

CA838401

LOCUS

DEFINITION MCT016B04 166733 Ice plant Lambda Uni-Zap XR expression library, 5

days 0.5 M NaCl treatment, Crassulacean acid metabolism phase IV

(5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT016B04 5,

mRNA sequence.

CA838401

VERSION

KEYWORDS

SOURCE

Mesembryanthemum crystallinum (common iceplant)

ORGANISM

Mesembryanthemum crystallinum
Bakryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Aizoaceae; Mesembryanthemum.
1 (bases 1 to 644)
Cushman, J.C.
An expressed sequence tag database for the common ice plant.
Mesembryanthemum crystallinum

AUTHORS

JOURNAL

COMMENT
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRIMERS
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 016 row: B column: 04
Seq primer: T3 20mer
High quality sequence stop: 644.
Location/Qualifiers

FEATURES

1..644
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT016B04"
/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoRI, Site 2: XhoI; library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:
Pred. No.: 9.57e-05 Length: 644
Score: 120.00 Matches: 41
Percent Similarity: 45.7% Conservative: 28
Best Local Similarity: 27.2% Mismatches: 64
Query Match: 15.1% Indels: 18
DB: Gaps: 6

US-09-978-274A-6 (1-154) x CA838401 (1-644)

QY 3 AantThrlleThrPheApsAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGlu 22
DB 205 AACACCGGTGACATTCGACCTC-----GCCCATCCGACACATATCCAAAGTTCATTGCC 258
QY 23 SerLeuArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuPro 42
DB 259 GATCTCCAAACTGACTATCTCCGGCAACCGCATGTCAA--ATCCCGGTGACACGG 315
QY 43 AspThrAsnSerThr-----ProLysTyrLeuLeuValLysLeuGlnGlyAlaAsn 59
DB 316 GCAACCGCAACCACTCAATGACCAACGATGCTCTGCTGACCTCGAAACACCTCG 375
QY 60 LeuLysThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAsp 79
DB 376 CAAAACCACTCACTCCGATGACGTGACGTACGTCGCTATCGCGAC 435
QY 80 ProPheAsnGlyAsn-----LysCysArgTyrHisIlePheAsnAspIleThr 95
DB 436 AAGTTCAAAGAAAGACGCAAAATGAGACCGTGCACACTTCCTCAAGATGACATCT 495
QY 96 SerThrGluArgThrAspValGluAsnThrLeuCysSerSerSerSerArgValAla 115
DB 496 ACGGTTCGCAAG-----GAGAAATCTCTTTCATGAGACACGTTCCGAACTTCG 546

QY 116 MetSerIleAsnTyrAsnSerLeuTyrProThrMetGluLysValAlaGluValAsnSer 135
DB 547 TTCAAAGGACCTTACACATCTTA-----GAGAAATGCTGCAACCAACGA 591
QY 136 ArgAsnGlnValGlnLeuGlyIleGlnIleLeu 146
DB 592 CGAAGACCAATGAGTTAGGGGTGATANACTA 624

Search completed: April 9, 2006, 06:20:25
Job time : 2800.92 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 8, 2006, 13:04:24 ; Search time 168.1 seconds
(without alignments)
1628.463 Million cell updates/sec

Title: US-09-978-274A-6

Perfect score: 753

Sequence: 1 MINTTPDAGNATINKYATF.....SRNQVQGIQLSSDGKIS 154

Scoring table: BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA -OPMT=fastlap -SUFFIX=p2n.rml -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsom62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NCPU=6 -ICPU=3 -NO MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MAIN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

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6: /cgn2_6/ptodata/1/ina/PP.COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	596	75.2	1195	2	US-08-373-858-1	Sequence 1, Appli
2	596	75.2	1195	2	US-08-342-7868-1	Sequence 1, Appli
3	596	75.2	1379	2	US-08-500-611-1	Sequence 1, Appli
4	596	75.2	1379	2	US-08-500-694-1	Sequence 1, Appli
5	596	75.2	1379	3	US-07-865-169-1	Sequence 1, Appli
6	596	75.2	1379	3	US-09-005-273-1	Sequence 1, Appli
7	596	75.2	1379	3	US-08-501-253A-1	Sequence 1, Appli
8	596	75.2	1379	6	PCT-US96-11546-1	Sequence 1, Appli
9	588	74.1	1379	3	US-07-865-169-2	Sequence 2, Appli

10	588	74.1	1379	3	US-09-005-273-3	Sequence 3, Appli
11	463.5	58.4	918	2	US-08-138-636-1	Sequence 1, Appli
12	463.5	58.4	918	2	US-08-319-622A-1	Sequence 1, Appli
13	463.5	58.4	918	2	US-08-471-564-1	Sequence 1, Appli
14	190.5	24.0	804	2	US-08-356-161-7	Sequence 7, Appli
15	190.5	24.0	804	3	US-08-718-904-23	Sequence 23, Appli
16	190.5	24.0	804	3	US-09-449-249-23	Sequence 23, Appli
17	190.5	24.0	804	6	PCT-US93-05702-7	Sequence 7, Appli
18	190.5	24.0	804	6	PCT-US95-10973A-7	Sequence 7, Appli
19	188.5	23.8	765	3	US-08-718-904-79	Sequence 79, Appli
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21	188.5	23.8	1167	6	PCT-US95-10973A-57	Sequence 57, Appli
22	188.5	23.8	1230	2	US-08-356-161-12	Sequence 12, Appli
23	188.5	23.8	1230	2	US-08-356-161-13	Sequence 13, Appli
24	188.5	23.8	1230	3	US-08-718-904-53	Sequence 53, Appli
25	188.5	23.8	1230	3	US-09-449-249-53	Sequence 53, Appli
26	188.5	23.8	1230	6	PCT-US93-05702-12	Sequence 12, Appli
27	188.5	23.8	1230	6	PCT-US93-05702-13	Sequence 13, Appli
28	188.5	23.8	1230	6	PCT-US95-10973A-12	Sequence 12, Appli
29	188.5	23.8	1230	6	PCT-US95-10973A-13	Sequence 13, Appli
30	188.5	23.8	1233	3	US-08-718-904-80	Sequence 80, Appli
31	188.5	23.8	1233	3	US-09-449-249-80	Sequence 80, Appli
32	188.5	23.8	1251	3	US-08-718-904-74	Sequence 74, Appli
33	188.5	23.8	1251	3	US-09-449-249-74	Sequence 74, Appli
34	188.5	23.8	1260	3	US-08-718-904-72	Sequence 72, Appli
35	188.5	23.8	1260	3	US-09-449-249-72	Sequence 72, Appli
36	188.5	23.8	1266	3	US-08-718-904-75	Sequence 75, Appli
37	188.5	23.8	1266	3	US-09-449-249-75	Sequence 75, Appli
38	188.5	23.8	1269	3	US-08-718-904-78	Sequence 78, Appli
39	188.5	23.8	1269	3	US-09-449-249-78	Sequence 78, Appli
40	188.5	23.8	1275	3	US-08-718-904-73	Sequence 73, Appli
41	188.5	23.8	1275	3	US-09-449-249-73	Sequence 73, Appli
42	188.5	23.8	1299	3	US-08-718-904-77	Sequence 77, Appli
43	188.5	23.8	1299	3	US-09-449-249-77	Sequence 77, Appli
44	188.5	23.8	1299	6	PCT-US95-10973A-58	Sequence 58, Appli
45	188.5	23.8	1320	3	US-08-718-904-76	Sequence 76, Appli

ALIGNMENTS

RESULT 1
US-08-373-858-1
; Sequence 1, Application US/08373858
; Patent No. 5633155
GENERAL INFORMATION:
; APPLICANT: Kim, Man-Keun
; APPLICANT: Lee, Kwan-Ho
; APPLICANT: Na, Byoung-Kook
; APPLICANT: Jeong, Han-Seung
; APPLICANT: Choi, Kyu-Whan
; APPLICANT: Moon, Young-Ho
; APPLICANT: Jeon, Hong-Seob
TITLE OF INVENTION: Expression Vector for Phytoacca
TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dady & Dady
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/373,858
FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

Db 339 GAACCAATTAATGCTGTACCATATCTTTAATGATCTCAGTACTGAACGCCAAGAT 398
Qy 102 ValGluAsnThrLeuCySerSerSerSerSerSerValAlaMetSerIleAsnTyrAsn 121
Db 339 GTAGAGACTACTCTTGTCCCAATATCCATTTCTGTGTAGTAAACATTAACCTTGTAT 458
Qy 122 SerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAsnGlnValGlnLeu 141
Db 459 AGTCATATCCAAATTCGAATCGAATCAAAAGCGAGATGAATCAAGAGTCAACTCCAACTG 518
Qy 142 GylIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
Db 519 GGAATTCAAATATCTGACAGATATATGTGAAAGATTCT 557

RESULT 3
US-08-500-611-1
Sequence 1, Application US/08500611
Patent No. 5756322
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun E.
TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSES: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,611
FILING DATE: 11-JUL-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-611-1
Alignment Scores:
Pred. No.: 1.5e-70 Length: 1379
Score: 596.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
DB: 2 Gaps: 0

US-09-978-274A-6 (1-154) x US-08-500-611-1 (1-1379)
Qy 2 IleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMet 21
Db 291 GTGAATCAATCAATCAATCAATGTGAATGACCACTTACCAATCAATCAATCAATCTG 350
Qy 22 GluSerLeuAspGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeu 41
Db 351 AATGATCTTGTAATGAGCCAAAGATCCAGTTTAAAGCTAATGAAATCCAAATGCTG 410
Qy 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
Db 411 CCCAATCAATATCAATATCCAAAGTACGTGTGTGAGCTCAAGGTTCAAATTAATAA 470
Qy 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
Db 471 ACCATCACTAAAGTCGAGCGAAGCAATTTGTATGTGAAGGGTTATTCGATCCCTTT 530
Qy 82 AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db 531 GAACCAATTAATGCTGTACCATATCTTTAATGATCTCAGTACTGAACGCCAAGAT 590
Qy 102 ValGluAsnThrLeuCySerSerSerSerSerSerValAlaMetSerIleAsnTyrAsn 121
Db 591 GTAGAGACTACTCTTGTCCCAATATCCATTTCTGTGTAGTAAACATTAACCTTGTAT 650
Qy 122 SerLeuTyrProThrMetGluLysLysAlaGluValAsnSerArgAsnGlnValGlnLeu 141
Db 651 AGTCATATCCAAATTCGAATCGAATCAAAAGCGAGATGAATCAAGAGTCAAGTCCAACTG 710
Qy 142 GylIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
Db 711 GGAATTCAAATATCTGACAGATATATGTGAAAGATTCT 749

RESULT 4
US-08-500-694-1
Sequence 1, Application US/08500694
Patent No. 5880329
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun E.
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSES: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,694
FILING DATE: 11-JUL-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:

```

; NAME/KEY: CDS
; LOCATION: 225..1163
; FEATURE: mutation
; NAME/KEY: mutation
; LOCATION: replace(233, "a")
; FEATURE: mutation
; NAME/KEY: replace(349, "g")
; FEATURE: mutation
; NAME/KEY: mutation
; LOCATION: replace(435, "c")
; US-08-500-694-1

Alignment Scores:
Pred. No.: 1.5e-70 Length: 1379
Score: 596.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
DB: 2 Gaps: 0

US-09-978-274A-6 (1-154) x US-08-500-694-1 (1-1379)

QY 2 ILeaenThrlleThrPheAepAlaGlyAaenAlaThrlleAenlyTyrlaThrPheMet 21
Db 291 GTGAATACATCAATCTCAATGTTGAAAGTACCCATTGCAATACGCCACTTTCTG 350
QY 22 GlSerleuArghAnGlnAlaLyAaPProlyleuTyCysTyrglylePrometleu 41
Db 351 AATGATCTTCGTATGAGCGAAGATCCAAAGTTTAAATGCTATGGAATACCAATCTG 410
QY 42 ProAepThraSerThrProlyTyrlleuValyleuGlnGlyAlaAaenleuLy 61
Db 411 CCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 470
QY 62 ThrlleThrlleuMetleuArghAaenleuTyrlaMetGlyTyrlSerAaPProPhe 81
Db 471 ACCATCACTAATGCTGAGACCAAAATTTGTATGTATGGTTATCTGATCCCTTT 530
QY 82 AenGlyAaenlyCySaTgTyrlHsllePheAaenAlleThrSerThrgluArghThraP 101
Db 531 GAAACCAATTAATGCTGTTTCCATATCTTTAATGATATCTCAAGTACTGAACGCCAAGT 590
QY 102 ValGluAaenThrlleuCySerSerSerSerSerArghValAlaMetSerlleAaenTyraa 121
Db 591 GTAGAGACTACTCTTGGCCCAATGCCCAATTCGTGTAGTAAAAACATTAACCTTGAT 650
QY 122 SerleuTyProThrlleuMetGlylyblybAlaGluValAaenSerArghAenGlnValGlnleu 141
Db 651 AGTCGATATCCAAATGGAATCAAAAGCGGAGATTAATCAAGAAAGTCAGTCCAACTG 710
QY 142 GlylleGlnleuSerSerAaPilleGlylyleSer 154
Db 711 GGAATCAATATCTCGACAGTAAATTTGGAAGATTTCT 749

RESULT 5
US-07-865-169-1
; Sequence 1, Application US/07865169
; Patent No. 6015940
; GENERAL INFORMATION:
; APPLICANT: Turner, Nilgun E.
; APPLICANT: Lodge, Jennifer K.
; APPLICANT: Kaniewski, Wojciech K.
; TITLE OF INVENTION: Virus Resistant Potato Plants
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. B94F
; STREET: 700 Chesterfield Parkway No. 6015940th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/865,169
; FILING DATE: 19920407
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10547)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6049
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1379 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-07-865-169-1

Alignment Scores:
Pred. No.: 1.5e-70 Length: 1379
Score: 596.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
DB: 3 Gaps: 0

US-09-978-274A-6 (1-154) x US-07-865-169-1 (1-1379)

QY 2 ILeaenThrlleThrPheAepAlaGlyAaenAlaThrlleAenlyTyrlaThrPheMet 21
Db 291 GTGAATACATCAATCTCAATGTTGAAAGTACCCATTGCAATACGCCACTTTCTG 350
QY 22 GlSerleuArghAnGlnAlaLyAaPProlyleuTyCysTyrglylePrometleu 41
Db 351 AATGATCTTCGTATGAGCGAAGATCCAAAGTTTAAATGCTATGGAATACCAATCTG 410
QY 42 ProAepThraSerThrProlyTyrlleuValyleuGlnGlyAlaAaenleuLy 61
Db 411 CCCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 470
QY 62 ThrlleThrlleuMetleuArghAaenleuTyrlaMetGlyTyrlSerAaPProPhe 81
Db 471 ACCATCACTAATGCTGAGACCAAAATTTGTATGTATGGTTATCTGATCCCTTT 530
QY 82 AenGlyAaenlyCySaTgTyrlHsllePheAaenAlleThrSerThrgluArghThraP 101
Db 531 GAAACCAATTAATGCTGTTTCCATATCTTTAATGATATCTCAAGTACTGAACGCCAAGT 590
QY 102 ValGluAaenThrlleuCySerSerSerSerSerArghValAlaMetSerlleAaenTyraa 121
Db 591 GTAGAGACTACTCTTGGCCCAATGCCCAATTCGTGTAGTAAAAACATTAACCTTGAT 650
QY 122 SerleuTyProThrlleuMetGlylyblybAlaGluValAaenSerArghAenGlnValGlnleu 141
Db 651 AGTCGATATCCAAATGGAATCAAAAGCGGAGATTAATCAAGAAAGTCAGTCCAACTG 710
QY 142 GlylleGlnleuSerSerAaPilleGlylyleSer 154
Db 711 GGAATCAATATCTCGACAGTAAATTTGGAAGATTTCT 749

RESULT 6
US-09-005-273-1
; Sequence 1, Application US/09005273
; Patent No. 6137030
; GENERAL INFORMATION:
; APPLICANT: Turner, Nilgun E.
; TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
```

TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
ADDRESSEE: MENTILIK
STREET: 600 South, Avenue West
CITY: Westfield
STATE: New Jersey
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,273
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,611
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE: 11-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
NAME/KEY: sig_peptide
LOCATION: 225..290
US-09-005-273-1
Alignment Scores:
Pred. No.: 1.5e-70 Length: 1379
Score: 596.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
Gaps: 0
US-09-978-274A-6 (1-154) x US-09-005-273-1 (1-1379)
QY 2 11aenThrlleThrPheAspAlaGlyAsnAlaThrlleAsnLysTyrAlaThrPheMet 21
DB 291 GTGATTCATCACTTCAATGAGTGAAGTACACCATTCAGCAATACGCACTTTCTG 350
QY 22 GluSerLeuArgAnglnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeu 41
DB 351 AATGATCTTCCTAATGAGCAAGATCCAGTTTAAATGCTATGGAATACCAATGCTG 410
QY 42 ProAspThrAsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLys 61
DB 411 CCGATATCAATATCAATCCAAAGTACGTTGTGTGAGCTCCAAAGGTTCAAAATRAAAA 470
QY 62 ThrIleThrLeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81

DB 471 ACCATTCACATTAAGCTGAGCGAACAATTGTATGTAGTGGTTATTCGATCCCTT 530
QY 82 AsnGlyAsnLysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
DB 531 GAAACCAATTAATGCTGTTACCATATCTTTATGATATCTCAGCTACGACCAAGAT 590
QY 102 ValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTyrAsn 121
DB 591 GTAGAGACTACTCTTGGCCAAATGCCAATTCCTGTTGTAGTAAAAACATTAACCTTGAT 650
QY 122 SerLeuTyrProThrMetGluLysAlaGluValAsnSerArgAnglnValGlnLeu 141
DB 651 AGTGATATTCACATTCGAAATCAAAACCGGAGTAAATCAAGAAATCAAGTCCAACTG 710
QY 142 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSer 154
DB 711 GGAATTCAAATATCTCGACAGTAATATTTGAAAGATTTCT 749
RESULT 7
US-08-501-253A-1
Sequence 1, Application US/08501253A
Patent No. 6146628
GENERAL INFORMATION:
APPLICANT: Uckun, Fatih
TITLE OF INVENTION: Biotherapeutic Agents Comprising
TITLE OF INVENTION: Recombinant Pap and Pap Mutants
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 6146628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: US
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,253A
FILING DATE: 11-JUL-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kettlerberger, Denise M.
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 600.323US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
US-08-501-253A-1
Alignment Scores:
Pred. No.: 1.5e-70 Length: 1379
Score: 596.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
Gaps: 0
US-09-978-274A-6 (1-154) x US-08-501-253A-1 (1-1379)

QY 2 115aantThrlleThrPheapAlaGlyAsnAlaThrlleAsnlySTyAlaThrPheMet 21
Db 291 GTGAATACATCATCTCAATGTTGGAAGTACCAACCATTTGCAAAATGCGCACTTTTCTG 350
QY 22 GluSerleuArganglnAlaYAspProlyleuLysCysTyGlyllePrometleu 41
Db 351 AATGATCTTGTATGAGGAGGAAAGATCCAAAGTTTAAAGCTATGGAATACCAATGCTG 410
QY 42 ProAspThrAsnSerThrProlySTyLeuLeuValLysleuGlnGlyAlaAsnLeuLys 61
Db 411 CCCAATCAATACCAATCCAAAGTACGTTGTTGTTGAGCTCCAAAGTTTCAATTAATAAAA 470
QY 62 ThrleThrlleuMetleuArgArgAsnAsnLeuTyValMetGlyTySerAspProPhe 81
Db 471 ACCATCACACTAATGCTGAGACGAAACAATTTGTATGTATGAGTTATTCGATCCCTTT 530
QY 82 AsnGlyAsnlySCysAlaGlyThrllePheAsnAspilleThrSerThrlGluArgThrAsp 101
Db 531 GAAACCAATTAAGTCTGATACCAATCTTAAATGATATCTCAGGTACTGAAACGCCAAGAT 590
QY 102 ValGluAsnThrlleuCysSerSerSerSerSerArgValAlaMetSerilleAsnTyraAsn 121
Db 591 GTGAGACTACTCTTTTCCCAATGCCAATCTCTGTGTGTAATAAACAATAAATTTGAT 650
QY 122 SerleuTyProThrMetGluTyValGluValAsnSerArganglnValGlnLeu 141
Db 651 AGTCGATATCCAACTTGAATCAAAAGCGGAGTAATAATCAAGAAGTCAAGTCCAACTG 710
QY 142 GlylleGlnlleleuSerSerAspilleGlylylleSer 154
Db 711 GGAATTCAAATACTCGACAGTAATATTGAAAGATTCTT 749

RESULT 8

PCT-US96-11546-1
Sequence 1, Application PC/TUS9611546
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein
TITLE OF INVENTION: Mutants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
PCT-US96-11546-1

Alignment Scores:

Pred. No.:	Length:
Score: 1.5e-70	1379
Percent Similarity: 596.00	Matches: 110
Best Local Similarity: 86.9%	Conservative: 23
Query Match: 71.9%	Mismatches: 20
DB: 6	Indels: 0
	Gaps: 0

US-09-978-274a-6 (1-154) x PCT-US96-11546-1 (1-1379)

QY 2 115aantThrlleThrPheapAlaGlyAsnAlaThrlleAsnlySTyAlaThrPheMet 21
Db 291 GTGAATACATCATCTCAATGTTGGAAGTACCAACCATTTGCAAAATGCGCACTTTTCTG 350
QY 22 GluSerleuArganglnAlaYAspProlyleuLysCysTyGlyllePrometleu 41
Db 351 AATGATCTTGTATGAGGAGGAAAGATCCAAAGTTTAAAGCTATGGAATACCAATGCTG 410
QY 42 ProAspThrAsnSerThrProlySTyLeuLeuValLysleuGlnGlyAlaAsnLeuLys 61
Db 411 CCCAATCAATACCAATCCAAAGTACGTTGTTGTTGAGCTCCAAAGTTTCAATTAATAAAA 470
QY 62 ThrleThrlleuMetleuArgArgAsnAsnLeuTyValMetGlyTySerAspProPhe 81
Db 471 ACCATCACACTAATGCTGAGACGAAACAATTTGTATGTATGAGTTATTCGATCCCTTT 530
QY 82 AsnGlyAsnlySCysAlaGlyThrllePheAsnAspilleThrSerThrlGluArgThrAsp 101
Db 531 GAAACCAATTAAGTCTGATACCAATCTTAAATGATATCTCAGGTACTGAAACGCCAAGAT 590
QY 102 ValGluAsnThrlleuCysSerSerSerSerSerArgValAlaMetSerilleAsnTyraAsn 121
Db 591 GTGAGACTACTCTTTTCCCAATGCCAATCTCTGTGTGTAATAAACAATAAATTTGAT 650
QY 122 SerleuTyProThrMetGluTyValGluValAsnSerArganglnValGlnLeu 141
Db 651 AGTCGATATCCAACTTGAATCAAAAGCGGAGTAATAATCAAGAAGTCAAGTCCAACTG 710
QY 142 GlylleGlnlleleuSerSerAspilleGlylylleSer 154
Db 711 GGAATTCAAATACTCGACAGTAATATTGAAAGATTCTT 749

RESULT 9

US-07-865-169-2
Sequence 2, Application US/07865169
Patent No. 6015940
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
APPLICANT: Lodge, Jennifer K.
APPLICANT: Kaniewski, Wojciech K.
TITLE OF INVENTION: Virus Resistant Potato Plants
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. B34F
STREET: 700 Chesterfield Parkway No. 6015940ch
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865,169
FILING DATE: 19920407
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10547)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-865-169-2

Alignment Scores:
Pred. No.: 1,82e-69 Length: 1379
Score: 588.00 Matches: 109
Percent Similarity: 86.3% Conservative: 23
Best Local Similarity: 71.2% Mismatches: 21
Query Match: 74.1% Indels: 0
Gaps: 0

US-09-978-274A-6 (1-154) x US-07-865-169-2 (1-1379)

QY 2 IleaThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLeuYrAlaThrPheMet 21
Db 291 GTGAATCAATCAATCAATCAATGTTGAGTACCAACCATTAAGCAATGTTTGG 350
QY 22 GluSerLeuArgAngInAlaLeuAspProlyLeuLeuYrGlyIleProMetLeu 41
Db 351 AATGATCTTGTAAATGAAGCAAGATCAAGTTTAAATCTTGAATACCAATGCTG 410
QY 42 ProAspThrAsnSerThrProlyLeuLeuValLeuGlnGlyAlaAsnLeuYs 61
Db 411 CCCAATCAATCAATCAATCAATGTTGAGTACCAACCATTAAGCAATGTTTGG 470
QY 62 ThrIleThrLeuMetLeuArgAsnAsnLeuYrValMetGlyYrSerAspProPhe 81
Db 471 ACCATCACTAATGCTGAGACGAACCAATTTGATGATGATGATGATGATGATGAT 530
QY 82 AsnGlyAsnLeuYrCybArgYrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db 531 GAAACCAATCAATCAATCAATGTTGAGTACCAACCATTAAGCAATGTTTGG 590
QY 102 ValGluAsnThrLeuCybSerSerSerSerSerArgValAlaMetSerIleAsnYrAsn 121
Db 591 GTAGAGACTACTCTTGGCCCAATGCCAATCTCTGTTAGTAAACATTAACCTTGAT 650
QY 122 SerLeuYrProThrMetGluLeuYrAlaGluValAsnSerArgAsnGlnValGlnLeu 141
Db 651 AGTCGATATCAATCAATGATCAAAAGCGGAGATTAATCAAGAGTCAAGTCAACTG 710
QY 142 GlyIleGlnIleLeuSerSerAspIleGlyYrIleSer 154
Db 711 GGAATTCAAATATCTCGACATGAATATGGAAGAATTCT 749

RESULT 10
US-09-005-273-3
Sequence 3, Application US/09005273
Patent No. 6137030
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun E.

TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: LERNER, DAVID, LITTENBERG, KRUMHOLTZ &
ADDRESSER: MENTILIK
STREET: 600 South, Avenue West
CITY: Westfield
STATE: New Jersey
COUNTRY: USA
ZIP: 07090

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,273
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,611
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE: 11-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 225..290
US-09-005-273-3

Alignment Scores:
Pred. No.: 1,82e-69 Length: 1379
Score: 588.00 Matches: 109
Percent Similarity: 86.3% Conservative: 23
Best Local Similarity: 71.2% Mismatches: 21
Query Match: 74.1% Indels: 0
Gaps: 0

US-09-978-274A-6 (1-154) x US-09-005-273-3 (1-1379)

QY 2 IleaThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLeuYrAlaThrPheMet 21
Db 291 GTGAATCAATCAATCAATGTTGAGTACCAACCATTAAGCAATGTTTGG 350
QY 22 GluSerLeuArgAngInAlaLeuAspProlyLeuLeuYrGlyIleProMetLeu 41
Db 351 AATGATCTTGTAAATGAAGCAAGATCAAGTTTAAATCTTGAATACCAATGCTG 410
QY 42 ProAspThrAsnSerThrProlyYrLeuLeuValLeuGlnGlyAlaAsnLeuYs 61
Db 411 CCCAATCAATCAATCAATCAATGTTGAGTACCAACCATTAAGCAATGTTTGG 470


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1 REFERENCE/DOCKET NUMBER: 0136/0A445
2
3 TELECOMMUNICATION INFORMATION:
4
5 TELEPHONE: 212-527-7700
6
7 TELEFAX: 212-753-6237
8
9 TELEX: 236687
10
11 INFORMATION FOR SER ID NO: 1:
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13 SEQUENCE CHARACTERISTICS:
14
15 LENGTH: 916 base pairs
16
17 TYPE: nucleic acid
18
19 STRANDEDNESS: single
20
21 TOPOLOGY: linear
22
23 MOLECULE TYPE: cDNA to mRNA
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25 HYPOTHEetical: NO
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27 ANTI-SENSE: NO
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29 ORIGINAL SOURCE:
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31 ORGANISM: Physalacca insularis Nakai
32
33 TISSUE TYPE: leaf
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35 IMMEDIATE SOURCE:
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37 CLONE: PIP
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Db 358 GTAGAGACTACTCTTGGCCCAATGCCGATCTCGTGTGGTAAACATMAACTATGAT 417
QY 122 SerleuTyPProThrMetGluLyAAlaGluValAaAserAryrAaAgluValGluA 141
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QY 142 GlylleGluAaAserSerSerSerSerSerSerSerSerSerSerSerSerSerSer 154
Db 478 GGAATTCGAACTACTCGACAGTGCATGGAAGATTTCT 516
RESULT 14
US-08-356-161-7
Sequence 7, Application US/08356161
Patent No. 5916772
GENERAL INFORMATION:
APPLICANT: Lappi, Douglas A.
APPLICANT: Baithelmy, Isabel
APPLICANT: Baird, J. Andrew
APPLICANT: Sosnowski, Barbara A.
TITLE OF INVENTION: RECOMBINANT PRODUCTION OF
TITLE OF INVENTION: SAPORIN-CONTAINING PROTEINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 701 Fifth Avenue, 6300 Columbia Center
City: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,161
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,161
FILING DATE: 13-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: No. 5916772tenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.404US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..804
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..804
OTHER INFORMATION: /notes= "Nucleotide sequence
OTHER INFORMATION: corresponding to the clone M13 mp18-G9 in Example 1.B.2."
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 46..804

OTHER INFORMATION: /product= "Saporin"
US-08-356-161-7
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Score: 190.50 Matches: 50
Percent Similarity: 55.0% Conserved: 38
Best Local Similarity: 31.2% Mismatches: 59
Query Match: 24.0% Indels: 13
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QY 22 GluSerleuAryrAaAAlaAlyAaAProlyAaAlyAaAlyAaAlyAaAlyAaAlyAaA 40
Db 106 GATTAATATCCGAACCAACGTAAGATCCAAACTGAATATAGGTATCCGATACGAC 165
QY 41 leuProAaAThrAaAserThrProlyAaAlyAaAlyAaAlyAaAlyAaAlyAaAlyAa 60
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QY 61 lyeThrlleThrlleuAaAlyAaAAlaAaAAlaAaAAlaAaAAlaAaAAlaAaAAlaA 78
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US-08-718-904-23
Sequence 23, Application US/08718904
Patent No. 6037329
GENERAL INFORMATION:
APPLICANT: Baird, J. Andrew
APPLICANT: Chandler, Lois Ann
APPLICANT: Sosnowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6037329tenburg Ph.D., Carol

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; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 760100.415C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 804 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..804
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..804
; OTHER INFORMATION: /note= "Nucleotide sequence
; OTHER INFORMATION: corresponding to the clone M13 mp18-69 in Example I.B.2."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 46..804
; OTHER INFORMATION: /product= "Saporin"
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US-08-718-904-23

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Alignment Scores:
Pred. No.: 5.21e-16 Length: 804
Score: 190.50 Matches: 50
Percent Similarity: 55.0% Conservative: 38
Best Local Similarity: 31.2% Mismatches: 19
Query Match: 24.0% Indels: 13
DB: 3 Gaps: 6

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US-09-978-274A-6 (1-154) x US-08-718-904-23 (1-804)

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 Job time : 172.1 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 9, 2006, 01:45:16 ; Search time 551.36 Seconds
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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5	596	75.2	1379	3	US-09-978-274A-30
6	596	75.2	1379	10	US-11-106-187-1
7	588	74.1	1368	3	US-09-978-274A-31

8	584.5	73.7	1376	8	US-10-467-009-1	Sequence 1, Appl
9	261	32.9	934	3	US-09-978-274A-32	Sequence 32, Appl
10	261	32.8	934	10	US-11-106-187-20	Sequence 3, Appl
11	260	32.8	855	10	US-11-106-187-20	Sequence 20, Appl
12	196.5	24.8	765	3	US-09-792-793A-66	Sequence 66, Appl
13	196.5	24.8	765	6	US-10-375-209A-66	Sequence 66, Appl
14	196.5	24.8	984	3	US-09-792-793A-60	Sequence 60, Appl
15	196.5	24.8	984	6	US-10-375-209A-60	Sequence 60, Appl
16	196.5	24.8	993	3	US-09-792-793A-63	Sequence 63, Appl
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18	196.5	24.8	999	3	US-09-792-793A-54	Sequence 54, Appl
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23	190.5	24.0	804	3	US-09-861-257-38	Sequence 38, Appl
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37	188.5	23.8	1269	6	US-10-189-360-78	Sequence 78, Appl
38	188.5	23.8	1275	3	US-09-861-257-76	Sequence 76, Appl
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40	188.5	23.8	1299	3	US-09-861-257-80	Sequence 80, Appl
41	188.5	23.8	1299	6	US-10-189-360-77	Sequence 77, Appl
42	188.5	23.8	1320	3	US-09-861-257-79	Sequence 79, Appl
43	188.5	23.8	1320	6	US-10-189-360-76	Sequence 76, Appl
44	184.5	23.3	804	3	US-09-861-257-35	Sequence 35, Appl
45	184.5	23.3	804	3	US-09-861-257-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-09-978-274A-5
Sequence 5, Application US/0978274A
Patent No. US20020116737A1

GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Ackinson, Howard
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 465
TYPE: DNA
ORGANISM: PhytoIaccia americana
US-09-978-274A-5

Alignment Scores:

Pred. No.: 6,78e-99
Score: 793.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
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Length: 465
Matches: 154
Conservative: 0
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US-09-978-274A-6 (1-154) x US-09-978-274A-5 (1-465)

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RESULT 2

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; Sequence 3, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Phytolacca americana
US-09-978-274A-3
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Alignment Scores:

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US-09-978-274A-6 (1-154) x US-09-978-274A-3 (1-792)

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RESULT 3

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; Sequence 19, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PAP-S/Cystatin fusion
US-09-978-274A-19
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Alignment Scores:

Pred. No.:	2.6e-98	Length:	1092
Score:	793.00	Matches:	154
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-09-978-274A-6 (1-154) x US-09-978-274A-19 (1-1092)

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QY 1 MetIleasanthrilethrpheaspaalaglyasnaalathrileasnytyralathrPhe 20
DB 1 ATGATTAATACGATCAGCTTTGATGCTGGAATGCCCATTTAACTTAACCAATATGCCACTTT 60
QY 21 MetGluserieuarganginalalyaspprolyaleuyscytyrglyilepromet 40
DB 61 ATGGAATCTCTTCGTATTCAGCGAAGATCCAAATCTAAATGCTATGCGATCCAAATG 120
QY 41 LeuProaspthrasnserrthproulytyrleuleuVallyleuenginglyalaasleu 60
DB 121 CTACCTGATACCTAATTCAGCCCTTAAGTACTTATTTGATTAAGCTCCAAAGGCGAAACCTA 180
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Qy 61 LysThrIleThrLeuMetLeuArgAsnAsnLeuTyValMetGlyTySerAspPro 80
Db 181 AAAACATTAACATTAATGCTGAGAGAAATACTTAATCGTAGGGCTATTCTGATCCC 240.
Qy 81 PheAsnGlyAsnLeuTySerAspTyHisIlePheAsnAspIleThrSerThrGluArgThr 100
Db 241 TTCAATGCGCAATTAAGTGTGCTTACCATATTAATGATTAATACAGACGCAAGCACT 300
Qy 101 AspValGluAsnThrLeuCySerSerSerSerSerArgValAlaMetSerIleAsnTy 120
Db 301 GATGGAGAAATACCTTGTCTCAAGTCTAGTCTCGTGTGCAATGTCATTAACTAC 360
Qy 121 AsnSerLeuTyProThrMetGluValLeuValGluValAsnSerArgAsnGlnValGln 140
Db 361 AATGCTTATATCCGACCATGGAAGAAAGCAAGAACTCAAGAAATCAAGTCCA 420
Qy 141 LeuGlyIleGlnIleLeuSerSerSerSerSerSerSerSerSerSerSerSerSer 154
Db 421 TTGGGAATTCAAATATCTCAGCAGTCACTGGAATAATCTCT 462

RESULT 4

US-09-978-274A-1
Sequence 1, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Ackinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
CURRENT FILING DATE: 2001-10-15
PRIORITY APPLICATION NUMBER: 0025225.4
PRIORITY FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 945
TYPE: DNA
ORGANISM: Phytolacca americana
US-09-978-274A-1

Alignment Scores:

Pred. No.: 1.01e-97 Length: 945
Score: 788.00 Matches: 153
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.4% Indels: 0
Gaps: 0

US-09-978-274A-6 (1-154) x US-09-978-274A-1 (1-945)

Qy 2 ILeaAnthrIleThrPheAspAlaGlyAsnAlaThrIleAsnLeuTyValaThrPheMet 21
Db 73 ATAAATAGCATCACTTTGATGCGGAATGCCACATTAACAATAGCCACTTTATG 132
Qy 22 GluSerLeuArgAsnGlnAlaLeuAspProLysLeuTySerTyGlyIleProMetLeu 41
Db 133 GAATCTCTTCCTAATCAAGCGAAAGATCCAAATCAAAATGCTATGGATACCAATGCTA 192
Qy 42 ProAspThrAsnSerThrProLysTyLeuLeuValLeuGlnGlyValaAsnLeuTy 61
Db 193 CCAATATCAATTAATGACCCCTTAAGTACTTAATGTTAGGCTCAAGGTCGCAACCTTAA 252
Qy 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTyValMetGlyTySerAspProPhe 81
Db 253 ACCATTAACATTAATGCTGAGCGAAATTAATTAATGCGATGGGCTATTCGATCCCTTC 312
Qy 82 AsnGlyAsnLeuTySerAspTyHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db 313 AATGGCAATTAAGTGTGCTTACCATATTAATGATTAATTAACAGACCGAAGCACTGAT 372

Qy 102 ValGluAsnThrLeuCySerSerSerSerSerArgValAlaMetSerIleAsnTyAsn 121
Db 373 GTGAGAAATACCTTTGCTCAAGTCTAGTCTCGTTCGCAATGCTCAATTAATCAAT 432
Qy 122 SerLeuTyProThrMetGluValLeuValGluValAsnSerArgAsnGlnValGln 141
Db 433 AGCTTATATCCGACCATGGAAGAAAGCAAGAAATCAAGAAATCAAGTCAATG 492
Qy 142 GlyIleGlnIleLeuSerSerSerSerSerSerSerSerSerSerSerSerSer 154
Db 493 GGAATTCAAATATCTCAGCAGTCACTGGAATAATCTCT 531

RESULT 5

US-09-978-274A-30
Sequence 30, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Ackinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
CURRENT FILING DATE: 2001-10-15
PRIORITY APPLICATION NUMBER: 0025225.4
PRIORITY FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 1379
TYPE: DNA
ORGANISM: Phytolacca americana
US-09-978-274A-30

Alignment Scores:

Pred. No.: 5.43e-71 Length: 1379
Score: 596.00 Matches: 110
Percent Similarity: 86.9% Conservative: 23
Best Local Similarity: 71.9% Mismatches: 20
Query Match: 75.2% Indels: 0
Gaps: 0

US-09-978-274A-6 (1-154) x US-09-978-274A-30 (1-1379)

Qy 2 ILeaAnthrIleThrPheAspAlaGlyAsnAlaThrIleAsnLeuTyValaThrPheMet 21
Db 291 GTGAATCAATCATCTCAATGTTGGAAGTACCACTTAAGCAATGCGCACATTTCTG 350
Qy 22 GluSerLeuArgAsnGlnAlaLeuAspProLysLeuTySerTyGlyIleProMetLeu 41
Db 351 AATGATCTTGTATATGAAGCGAAAGATCCAAATTAAGTATGATGGAATTAACCAATGCTG 410
Qy 42 ProAspThrAsnSerThrProLysTyLeuLeuValLeuGlnGlyValaAsnLeuTy 61
Db 411 CCCAATCAAAATTAATCAATCAAAATGCTGTTGTTGAGTCCAAAGTTCAAAATTAATA 470
Qy 62 ThrIleThrLeuMetLeuArgAsnAsnLeuTyValMetGlyTySerAspProPhe 81
Db 471 ACCATCACTAATGCTGAGACCAAAATTTGATGATGATGATGATGATGATGATGAT 530
Qy 82 AsnGlyAsnLeuTySerAspTyHisIlePheAsnAspIleThrSerThrGluArgThrAsp 101
Db 531 GAAACCAATTAAGTGTGCTTACCAATCTTAATGATTAATGACGATCAAGCGCAAGAT 590
Qy 102 ValGluAsnThrLeuCySerSerSerSerSerSerSerSerSerSerSerSerSer 121
Db 591 GTGAGATCACTCTTTGCGCAAAATGCCAATTCGATGTTAATTAATTAATTAATTAAT 650
Qy 122 SerLeuTyProThrMetGluValLeuValGluValAsnSerArgAsnGlnValGln 141
Db 651 AGTCATATCAACATTCGATGGAATCAAAAGCGGAGTAAATCAAGAAATGATGATCACTG 710

Pred. No.:	3.82e-16	length:	984
Percent:	196.50	Matches:	51
Percent Similarity:	55.3%	Conservative:	38
Best Local Similarity:	31.7%	Mismatches:	59
Query Match:	24.8%	Indels:	13
DB:	3	Gaps:	6

US-09-978-274A-6 (1-154) X US-09-792-793A-60 (1-984)

Qy	MeLleasnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnValAlaThrPhe	20
Dp	220 ATGGTACTAGATTACCTCGACCTGGTCATCCGACCGCGGCATTATGACGCTTC	279
Qy	21 MetGluSerLeuAlaArgAsnAlaIleValAspProIleValLeuIleValMet	40
Dp	280 GTGGATTAAATTGTTAACAACGTAAAGATCCGAATCTGAATACGGTGTATCTGAATAT	339
Qy	41 ---LeuProAspThrAsnSerThrProIleValLeuValIleValGlnGlyAlaAsn	59
Dp	340 GCGGTATCCGTCGCCCGACCAAGAAAGTTCTGGCATTAACTTTCAAAGCTCCCGT	399
Qy	60 LeuIleThrIleThrLeuMetLeuAlaArgAsnAsnLeuIleValMetGlyTyr----	77
Dp	400 ---GGCACTGTTTCTCTGGGGCTGAAGCCGCAATACTGTATGTTGTGGCTATCTGGCG	456
Qy	78 SerAspProPheAsnGlyAsnIleValGlyGlnIlePheAsnAspIleThrSerThr	97
Dp	457 ATGATATATACGAACGTGAACCGCGCC--TACTACTTTCGTGAAGATTAACAAGCGG	513
Qy	98 GluArgThrAspValGluAsnThrIleCysSerSerSerSerSerArgValAlaMetSer	117
Dp	514 GAATTCACACT-----GCTCGTTCCCGAGGCGACACATCGCAACCAAAAAGCA	561
Qy	118 IleAsnThrAsnSerLeuTyrProThrMetGluValGlyValAlaGluVal-----	133
Dp	562 CTGAAGATATCGGAAGATTACCAATCATCAATCGAAGAAACGGCAATATCAACGAGGCGAT	621
Qy	134 AsnSerArgAsnGlnIleValGlnIleGlnIleGlnIleLeuSerSerAspIleGlyAsIle	153
Dp	622 CAATCCCGCAAAAGAACTGGGTCTGGGTATTGATCTCTGAAGACAGATCGAAGCGGCTC	681
Qy	154 Ser	154
Dp	682 AAC	684

RESULT 15
US-10-375-209A-60
; Sequence 60, Application US/10375209A
; Publication No. US20030215421A1

Alignment Scores:	
Pred. No.:	3.82e-16
Length:	984

Score:	196.50	Matches:	57
Percent Similarity:	55.34	Conservative:	35
Best Local Similarity:	21.74	Mismatches:	55
Query Match:	24.84	Indels:	1
DB:	6	Gaps:	6

US-09-978-274A-6 (1-154) X US-10-375-209A-60 (1-984)

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Job time : 554.36 secs
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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 9, 2006, 01:48:26 ; Search time 403.952 Seconds
(without alignments)
1525.144 Million cell updates/sec

Title: US-09-978-274A-6

Perfect score: 793

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 9267905 seqs, 2000278028 residues

Total number of hits satisfying chosen parameters: 18535810

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/abs/ABSSWB_spool/US09978274/runat_07042006_173042_28604/app_query.fasta.1
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blowm62
-TRANS=numan40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs803p
-USER=US09978274.ecgn_1_2451@runat.07042006_173042_28604 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:
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2: /SIDS5/ptodata/1/pubpna/US07_NEW_PUB.seq:
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12: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:
13: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:
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15: /SIDS5/ptodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No. Score Query Match Length DB ID Description
1 596 75.2 1360 14 US-11-010-795-19 Sequence 19, Appl
2 261 32.9 934 14 US-11-010-795-21 Sequence 21, Appl

3 112 14.1 1855 8 US-10-893-584-3 Sequence 3, Appl
4 112 14.1 1855 8 US-10-893-584-5 Sequence 5, Appl
5 112 14.1 1855 8 US-10-893-584-7 Sequence 7, Appl
6 112 14.1 1855 8 US-10-893-584-9 Sequence 9, Appl
7 112 14.1 1855 8 US-10-893-584-13 Sequence 13, Appl
8 112 14.1 1855 8 US-10-893-584-15 Sequence 15, Appl
9 112 14.1 1855 8 US-10-893-584-17 Sequence 17, Appl
10 112 14.1 1855 8 US-10-893-584-19 Sequence 19, Appl
11 112 14.1 1855 8 US-10-893-584-21 Sequence 21, Appl
12 112 14.1 1855 8 US-10-893-584-23 Sequence 23, Appl
13 112 14.1 1855 8 US-10-893-584-25 Sequence 25, Appl
14 112 14.1 1855 8 US-10-893-584-27 Sequence 27, Appl
15 112 14.1 1855 8 US-10-893-584-29 Sequence 29, Appl
16 112 14.1 1855 8 US-10-893-584-31 Sequence 31, Appl
17 112 14.1 1855 8 US-10-893-584-33 Sequence 33, Appl
18 112 14.1 1855 8 US-10-893-584-35 Sequence 35, Appl
19 112 14.1 1855 8 US-10-893-584-37 Sequence 37, Appl
20 112 14.1 1855 8 US-10-893-584-39 Sequence 39, Appl
21 112 14.1 1855 8 US-10-893-584-41 Sequence 41, Appl
22 112 14.1 1855 8 US-10-893-584-43 Sequence 43, Appl
23 112 14.1 1855 8 US-10-893-584-45 Sequence 45, Appl
24 112 14.1 1855 8 US-10-893-584-47 Sequence 47, Appl
25 112 14.1 1855 8 US-10-893-584-49 Sequence 49, Appl
26 112 14.1 1855 8 US-10-893-584-51 Sequence 51, Appl
27 112 14.1 1855 8 US-10-893-584-53 Sequence 53, Appl
28 112 14.1 1855 8 US-10-893-584-55 Sequence 55, Appl
29 112 14.1 1855 8 US-10-893-584-57 Sequence 57, Appl
30 112 14.1 1855 8 US-10-893-584-59 Sequence 59, Appl
31 112 14.1 1855 8 US-10-893-584-61 Sequence 61, Appl
32 112 14.1 1855 8 US-10-893-584-63 Sequence 63, Appl
33 112 14.1 1855 8 US-10-893-584-65 Sequence 65, Appl
34 112 14.1 1855 8 US-10-893-584-67 Sequence 67, Appl
35 112 14.1 1855 8 US-10-893-584-69 Sequence 69, Appl
36 112 14.1 1855 8 US-10-893-584-71 Sequence 71, Appl
37 112 14.1 1855 8 US-10-893-584-73 Sequence 73, Appl
38 112 14.1 1855 8 US-10-893-584-75 Sequence 75, Appl
39 112 14.1 1855 8 US-10-893-584-77 Sequence 77, Appl
40 112 14.1 1855 8 US-10-893-584-79 Sequence 79, Appl
41 112 14.1 1855 8 US-10-893-584-81 Sequence 81, Appl
42 112 14.1 1855 8 US-10-893-584-83 Sequence 83, Appl
43 112 14.1 1855 8 US-10-893-584-85 Sequence 85, Appl
44 112 14.1 1855 8 US-10-893-584-87 Sequence 87, Appl
45 112 14.1 1855 8 US-10-893-584-89 Sequence 89, Appl

ALIGNMENTS

RESULT 1
US-11-010-795-19
Sequence 19, Application US/11010795
Publication No. US20060005271A1
GENERAL INFORMATION:
APPLICANT: TUMER, NINGUN E.
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
TITLE OR INVENTION: RESISTANT TO TRICHOHEPENE FUNGAL TOXINS
FILE REFERENCE: OCTRS 3.0-085
CURRENT APPLICATION NUMBER: US/11/010.795
PRIOR APPLICATION NUMBER: 2004-12-13
PRIOR FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 19
LENGTH: 1360
TYPE: DNA
ORGANISM: Phytolacca americana
FEATURE:
NAME/KEY: CDS
LOCATION: (207)..(1145)
US-11-010-795-19
Alignment Scores:

Db 136 ATAACTTTACCAACAGCGGTCCTGCTGCAAGCTTACCAACTTTATCAGACTGTT 195
 Qy 25 ArgAnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 44
 Db 196 CGCGGTCGTTTAAACAACGAGCTGATGTGAGACATGATATACAGTGTGGCCAAACAGA 255
 Qy 45 AenSerThrPro-----LysTyrLeuLeuValLysLeuGlnGlyValAsnLeuLys 61
 Db 256 GTTGGTTGGCCATTAACCAACGAGTTTATTTAGTTGGAACCTCAAAATCAGCAGACTT 315
 Qy 62 ThrIleThrMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
 Db 316 TCTGTACATTCAGCCCTGATGTCAACCAATGATATGTGCTGCTACCGT----- 366
 Qy 82 AenGlyAsnLysCysArgTyr----- 88
 Db 367 GCTGGAATATAGCGCATATTTCTTTCATCTGACATCAGAAAGATCAGAACCAATCACT 426
 Qy 89 HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCySer 108
 Db 427 CATCTTTC-----ACTGATGTTCAAAAT----- 450
 Qy 109 SerSerSerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGlu 128
 Db 451 -----CGATATACATTCGCTTGTGTGTAAT-----TATGATAGACTTGA 492
 Qy 129 LysLysAlaGluValAsnSerArgAsnGlnValGlnLeuGly 142
 Db 493 CACTTGTCTGCT--AACTGTGAGAGAAATATCGAGTTGGGA 531

RESULT 8
 US-10-893-584-15
 ; Sequence 15, Application US/10893584
 ; Publication No. US20050272048A1

GENERAL INFORMATION:
 APPLICANT: Borgford, Thor
 APPLICANT: Braun, Curtis
 APPLICANT: Purac, Admir
 APPLICANT: Stoll, Dominik
 TITLE OF INVENTION: Ricin-like Toxin Variants for Treatment of Cancer.
 TITLE OF INVENTION: Viral or Parasitic Infections
 FILE REFERENCE: 10447-025
 CURRENT APPLICATION NUMBER: US/10/893,584
 PRIOR FILING DATE: 2004-07-19
 PRIOR APPLICATION NUMBER: US 09/551,151
 PRIOR FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: US 09/403,752
 PRIOR FILING DATE: 1999-10-29
 PRIOR APPLICATION NUMBER: US 10/089,058
 PRIOR FILING DATE: 2000-10-04
 NUMBER OF SEQ ID NOS: 274
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 15
 LENGTH: 1855
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: pAP-226 insert
 US-10-893-584-15

Alignment Scores:
 Pred. No.: 0.00613 Length: 1855
 Score: 112.00 Matches: 40
 Percent Similarity: 40.9% Conservative: 23
 Best Local Similarity: 26.0% Mismatches: 53
 Query Match: 14.1% Indels: 38
 DB: 8 Gaps: 7

US-09-978-274A-6 (1-154) x US-10-893-584-15 (1-1855)

Qy 5 IleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGluSerLeu 24
 Db 136 ATAACTTTACCAACAGCGGTCCTGCTGCAAGCTTACCAACTTTATCAGACTGTT 195

Qy 25 ArgAnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 44
 Db 196 CGCGGTCGTTTAAACAACGAGCTGATGTGAGACATGATATACAGTGTGGCCAAACAGA 255
 Qy 45 AenSerThrPro-----LysTyrLeuLeuValLysLeuGlnGlyValAsnLeuLys 61
 Db 256 GTTGGTTGGCCATTAACCAACGAGTTTATTTAGTTGGAACCTCAAAATCAGCAGACTT 315
 Qy 62 ThrIleThrMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPhe 81
 Db 316 TCTGTACATTCAGCCCTGATGTCAACCAATGATATGTGCTGCTACCGT----- 366
 Qy 82 AenGlyAsnLysCysArgTyr----- 88
 Db 367 GCTGGAATATAGCGCATATTTCTTTCATCTGACATCAGAAAGATCAGAACCAATCACT 426
 Qy 89 HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCySer 108
 Db 427 CATCTTTC-----ACTGATGTTCAAAAT----- 450
 Qy 109 SerSerSerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGlu 128
 Db 451 -----CGATATACATTCGCTTGTGTGTAAT-----TATGATAGACTTGA 492
 Qy 129 LysLysAlaGluValAsnSerArgAsnGlnValGlnLeuGly 142
 Db 493 CACTTGTCTGCT--AACTGTGAGAGAAATATCGAGTTGGGA 531

RESULT 9
 US-10-893-584-17
 ; Sequence 17, Application US/10893584
 ; Publication No. US20050272048A1

GENERAL INFORMATION:
 APPLICANT: Borgford, Thor
 APPLICANT: Braun, Curtis
 APPLICANT: Purac, Admir
 APPLICANT: Stoll, Dominik
 TITLE OF INVENTION: Ricin-like Toxin Variants for Treatment of Cancer.
 TITLE OF INVENTION: Viral or Parasitic Infections
 FILE REFERENCE: 10447-025
 CURRENT APPLICATION NUMBER: US/10/893,584
 PRIOR FILING DATE: 2004-07-19
 PRIOR APPLICATION NUMBER: US 09/551,151
 PRIOR FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: US 09/403,752
 PRIOR FILING DATE: 1999-10-29
 PRIOR APPLICATION NUMBER: US 10/089,058
 PRIOR FILING DATE: 2000-10-04
 NUMBER OF SEQ ID NOS: 274
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 17
 LENGTH: 1855
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: pAP-228 insert
 US-10-893-584-17

Alignment Scores:
 Pred. No.: 0.00613 Length: 1855
 Score: 112.00 Matches: 40
 Percent Similarity: 40.9% Conservative: 23
 Best Local Similarity: 26.0% Mismatches: 53
 Query Match: 14.1% Indels: 38
 DB: 8 Gaps: 7

US-09-978-274A-6 (1-154) x US-10-893-584-17 (1-1855)

Qy 5 IleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGluSerLeu 24
 Db 136 ATAACTTTACCAACAGCGGTCCTGCTGCAAGCTTACCAACTTTATCAGACTGTT 195

QY	25	AtgAaagcinalalysaepProlylsuLeuylsCyStyrglylleProMetLeuProAspThr	44
		:::	:::
Db	196	CGCGCGTGGTTAAACAACTGAGCGTAGTGTGAGACATGATATACCAAGTGTGGCAACACA	255
QY	45	AaaserThrPro-----LyStyLeuLeuValylsLeuGlnlyalAsaenLeuys	61
		:::	:::
Db	256	GTTGGTTGGCTTAATAAACCAACGGTTTATTTAGTTGAACCTCTCAATCATGACAGACTT	315
QY	62	ThrIleThrLeuMetLeuArgArgAsnAsnLeuTyValMetGlnTyTserAspProPhe	81
		:::	:::
Db	316	TCTGTACATTATGACGCTGAGATGTCAACCAATGATATGTGTGGCTAACCGT	366
QY	82	AsnGlyAsnLysCyArgTyT-----	88
		:::	:::
Db	367	GCTGGAAAATAGCGCATATTTCTTTTCATCTGTACATCAGAAAGATCAGAAACATCACT	426
QY	89	HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCySer	108
		:::	:::
Db	427	CATCTTTT-----ACTGATGTTCAAAAT-----	450
QY	109	SerSerSerSerArgValAlaMetSerIleAsnTyAsnSerLeuTyProThrMetGlu	128
		:::	:::
Db	451	CGATATATCATTTCCGCTTGTGTGTAAAT-----TATGATAGACCTTGAA	492
QY	129	LysLysAlaGluValAsnSerArgAsnGlnValGlnLeuGly	142
		:::	:::
Db	493	CAACTTGCTGGT--AATCTGAGAGAAAATATGCAAGTTGGGA	531

RESULT 10
US-10-893-584-19
; Sequence 19, Application US/10893584
; Publication No. US20050272048A1

```

; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Rizin-Like Toxin Variants for Treatment of Cancer
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PAP-230 insert
; US-10-893-584-19

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Alignment Scores:	
Pred. No.:	0.00613
Score:	112.00
Percent Similarity:	40.9%
Best Local Similarity:	26.0%
Query Match:	14.1%
DB:	8
Gaps:	7
Length:	1855
Matches:	40
Conservative:	23
Mismatches:	53
Indels:	38

US-09-978-274A-6 (1-154) X US-10-893-584-19 (1-1855)

QY 5 IleThrPheAsnAlaGlyAsnAlaThrIleAsnLysTrpAlaThrPheMetGluSerLeu 24
||| ||| |||||||::: ||| |||::: :::::
Db 136 ATAAACTTTACCAAGCGGGTGCCTGTGAAAGCTACCAAATTCACAGAGCTTT 19
ArgbaGlnAlaLysaaPProLyLeuLysCysTrpGlyLePProMetLeuProAspThr 44
QY 25

Dbb
196 CCGGGTCGTTTAAACAATCGAGCTGTAGACATATATTACCAAGTTGCCCAAACAGA 255

Oy
45 AamSerThPro-----LySeTyLeuMetValLysLeuGlnGlyAlaIleAenLeuYs 61

Dbb
256 GTTGCTTTGCCTATAATTAACAACGCGTTTATTTAATTGAAGCTCCCAATCAYGAGACTT 315

Oy
62 ThlLeThrLeuMetLeuArgArgAenLeuTyValMetGlyTyrsSerAapProPhe 81

Dbb
316 TCGTTACTTAGCGCTGGAGTGCACCAATCATATGCGTGGCTACCGT----- 366

Oy
82 AangLYAenLYsCyahrgTYr----- 88

Dbb
367 GCGGAATATAGGCAATATTCTTTCATCTGCACATCAGAAAGATGCAAGAACATCACT 426

Oy
89 HisILepheaAenApILeThrSerThrdQuArgHraAPValIGuaenThrLeuCySer 108

Dbb
427 CATCTTTTC-----ACTGATGTTCAAAAAT----- 450

Oy
109 SerSerSerSerArgValAlaMetSerILEaenTyzAenSerLeuTyProThrMetGLn 128

Dbb
451 -----CGAATACATTCGCCCTTTGGTGTAAAT-----TATGATAGCTTGA 492

Oy
129 LysLeuAlaGLuValAenSerArgAenGlnValGlnLeuGly 142

Dbb
493 CAACCTGCTGGT---AATCTGAGAGAAAAATATCAGACTGGGA 531

RESULT 11
US-10-893-584-21
; Sequence 21, Application US/10893584
; Publication No. US20050272048A1

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/ GENERAL INFORMATION:
/ APPLICANT: Borgford, Thor
/ APPLICANT: Braun, Curtis
/ APPLICANT: Parac, Admir
/ APPLICANT: Scoll, Dominik
/ TITLE OF INVENTION: Richn-like Toxin Variants for Treatment of Cancer
/ TITLE OF INVENTION: Viral or Parasitic Infections
/ FILE REFERENCE: 10447-025
/ CURRENT APPLICATION NUMBER: US/10/893,584
/ CURRENT FILING DATE: 2004-07-19
/ PRIOR APPLICATION NUMBER: US 09/551,151
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: US 09/403,752
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 10/089,058
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 274
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 21
/ LENGTH: 1855
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: PAP-232 Inbert
US-10-893-584-21

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Alignment scores:	
Pred. No.:	0.00613
Score:	112.00
Percent Similarity:	40.9%
Best Local Similarity:	26.0%
Query Match:	14.1%
DB:	8
	7
Length:	1855
Matches:	40
Conservative:	23
Mismatches:	53
Indels:	38
Gaps:	7

US-09-978-274A-6 (1-154) X US-10-893-584-21 (1-1855)

Qy 5 IleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetClnSerIeu 24
Db 136 ATTAACCTTTCACACAGCGGGCGACATGTGCAAGACTACACAACTTATACAGAGCTTT 19
Qy 25 ArgAsnGlnAlaLysAspProLysPheLysLeuGlyTyrGlyIleProMetLeuProAspThr 44

```
Db 196 CGCGTCTTTAAACAATGAGCTGATGTGACATGATATATACAGTGTGGCAAAACAGA 255
Qy 45 AenSerThrPro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAenLeuLys 61
Db 256 GTTGGTTGGCTTAAACCAACGAGGTTTATTTAGTTGAAGCTCTCAATATCATGCAGAGCTT 315
Qy 62 ThrIleThrLeuMetLeuArgArgAenAenLeuTyrValMetGlyTyrSerAspProPhe 81
Db 316 TCTGTTACATTAGCGCTGATGTACCAATGATATGTGTGGCTACCGT----- 366
Qy 82 AenGlyAenLysCysArgTyr----- 88
Db 367 GCTGGAATAAGCGCATATATTTCTTCATCCCTGACAAATCAGAAAGATCAGAAACATCACT 426
Qy 89 HisIlePheAenAspIleThrSerThrGluArgThrAspValGluAenThrLeuCySer 108
Db 427 CATCTTTC-----ACTGATGTTCAAAAT----- 450
Qy 109 SerSerSerSerArgValAlaMetSerIleAenTyrAenSerLeuTyrProThrMetGlu 128
Db 451 -----CGATATACATTCGCTTGTGTGTAAT-----TATGATAGACTTGAA 492
Qy 129 LysLysAlaGluValAenSerArgAenGlnValGlnLeuGly 142
Db 493 CAACTTGCTGGT---AATCTGAGAGAAATATCGAGTTGGGA 531
```

RESULT 12

```
US-10-893-584-23
; Sequence 23, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admitr
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PAP-234 insert
US-10-893-584-23
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Alignment Scores:

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Pred. No.: 0.00613 Length: 1855
Score: 112.00 Matches: 40
Percent Similarity: 40.9% Conservative: 23
Best Local Similarity: 26.0% Mismatches: 53
Query Match: 14.1% Indels: 38
DB: 8 Gaps: 7
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US-09-978-274A-6 (1-154) x US-10-893-584-23 (1-1855)

```
Qy 5 IlleThrPheAspAlaGlyAenAlaThrIleAenLysTyrAlaThrPheMetGluSerLeu 24
Db 136 ATAACCTTACCAACAGCGGTGCCACTGTGCAGAAAGCTACAAACTTATACAGAGCTGT 195
Qy 25 ArgAenGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 44
Db 196 CGCGTCTTTAAACAATGAGCTGATGTGACATGATATATACAGTGTGGCAAAACAGA 255
```

```
Qy 45 AenSerThrPro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAenLeuLys 61
Db 256 GTTGGTTGGCTTAAACCAACGAGGTTTATTTAGTTGAAGCTCTCAATATCATGCAGAGCTT 315
Qy 62 ThrIleThrLeuMetLeuArgArgAenAenLeuTyrValMetGlyTyrSerAspProPhe 81
Db 316 TCTGTTACATTAGCGCTGATGTACCAATGATATGTGTGGCTACCGT----- 366
Qy 82 AenGlyAenLysCysArgTyr----- 88
Db 367 GCTGGAATAAGCGCATATATTTCTTCATCCCTGACAAATCAGAAAGATCAGAAACATCACT 426
Qy 89 HisIlePheAenAspIleThrSerThrGluArgThrAspValGluAenThrLeuCySer 108
Db 427 CATCTTTC-----ACTGATGTTCAAAAT----- 450
Qy 109 SerSerSerSerArgValAlaMetSerIleAenTyrAenSerLeuTyrProThrMetGlu 128
Db 451 -----CGATATACATTCGCTTGTGTGTAAT-----TATGATAGACTTGAA 492
Qy 129 LysLysAlaGluValAenSerArgAenGlnValGlnLeuGly 142
Db 493 CAACTTGCTGGT---AATCTGAGAGAAATATCGAGTTGGGA 531
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RESULT 13

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US-10-893-584-25
; Sequence 25, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admitr
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PAP-236 insert
US-10-893-584-25
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Alignment Scores:

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Pred. No.: 0.00613 Length: 1855
Score: 112.00 Matches: 40
Percent Similarity: 40.9% Conservative: 23
Best Local Similarity: 26.0% Mismatches: 53
Query Match: 14.1% Indels: 38
DB: 8 Gaps: 7
```

US-09-978-274A-6 (1-154) x US-10-893-584-25 (1-1855)

```
Qy 5 IlleThrPheAspAlaGlyAenAlaThrIleAenLysTyrAlaThrPheMetGluSerLeu 24
Db 136 ATAACCTTACCAACAGCGGTGCCACTGTGCAGAAAGCTACAAACTTATACAGAGCTGT 195
Qy 25 ArgAenGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 44
Db 196 CGCGTCTTTAAACAATGAGCTGATGTGACATGATATATACAGTGTGGCAAAACAGA 255
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Db      256 GTTGGTTGCTATAACCAACGTTTATTAGTTGAACCTCTCAATCATGCAGACTT 315
Qy      62 ThrIleThrLeuMetLeuArgArgAsnLeuTyrValMetGlyTyrSerAspProPhe 81
Db      316 TCTGTTACATTAGCGCTGATGTGACCAATGATATGTGTGGCTACCGT----- 366
Qy      82 AsnGlyAsnLysCysArgTyr----- 88
Db      367 GCTGAAATAGCGCATATTCTTTTCATCCTGACAAATCAGAGATGACAGAACATCACT 426
Qy      89 HisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSer 108
Db      427 CATCTTTC-----ACTGATGTTCAAAAT----- 450
Qy      109 SerSerSerSerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGlu 128
Db      451 -----CGATATACATTGCGCTTGGTGGTAAAT-----TATGATAGACTTGAA 492
Qy      129 LysLysAlaGluValAsnSerArgAsnGlnValGlnLeuGly 142
Db      493 CAACTTGCTGGT---AATCTGAGAGAAATAATCGAGTTGGGA 531

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 Job time : 406.952 secs

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:06:24 ; Search time 1958.59 Seconds
(without alignments)
9664.530 Million cell updates/sec

Title: US-09-978-274A-7

Perfect score: 333
Sequence: 1 atcgagagtcgattcattcccc.....gaacctgcagacaacttaa 333

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBank: 1: gb_ba: 2: gb_in: 3: gb_env: 4: gb_om: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pr: 9: gb_ro: 10: gb_srb: 11: gb_sy: 12: gb_un: 13: gb_vl: 14: gb_hcg: 15: gb_pl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	333	100.0	333	6	AX427708 Sequence
2	329	98.8	945	6	AX427702 Sequence
3	328.4	98.6	792	6	AX427704 Sequence
4	325.8	97.8	1249	15	PAPAPSRIP
5	319	95.8	786	15	AB071855
6	302.4	90.8	1092	6	AX427720 Sequence
7	245.8	73.8	1052	15	AY137202
8	245.8	73.8	2472	6	E05033
9	245.8	73.8	2472	15	PTCAPAP
10	233	70.0	942	15	AY547315
11	233	70.0	942	15	AY547315 Phytolacc
12	233	70.0	1164	15	AY572976
13	233	70.0	1164	15	PAPAP
14	233	70.0	1195	6	A42103
15	233	70.0	1195	6	A42103 Sequence 1
16	233	70.0	1195	6	I43835
17	233	70.0	1195	6	I55866
18	233	70.0	1378	6	AX427732 Sequence
			1379	6	AR009535

19	233	70.0	1379	6	AR136704
20	233	70.0	1379	6	AR136705
21	233	70.0	1379	6	AX427731
22	231.4	69.5	1114	15	AF533515
23	231.4	69.5	1179	6	AR141172
24	229.8	69.0	1164	15	AY049785
25	227.8	68.4	783	15	AB071854
26	225	67.6	951	6	A67185
27	225	67.6	2269	15	AR141331
28	223.4	67.1	882	6	A67183
29	221.8	66.6	918	6	A43003
30	221.8	66.6	918	6	A48150
31	221.8	66.6	918	6	I60482
32	221.8	66.6	918	6	I89987
33	215.4	64.7	939	15	AY327475
34	205.2	61.6	1113	15	AY071928
35	176.8	53.1	714	15	AY603352
36	176.8	53.1	714	15	AY603354
37	175.2	52.6	711	15	AF338910
38	175.2	52.6	714	15	AF603353
39	136.4	41.0	1226	15	CAANTIPR
40	136.4	41.0	1226	15	CAAV
41	84.2	25.3	926	15	AY491967
42	84.2	25.3	1080	15	BVBETRAVUL
43	79.8	24.0	1137	15	AF228508
44	78.8	23.7	1085	15	AY437531
45	78.8	23.7	1387	15	AR445416

ALIGNMENTS

RESULT 1	AX427708	333 bp	DNA	linear	PAT 20-JUN-2002
LOCUS	AX427708	Sequence 7 from Patent WO0233107.			
DEFINITION	AX427708				
ACCESSION	AX427708				
VERSION	AX427708.1	GI:21537818			
KEYWORDS					
SOURCE					
ORGANISM	Phytolacca americana (American pokeweed)				
	Phytolacca americana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;				
	Caryophyllales; Phytolaccaceae; Phytolacca.				
REFERENCE					
AUTHORS	Neelam, A., Atkinson, H.J., McPherson, M.J. and Thomas, C.J.R.				
TITLE	Plant cell death system				
JOURNAL	Patent: WO 0233107-A 7 25-APR-2002;				
	CAMBRIDGE ADVANCED TECH (GB)				
FEATURES					
source	1..333	Location/Qualifiers			
	/organism="Phytolacca americana"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:3527"				
misc_feature	1..333				
misc_feature	/note="initiation codon added via PCR primer"				
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Query Match	100.0%; Score 333; DB 6; Length 333;				
Best Local Similarity	100.0%; Pred. No. 1.3e-79;				
Matches	333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 ATGGAGTTGATTCTATCCCTGTAATAAATGAGGCTTTTCTACTGATGCAATCCAA	60			
DB	1 ATGGAGTTGATTCTATCCCTGTAATAAATGAGGCTTTTCTACTGATGCAATCCAA	60			
QY	61 ATGTTTCAAGGAGCGGCGGATTCAGATCAATAGAAACCAAGTCAAGACTAATTTTAT	120			
DB	61 ATGTTTCAAGGAGCGGCGGATTCAGATCAATAGAAACCAAGTCAAGACTAATTTTAT	120			
QY	121 AGAGATTCTACCTGATCCCAAGTAATTAATTGGAGGAAGTGGGCAAAATCTCT	180			

Db 121 AGACATTTCTACCTGATCCCAAGTAATTATTTGGAGAGAGTGGGCAAAATCTCT 180
Qy 181 GAGCAATTGCACATGCGAAGATGGGGCTTTACCAACCACTTGAAGTGGATGCC 240
Db 181 GAGCAATTGCACATGCGAAGATGGGGCTTTACCAACCACTTGAAGTGGATGCC 240
Qy 241 AAGGATCAAGATGATAGTTCTTAGAGTGATGAATCAATCGTATGGGCACTCTT 300
Db 241 AAGGATCAAGATGATAGTTCTTAGAGTGATGAATCAATCGTATGGGCACTCTT 300
Qy 301 AAGTACGTTAATGCAACCTGTCAAGCAACTTAA 333
Db 301 AAGTACGTTAATGCAACCTGTCAAGCAACTTAA 333

RESULT 2
AX427702 945 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 1 from Patent WO0233107.
DEFINITION AX427702
ACCESSION AX427702
VERSION AX427702.1 GI:21537815
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
1 Neelam, A.; Atkinson, H.J., McPherson, M.J. and Thomas, C.J.R.
AUTHORS
TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A 1 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES
Location/Qualifiers
source
1..945
/organism="Phytolacca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"
misc_feature
1..24
/note="Binding site for primer PPS1BF"
misc_feature
complement(735..776)
/note="Binding site for primer PSXDR"
misc_feature
736..777
/note="Binding site for primer PSXDF"
variation
750..759
/note="Sequence replacing removed XbaI site"
misc_feature
complement(922..945)
/note="Binding site for primer PPS2SR"

ORIGIN
Query Match 98.8%; Score 329; DB 6; Length 945;
Best Local Similarity 100.0%; Pred. No. 1.3e-78;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GAGATTGATTCATTCCTCTGTAATAAAGTGAAGCTTTTCTACTGTTAGCCATCCAAATG 63
Db 532 GAGATTGATTCATTCCTCTGTAATAAAGTGAAGCTTTTCTACTGTTAGCCATCCAAATG 591
Qy 64 GTTTCAGAGGACGCGGATTCATAGTACATAGAGCAAGTCAAGTAAATTTTAAATAGA 123
Db 592 GTTTCAGAGGACGCGGATTCATAGTACATAGAGCAAGTCAAGTAAATTTTAAATAGA 651
Qy 124 GCAATTCACCTGATCCCAAGTAATTAATTTGGAGAGAGTGGGCAAAATCTCTGAG 183
Db 652 GCAATTCACCTGATCCCAAGTAATTAATTTGGAGAGAGTGGGCAAAATCTCTGAG 711
Qy 184 GCAATTCACATGCGCAAGATGGGGCTTTACCAACCACTTGAAGTGAATGCCAA 243
Db 712 GCAATTCACATGCGCAAGATGGGGCTTTACCAACCACTTGAAGTGAATGCCAA 771
Qy 244 GGTACCAAGTGAATGTTCTTAGAGTGATGAATCAATGCTGATGGGCACTCCTTAAG 303
Db 772 GGTACCAAGTGAATGTTCTTAGAGTGATGAATCAATGCTGATGGGCACTCCTTAAG 831

Qy 304 TACGTTAATGGAACTGTGACAGCACTTA 332
Db 832 TACGTTAATGGAACTGTGACAGCACTTA 860

RESULT 3
AX427704 792 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 3 from Patent WO0233107.
DEFINITION AX427704
ACCESSION AX427704
VERSION AX427704.1 GI:21537816
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE
1 Neelam, A.; Atkinson, H.J., McPherson, M.J. and Thomas, C.J.R.
AUTHORS
TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A 3 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES
Location/Qualifiers
source
1..792
/organism="Phytolacca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"
misc_feature
1..29
/note="Binding site for primer PS1BF"
misc_feature
1..3
/note="Initiation codon added via PCR primer"
misc_feature
complement(436..462)
/note="Binding site for primer PS1SR"
misc_feature
463..492
/note="Binding site for primer PS2BF"
variation
612
/note="Nucleotide change from published sequence"
variation
681..686
/note="Sequence replacing removed XbaI site"
misc_feature
complement(765..792)
/note="Binding site for primer PS2SR"
misc_feature
790..792
/note="Stop codon added via PCR primer"

ORIGIN
Query Match 98.6%; Score 328.4; DB 6; Length 792;
Best Local Similarity 99.7%; Pred. No. 2e-78;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 GAGATTGATTCATTCCTCTGTAATAAAGTGAAGCTTTTCTACTGTTAGCCATCCAAATG 63
Db 463 GAGATTGATTCATTCCTCTGTAATAAAGTGAAGCTTTTCTACTGTTAGCCATCCAAATG 522
Qy 64 GTTTCAGAGGACGCGGATTCATAGTACATAGAGCAAGTCAAGTAAATTTTAAATAGA 123
Db 523 GTTTCAGAGGACGCGGATTCATAGTACATAGAGCAAGTCAAGTAAATTTTAAATAGA 582
Qy 124 GCAATTCACCTGATCCCAAGTAATTAATTTGGAGAGAGTGGGCAAAATCTCTGAG 183
Db 583 GCAATTCACCTGATCCCAAGTAATTAATTTGGAGAGAGTGGGCAAAATCTCTGAG 642
Qy 184 GCAATTCACATGCGCAAGATGGGGCTTTACCAACCACTTGAAGTGAATGCCAA 243
Db 643 GCAATTCACATGCGCAAGATGGGGCTTTACCAACCACTTGAAGTGAATGCCAA 702
Qy 244 GGTACCAAGTGAATGTTCTTAGAGTGATGAATCAATGCTGATGGGCACTCCTTAAG 303
Db 703 GGTACCAAGTGAATGTTCTTAGAGTGATGAATCAATGCTGATGGGCACTCCTTAAG 762
Qy 304 TACGTTAATGGAACTGTGACAGCACTTA 333
Db 763 TACGTTAATGGAACTGTGACAGCACTTA 792

RESULT 4
PAPAPSRIP 1249 bp mRNA linear PLN 18-APR-2005
LOCUS P.americana mRNA for pokeweed antiviral protein.
DEFINITION X98079.1 GI:1707648
ACCESSION X98079.1
VERSION
KEYWORDS PAP-S gene; pokeweed antiviral protein (PAP); ribosome-inactivating protein.
SOURCE Phytolacca americana (American pokeweed)
ORGANISM Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE 1
AUTHORS Poyet, J.L. and Hoeveler, A.
TITLE cDNA cloning and expression of pokeweed antiviral protein from seeds in Escherichia coli and its inhibition of protein synthesis in vitro
JOURNAL FEBS Lett. 406 (1-2), 97-100 (1997)
PUBMED 9109394
REFERENCE 2 (bases 1 to 1249)
AUTHORS Poyet, J.L.
TITLE Direct Submission
DEFINITION Submitted (22-MAY-1996) J.L. Poyet, Laboratoire de Biochimie-Biologie Molculaire, UFR Sciences et Techniques, 16 route de Gray, 25030 Besancon Cedex, FRANCE
REMARK Revised by author 20-SEP-1996
FEATURES
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1. .1249
/organism="Phytolacca americana"
/mol_type="mRNA"
/db_xref="taxon:3527"
/feature_type="seeds"
1. .1249
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106. .1050
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/note="ribosome-inactivating protein type I"
/codon_start=1
/product="pokeweed antiviral protein"
/protein_id="CA66702.1"
/db_xref="GI:1707649"
/db_xref="COA:P93444"
/db_xref="InterPro:IPR001574"
/db_xref="UniProt/TREMBL:P93444"
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106. .177
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178. .1047
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polyA_site
polyA_signal
mat_peptide
sig_peptide
ORIGIN
Query Match 97.8%; Score 325.8; DB 15; Length 1249;
Best Local Similarity 99.4%; Pred. No. 9.4e-78;
Matches 327; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 697 GTTTCAGAGCAGCGCATTCAGATACATAGAGAACCAAGTCACCTAATTTTATATGA 756
QY 124 GCATTCACCTGATCCCAAGTAAATTAATTGAGAGAGAGAGGCGCAAAATCTTGAG 183
Db 757 GCATTCACCTGATCCCAAGTAAATTAATTGAGAGAGAGAGGCGCAAAATCTTGAG 816
QY 184 GCATTCACCAATGCAAGAAATGAGGCTTTACCCCAACCACTTGAGCTAGAGGCCAAA 243
Db 817 GCATTCACCAATGCAAGAAATGAGGCTTTACCCCAACCTTGAGCTAGAGGCCAAA 876
QY 244 GGTACCAAGTGAATGTTCTTAGAGTGATGAATCAATGATGATGAGCACTCTTAAG 303
Db 877 GTTACCAAGTGAATGTTCTTAGAGTGATGAATCAATGATGATGAGCACTCTTAAG 936
QY 304 TACGTTAATGAACCTTCAGACACTTA 332
Db 937 TACGTTAATGAACCTTCAGACACTTA 965
RESULT 5
AB071855 786 bp DNA linear PLN 19-MAR-2002
LOCUS Phytolacca americana pap2 gene for PAP-S2, partial cds.
DEFINITION AB071855
ACCESSION AB071855.1 GI:19570839
VERSION
KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)
Phytolacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.
REFERENCE 1
AUTHORS Honjo, E. and Watanabe, K.
TITLE Cloning of genomic DNA encoding two types of pokeweed antiviral protein in seeds, PAP-S1 and PAP-S2, and functional comparison of their recombinant proteins with other PAP isoforms
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 786)
AUTHORS Watanabe, K. and Honjo, E.
TITLE Direct Submission
DEFINITION Submitted (19-SEP-2001) Keiichi Watanabe, Saga University, Department of Applied Biological Sciences, Honjo-machi, Saga city, Saga 840-8502, Japan (E-mail:watanabe@cc.saga-u.ac.jp, Tel:81-952-28-8774, Fax:81-952-28-8774)
FEATURES
source
1. .786
/organism="Phytolacca americana"
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/codon_start=1
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/protein_id="BAB86350.1"
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CDS
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ORIGIN
Query Match 95.8%; Score 319; DB 15; Length 786;
Best Local Similarity 98.5%; Pred. No. 7.1e-76;
Matches 322; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 64 GTTTCAGAGGCGGCGGATTCAGTACATGAGAACCAAGTCAAGACTAATTTTAATAGA 123
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DB 520 GTTTCAGAGGCGGCGGATTCAGTACATGAGAACCAAGTCAAGACTAATTTTAATAGA 579
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QY 124 GCATTCTACCTCGTATCCCAAGTAATTAATTTGGAGAGAAAGGGGCAAAATCTCTGAG 183
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DB 580 GCATTCTACCTCGTATCCCAAGTAATTAATTTGGAGAGAAAGGGGCAAAATCTCTGAG 639
| | | | |
QY 184 GCATTCAAGATGCCAAGATGAGGCTTTACCCAAACCACTTGAGCTAGTGCACAA 243
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DB 640 GCATTCAAGATGCCAAGATGAGGCTTTACCCAAACCACTTGAGCTAGTGCACAA 699
| | | | |
QY 244 GTTACCAAGTGAATGTTCTTGAAGTGAATCAATCGTATGAGCACTCTTTAG 303
| | | | |
DB 700 GTTACCAAGTGAATGTTCTTGAAGTGAATCAATCGTATGAGCACTCTTTAG 759
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QY 304 TACGTTAATGAACTGTGACAACT 330
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DB 760 TACGTTAATGAACTGTGACAACT 786
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RESULT 6
AX427720 1092 bp DNA linear PAT 20-JUN-2002
LOCUS AX427720
DEFINITION Sequence 19 from Patent WO0233107.
ACCESSION AX427720
VERSION AX427720.1 GI:21537829
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct; artificial sequences.
other sequences; other sequences.
REFERENCE 1
AUTHORS Neelam, A., Ackinson, H. J., Mcpherson, M. J. and Thomas, C. J. R.
TITLE Plant cell death system
JOURNAL Patent: WO 0233107-A 19 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES
source 1. .1092
location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PAP-S/Cystatin fusion"
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/note="Binding site for primer p81BP"
variation 681. .686
/note="Modified XbaI site"
misc_feature complement(742. .786)
/note="Binding site for primer PCS-PAPSR"
misc_feature 766. .806
/note="Binding site for primer PCS-Delta86P"
misc_feature 766. .786
/note="TRV N1A protease cleavage site"
misc_feature complement(1066. .1092)
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ORIGIN
Query Match 90.8%; Score 302.4; DB 6; Length 1092;
Best Local Similarity 99.7%; Pred. No. 2.2e-71;
Matches 303; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 GGAGTTGATTCATTCCTCTTAATAAAGTGGGCTTTTCTACTGTAGCCATCCAAATG 63
| | | | |
DB 463 GGAGTTGATTCATTCCTCTTAATAAAGTGGGCTTTTCTACTGTAGCCATCCAAATG 522
| | | | |
QY 64 GTTTCAGAGGCGGCGGATTCAGTACATGAGAACCAAGTCAAGACTAATTTTAATAGA 123
| | | | |
DB 523 GTTTCAGAGGCGGCGGATTCAGTACATGAGAACCAAGTCAAGACTAATTTTAATAGA 582
| | | | |
QY 124 GCATTCTACCTCGTATCCCAAGTAATTAATTTGGAGAGAAAGGGGCAAAATCTCTGAG 183
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DB 583 GCATTCTACCTCGTATCCCAAGTAATTAATTTGGAGAGAAAGGGGCAAAATCTCTGAG 642
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QY 184 GCATTTCAGATGCCAAGATGAGGCTTTACCCAAACCACTTGAGCTAGTGCACAA 243
| | | | |
DB 643 GCATTTCAGATGCCAAGATGAGGCTTTACCCAAACCACTTGAGCTAGTGCACAA 702
| | | | |
QY 244 GTTACCAAGTGAATGTTCTTGAAGTGAATCAATCGTATGAGCACTCTTTAG 303
| | | | |
DB 703 GTTACCAAGTGAATGTTCTTGAAGTGAATCAATCGTATGAGCACTCTTTAG 762
| | | | |
QY 304 TACG 307
| | | | |
DB 763 TACG 766
| | | | |
RESULT 7
AY137202 1052 bp DNA linear PLN 28-SEP-2002
LOCUS AY137202
DEFINITION Phytolectra americana anti-virus protein (papn) gene, complete cds.
ACCESSION AY137202
VERSION AY137202.1 GI:23343924
KEYWORDS
SOURCE Phytolectra americana (red stem pokeweed)
ORGANISM
REFERENCE 1
AUTHORS Gao, B.
TITLE Pokeweed anti-virus protein
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1052)
AUTHORS Gao, B.
TITLE Direct Submission
JOURNAL Department of Plant Pathology, Hunan
Submitted (29-JUN-2002) Fuzong District, Changsha, Hunan 410128,
Agricultural University, Fuzong District, Changsha, Hunan 410128,
China
FEATURES
source 1. .1052
location/Qualifiers
/organism="Phytolectra americana"
/mol_type="genomic DNA"
/db_xref="taxon:3527"
/country="China: Hunan province"
/note="Common: red stem pokeweed"
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mRNA <76. .>960
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CDS /product="anti-virus protein"
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/protein_id="AA116078.1"
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TYNKKRHYHFKDISNTERNDWTTICPNSSRVGKINIVDSYPLLEKVGPRSG
VQLEIGLINSIGIKYGVDSPTKTEBFLVALQWSEARFRTYINOVKTNRAR
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ORIGIN
Query Match 73.8%; Score 245.8; DB 15; Length 1052;
Best Local Similarity 84.2%; Pred. No. 5.4e-56;
Matches 277; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
QY 4 GGAGTTGATTCATTCCTCTTAATAAAGTGGGCTTTTCTACTGTAGCCATCCAAATG 63
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DB 604 GGAGTTGATTCATTCCTCTTAATAAAGTGGGCTTTTCTACTGTAGCCATCCAAATG 663
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QY 64 GTTTCAGAGGCGGCGGATTCAGTACATGAGAACCAAGTCAAGACTAATTTTAATAGA 123
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DB 664 GTTTCAGAGGCGGCGGATTCAGTACATGAGAACCAAGTCAAGACTAATTTTAATAGA 723
| | | | |

QY 124 GCATTCTACCTGATCCCAAGTAATTAATTGGAGAGAGAGGCGCAAAATCTCGAG 183
 DB 724 GCATTCTACCTGATCCCAAGTAATTAATTGGAGAGAGAGGCGTAAGATCTTACG 783
 QY 184 GCATTCTACCAATGCGCAAGATGAGGCTTTTACCCAAACCACTTGAAGTGAATGCCAA 243
 DB 784 GCATTCTACCAATGCGCAAGATGAGGCTTTTACCCAAACCACTTGAAGTGAATGCCAA 843
 QY 244 GGTACCAAGTGAATGATCTTGAAGTGAATGAATCAATGATGATGCACTCTTAAG 303
 DB 844 GGTACCAAGTGAATGATCTTGAAGTGAATGAATCAATGATGATGCACTCTTAAG 903
 QY 304 TACGTTAATGGAACCTGTGACCAACTTA 332
 DB 904 TATGTTAATGGACCTGCGCAGCAACTTA 932

RESULT 8
 LOCUS E05033 2472 bp DNA linear PAT 29-SEP-1997
 DEFINITION DNA encoding antiviral protein.
 ACCESSION E05033
 VERSION E05033.1 GI:2173227
 KEYWORDS JP 1993137580-A/1.
 SOURCE PhytoIaccas americana (American pokeweed)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.
 REFERENCE 1 (bases 1 to 2472)
 Katoaka,J., Habuka,N., Masuda,O., Miyano,M. and Koiwai,A.
 NEW PROTEIN AND GENE CAPABLE OF CODING THE SAME
 PATENT: JP 1993137580-A 1 01-JUN-1993;
 JAPAN TOBACCO INC
 COMMENT OS PhytoIaccas americana
 PN JP 1993137580-A/1
 PD 01-NOV-1991
 PF 20-NOV-1991 JP 1991329672
 PI KATOKA JIRO, HABUKA NORIYUKI, MASUDA OSAMU, MIYANO MASASHI,
 PI KOIWA AKIRA
 PC C12N15/29,C12N15/73,C12P21/02//C12N1/21,C12P21/02,C12R1/19),
 PC (C12N1/21,
 PC C12R1/19);
 CC strandedness: Double;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 CC feature is identified by similarity;
 FH Key Location/Qualifiers
 FT CAAT_signal 549..552
 FT TATA_signal 627..630
 FT TATA_signal 845..850
 FT sig_peptide 1014..1085
 FT mat_peptide 1086..1895
 FT /product:'antiviral protein'
 FT CDS 1014..1898
 FT polyA_site 2130..2135.
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ORIGIN
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 Best Local Similarity 84.2%; Pred. No. 4.8e-56;
 Matches 277; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCCTCCCTTAATAAACTGAGGCTTTTCTTCTAGTGAACCAATCCAAATG 63
 DB 1542 GGAGTTGATTCCTCCCTTAATAAACTGAGGCTTTTCTTCTAGTGAACCAATCCAAATG 1601

QY 64 GTTTCAGAGGACGCGCATTCAGATCATAGAGACCAATCAAGACTAATTTTATAGA 123
 DB 1602 GTTTCAGAGGACGCGCATTCAGATCATAGAGACCAATCAAGACTAATTTTATAGA 1661
 QY 124 GCATTCTACCTGATCCCAAGTAATTAATTGGAGAGAGAGGCGCAAAATCTCGAG 183
 DB 1662 GCATTCTACCTGATCCCAAGTAATTAATTGGAGAGAGAGGCGGTAAGATCTTACG 1721
 QY 184 GCATTCTACCAATGCGCAAGATGAGGCTTTTACCCAAACCACTTGAAGTGAATGCCAA 243
 DB 1722 GCATTCTACCAATGCGCAAGATGAGGCTTTTACCCAAACCACTTGAAGTGAATGCCAA 1781
 QY 244 GGTACCAAGTGAATGATCTTGAAGTGAATGAATCAATGATGATGCACTCTTAAG 303
 DB 1782 GGTACCAAGTGAATGATCTTGAAGTGAATGAATCAATGATGATGCACTCTTAAG 1841
 QY 304 TACGTTAATGGAACCTGTGACCAACTTA 332
 DB 1842 TATGTTAATGGACCTGCGCAGCAACTTA 1870

RESULT 9
 LOCUS PTCAPAP 2472 bp DNA linear PLN 01-FEB-2000
 DEFINITION P. americana DNA for alpha-PAP (pokeweed antiviral protein),
 complete cds.
 ACCESSION D10600 D90537
 VERSION D10600.1 GI:218010
 KEYWORDS alpha-PAP; antiviral protein; pokeweed antiviral protein (PAP); ribosome-inactivating protein.
 SOURCE PhytoIaccas americana (American pokeweed)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.
 REFERENCE 1 (bases 1 to 2472)
 Katoaka,J., Habuka,N., Masuda,O., Miyano,M. and Koiwai,A.
 Isolation and analysis of a genomic clone encoding a pokeweed
 antiviral protein
 Plant Mol. Biol. 20 (5), 879-886 (1992)
 JOURNAL 1281438
 PUBMED 2 (bases 1 to 2472)
 Katoaka,J.
 DIRECT SUBMISSION
 REFERENCE Submitted (23-OCT-1991) Jiro Katoaka, Japan Tobacco Inc., Life
 Science Research Laboratory; 6-2 Umesaoka, Midori-ku, Yokohama,
 Kanagawa 227, Japan (Tel:045-972-5901, Fax:045-972-6205)
 Submitted (23-Oct-1991) to DDBJ by:
 Jiro Katoaka
 Life Science Research Laboratory
 Japan Tobacco Inc.
 6-2 Umesaoka, Midori-ku
 Yokohama 227
 Japan
 Phone: 045-972-5901
 Fax: 045-972-6205
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 /mol_type="genomic DNA"
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 549..552
 845..850
 1014..1898
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ORIGIN

LRNBAKPSLCKYIGI PMLPNTNTPKXVLYELQSNKKTITLMLRNNLYVMGYSDPF
ETNKRCHIFNDISGERODVETLLCPNANRSVKINIFDSRYPTLSSKAGVRSOV
QIGIOLDSNIGKISGVMSFTEKTEAEFLVLAIOVMSBAARFKYIENOVNFRARN
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Query Match 70.0%; Score 233; DB 15; Length 942;
Best Local Similarity 81.8%; Pred. No. 1.7e-52;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTAATAAAGCTGAGGCTTTTCTTCTAGTGGAGCCATCAATG 63
DB 526 GGAGTGAATGTCATTCCTGTAATAAAGCTGAGGCTTTTCTTCTAGTGGAGCCATCAATG 585
QY 64 GTTTCAGAGGCGAGGATTCATTCATAGAGAACCAAGCTCAAGCTAATTTAATAGA 123
DB 586 GTATCAGAGGCGAGGATTCATTCATAGAGAACCAAGCTCAAGCTAATTTAATAGA 645
QY 124 GCATTCACCTGATCCCAAGTAATTAATTTGAGAGAGAGTGGGCAAAATCTGAG 183
DB 646 GCATTCACCTGATCCCAAGTAATTAATTTGAGAGAGAGTGGGCAAAATCTGAG 705
QY 184 GCATTCACATGCGCAAGAAATGGGCTTTTACCCAAACCACTTGAAGTGAATGCCAA 243
DB 706 GCATTCACATGCGCAAGAAATGGGCTTTTACCCAAACCACTTGAAGTGAATGCCAA 765
QY 244 GGTAACCAAGTGAATGTTCTTAGAGTGAATGAATCATGTGATGTCGACTCTTAAG 303
DB 766 GGTAACCAAGTGAATGTTCTTAGAGTGAATGAATCATGTGATGTCGACTCTTAAG 825
QY 304 TACGTTAATGAACTGTGACAGCACTTA 332
DB 826 TACGTTGTTGGAGCTGTGACAGCACTTA 854

RESULT 12

PAPAP 1164 bp mRNA linear PLN 18-NOV-1991
LOCUS P.americana PAP gene for anti-viral protein.
DEFINITION X55383
ACCESSION X55383
VERSION X55383.1 GI:20421

KEYWORDS antiviral protein; cell wall protein; PAP gene; ribosome
inactivating protein.

SOURCE Phytophthora americana (American pokeweed)

ORGANISM

Bacteriophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE

AUTHORS Lin, Q., Chen, Z. C., Antoniw, J. F. and White, R. F.

TITLE 1 (bases 1 to 1164)

JOURNAL Submitted (05-NOV-1990) Antoniw J. F., AFRC Inst of Arable Crops
Research, Dept. of Plant Pathology, Rothamsted Experimental
Station, Harpenden, Hert, AL5 2JQ, UK

FEATURES

source

1. 1164
/organism="Phytolacca americana"
/mol_type="mRNA"
/db_xref="taxon:3527"
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2. 943
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gene
CDS

ORIGIN

/product="anti-viral protein"
/protein_id="CAA39054.1"
/db_xref="GI:20422"
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VGSQCTTYNQNMFPOLIMSTYNNVNLGDLPEGR"

Query Match 70.0%; Score 233; DB 15; Length 1164;
Best Local Similarity 81.8%; Pred. No. 1.6e-52;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTAATAAAGCTGAGGCTTTTCTTCTAGTGGAGCCATCAATG 63
DB 527 GGAGTGAATGTCATTCCTGTAATAAAGCTGAGGCTTTTCTTCTAGTGGAGCCATCAATG 586
QY 64 GTTTCAGAGGCGAGGATTCATTCATAGAGAACCAAGCTCAAGCTAATTTAATAGA 123
DB 587 GTATCAGAGGCGAGGATTCATTCATAGAGAACCAAGCTCAAGCTAATTTAATAGA 646
QY 124 GCATTCACCTGATCCCAAGTAATTAATTTGAGAGAGAGTGGGCAAAATCTGAG 183
DB 647 GCATTCACCTGATCCCAAGTAATTAATTTGAGAGAGAGTGGGCAAAATCTGAG 706
QY 184 GCATTCACAAAGCCAAAGAAATGGGCTTTTACCCAAACCACTTGAAGTGAATGCCAA 243
DB 707 GCATTCACAAAGCCAAAGAAATGGGCTTTTACCCAAACCACTTGAAGTGAATGCCAA 766
QY 244 GGTAACCAAGTGAATGTTCTTAGAGTGAATGAATCATGTGATGTCGACTCTTAAG 303
DB 767 GGTAACCAAGTGAATGTTCTTAGAGTGAATGAATCATGTGATGTCGACTCTTAAG 826
QY 304 TACGTTAATGAACTGTGACAGCACTTA 332
DB 827 TACGTTGTTGGAGCTGTGACAGCACTTA 855

RESULT 13

A36639 1195 bp DNA linear PAT 05-MAR-1997
LOCUS A36639
DEFINITION Sequence 1 from Patent EP0585554.
ACCESSION A36639
VERSION A36639.1 GI:2293943

KEYWORDS

unidentified

SOURCE

unclassified

unclassified sequences.

1 (bases 1 to 1195)

AUTHORS Kim, M., Lee, K., Na, B., Jeong, H. S., Choi, K., Moon, Y. and Jeon, H.

TITLE Process for preparing a transgenic plant expressing phytophthora

antiviral protein

Patent: EP 0585554-A 1 09-MAR-1994;

JINRO LIMITED (KR)

Other publication JP 6078775 940322

Other publication KR 9512900 951023.

COMMENT

Other publication KR 9512900 951023.

FEATURES

source

1. 1195
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/mol_type="unassigned DNA"
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ORIGIN

Query Match 70.0%; Score 233; DB 6; Length 1195;
Best Local Similarity 81.8%; Pred. No. 1.6e-52;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTAATAAAGCTGAGGCTTTTCTTCTAGTGGAGCCATCAATG 63
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Mon Apr 10 07:26:52 2006

us-09-978-274a-7.1g

Db 558 GGAGTGTGTCATTCATGAGAAAACCGAAGCCGAATTCCTATTGTAGCCATACAAATG 617
 QY 64 GTTTCAGAGGACGCGCATTCAGATACATAGAGAACCAAGTCAAGATTTTAAATAGA 123
 Db 618 GTATCAGAGGACGAGAAATTCAGATACATAGAGAAATCAGGTGAATCTTAATTTAAACGA 677
 QY 124 GCATTTCACCTGATCCCAAGTAATTAATTGGAGGAGAAAGTGGGCAAAATCTGAG 183
 Db 678 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAGATTTCAACA 737
 QY 184 GCATTTCACATGCCAAGATGGGCTTTACCCAAACCACTTGAGCTGTGATGCCAAA 243
 Db 738 GCAATTCATGATGCCAAGATGAGATTTTACCAAACTCTCGAGCTAGTGAGTCCAGT 797
 QY 244 GGTACCAAGTGATGTTCTTAGAGTGCATGAAATCAATCGATGTGGCACTCCTTAG 303
 Db 798 GGTGCCAAGTGATGTTGTTAGAGATGATGAATCAACCTGATGTAGCACTTTAAAC 857
 QY 304 TACGTTAATGAACTGTGACGAACTTA 332
 Db 858 TACGTTGTGGAGCTGTGACGAACTTA 886

RESULT 14
 A42103 1195 bp DNA linear PAT 05-MAR-1997

LOCUS A42103
 DEFINITION Sequence 1 from Patent EP0637591.
 ACCESSION A42103
 VERSION A42103.1 GI:2297595
 KEYWORDS
 SOURCE
 ORGANISM
 PhytoIacc americana (American pokeweed)

REFERENCE
 AUTHORS Moon, Y., Jeon, H., Choi, K., Lee, K. and Kim, M.
 TITLE A novel expression vector for phytoIacc antiviral protein
 JOURNAL Patent: EP 0637591-A 1 08-FEB-1995;
 JINRO LIMITED (KR)
 COMMENT Other publication AU 662844 950914
 Other publication JP 7067660 950314
 Other publication CA 2102859 950103
 Other publication AU 5064293 950119.
 Location/Qualifiers

FEATURES
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 1..1195
 /organism="PhytoIacc americana"
 /mol_type="unassigned DNA"
 /db_xref="taxon:3527"

ORIGIN

Query Match 70.0%; Score 233; DB 6; Length 1195;
 Best Local Similarity 81.8%; Pred. No. 1.6e-52;
 Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAAGTTGATTCATTCCTGTTAAACCTGAGGCTTTTCTACTGTGTAACCAATCAATG 63
 Db 558 GGAAGTGTGATTCATTCATGAGAAAACCGAAGCCGAATTCCTATTGTGATCCATACAAATG 617
 QY 64 GTTTCAGAGGACGCGCATTCAGATACATAGAGAACCAAGTCAAGATTTTAAATAGA 123
 Db 618 GTATCAGAGGACGAGAAATTCAGATACATAGAGAAATCAGGTGAATCTTAATTTAAACGA 677
 QY 124 GCATTTCACCTGATCCCAAGTAATTAATTGGAGGAGAAAGTGGGCAAAATCTGAG 183
 Db 678 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAGATTTCAACA 737
 QY 184 GCAATTCACATGCCAAGATGGGCTTTACCCAAACCACTTGAGCTGTGATGCCAAA 243
 Db 738 GCAATTCATGATGCCAAGATGAGATTTTACCAAACTCTCGAGCTAGTGAGTCCAGT 797
 QY 244 GGTACCAAGTGATGTTCTTAGAGTGCATGAAATCAATCGATGTGGCACTCCTTAG 303

Db 798 GGTGCCAAGTGATGTTGAGAGTGATGAATCAAGCCTGATGTAGCACTTTAAAC 857

QY 304 TACGTTAATGAACTGTGACGAACTTA 332
 Db 858 TACGTTGTGGAGCTGTGACGAACTTA 886

RESULT 15
 I43835 1195 bp DNA linear PAT 07-OCT-1997

LOCUS I43835
 DEFINITION Sequence 1 from patent US 5633155.
 ACCESSION I43835
 VERSION I43835.1 GI:2468933
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1195)
 AUTHORS Kim, M.-K., Lee, K.-H., Na, B.-K., Jeong, H.-S., Choi, K.-W., Moon, Y.-H.

TITLE Expression vector for phytoIacc antiviral protein and process for
 preparing transgenic plant transformed therewith
 JOURNAL Patent: US 5633155-A 1 27-MAY-1997;
 Location/Qualifiers

FEATURES
 source
 1..1195
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 70.0%; Score 233; DB 6; Length 1195;
 Best Local Similarity 81.8%; Pred. No. 1.6e-52;
 Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAAGTTGATTCATTCCTGTTAAACCTGAGGCTTTTCTACTGTGTAACCAATCAATG 63
 Db 558 GGAAGTGTGATTCATTCATGAGAAAACCGAAGCCGAATTCCTATTGTGATCCATACAAATG 617
 QY 64 GTTTCAGAGGACGCGCATTCAGATACATAGAGAACCAAGTCAAGATTTTAAATAGA 123
 Db 618 GTATCAGAGGACGAGAAATTCAGATACATAGAGAAATCAGGTGAATCTTAATTTAAACGA 677
 QY 124 GCATTTCACCTGATCCCAAGTAATTAATTGGAGGAGAAAGTGGGCAAAATCTGAG 183
 Db 678 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAGATTTCAACA 737
 QY 184 GCAATTCACATGCCAAGATGGGCTTTACCCAAACCACTTGAGCTGTGATGCCAAA 243
 Db 738 GCAATTCATGATGCCAAGATGAGATTTTACCAAACTCTCGAGCTAGTGAGTCCAGT 797
 QY 244 GGTACCAAGTGATGTTCTTAGAGTGCATGAAATCAATCGATGTGGCACTCCTTAG 303
 Db 798 GGTGCCAAGTGATGTTGTTAGAGATGATGAATCAAGCCTGATGTAGCACTTTAAAC 857
 QY 304 TACGTTAATGAACTGTGACGAACTTA 332
 Db 858 TACGTTGTGGAGCTGTGACGAACTTA 886

Search completed: April 9, 2006, 04:15:04
 Job time : 1958.59 secs

specific cells of a plant. The method involves transforming the plant with chimeric gene(s) which encodes a pokeweed antiviral protein namely PAP', PAPRI and PAP-S, where the gene(s) comprises a promoter which acts in response to the application of a specific stimulus to the plant so as to facilitate expression of the pokeweed antiviral protein in specific cells of the plant. The method is useful for inducing a necrotic effect in specific cells of a plant. The present sequence is pokeweed PAP-Sbeta protein encoding DNA

CC Sequence 333 BP; 106 A; 63 C; 76 G; 88 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 333; DB 6; Length 333;

XX Best Local Similarity 100.0%; Pred. No. 5.4e-95; Indels 0; Gaps 0;

XX Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGAGTTGATTCATTCCTGTAATAAAGTGAAGCTTTTCTTCTAGTGGCAATCCAA 60

DB 1 ATGGGAGTTGATTCATTCCTGTAATAAAGTGAAGCTTTTCTTCTAGTGGCAATCCAA 60

QY 61 ATGGTTTCAGAGGCGCGCATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTAA 120

DB 61 ATGGTTTCAGAGGCGCGCATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTAA 120

QY 121 AGAGCATTTTACCTGATCCCAAGTAATTAATTGGAGAGAGAGTGGGCAAAATCTCT 180

DB 121 AGAGCATTTTACCTGATCCCAAGTAATTAATTGGAGAGAGAGTGGGCAAAATCTCT 180

QY 181 GAGGCATTCACATGCGCAAGATGGGGCTTACCACCAACCACTTGAAGTGGATGCC 240

DB 181 GAGGCATTCACATGCGCAAGATGGGGCTTACCACCAACCACTTGAAGTGGATGCC 240

QY 241 AAAGTACCAAGTGAATGTTCTTGAAGTGAATGAATCAATGATGGGCACTCTCT 300

DB 241 AAAGTACCAAGTGAATGTTCTTGAAGTGAATGAATCAATGATGGGCACTCTCT 300

QY 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

DB 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

QY 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

DB 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

QY 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

DB 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

QY 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

DB 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

QY 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

DB 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

QY 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

DB 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

QY 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

DB 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

QY 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

DB 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

QY 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

DB 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

QY 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

DB 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

QY 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

DB 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

QY 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

DB 301 AAGTACGTTAATGAACTGTCAAGCAACTTAA 333

FT /bound_molecy= "Primer PPS2BR"

XX WO200233107-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-GB004593.

XX 14-OCT-2000; 2000GB-00025217.

XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.

XX Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;

XX WPI, 2002-489891/52.

XX P-PDB; AAE25918.

XX Inducing necrotic effect in specific cells of plant by transforming plant with a chimeric gene encoding pokeweed antiviral protein and a promoter

XX which acts in response to application of specific stimulus to plant.

XX Claim 24; Page 73-74; 87pp; English.

XX The invention relates to a method of inducing a necrotic effect in

XX specific cells of a plant. The method involves transforming the plant

XX with chimeric gene(s) which encodes a pokeweed antiviral protein namely

XX PAP', PAPRI and PAP-S, where the gene(s) comprises a promoter which acts

XX in response to the application of a specific stimulus to the plant so as

XX to facilitate expression of the pokeweed antiviral protein in specific

XX cells of the plant. The method is useful for inducing a necrotic effect

XX in specific cells of a plant. The present sequence is pokeweed pro-PAP-S

XX protein encoding DNA

XX Sequence 945 BP; 307 A; 187 C; 180 G; 271 T; 0 U; 0 Other;

XX Query Match 98.8%; Score 329; DB 6; Length 945;

XX Best Local Similarity 100.0%; Pred. No. 1.5e-93; Indels 0; Gaps 0;

XX Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGAAGTGAATTCATTCCTGTAATAAAGTGAAGCTTTTCTTCTAGTGGCAATCCAAATG 63

DB 532 GGAAGTGAATTCATTCCTGTAATAAAGTGAAGCTTTTCTTCTAGTGGCAATCCAAATG 63

QY 64 GTTTCAGAGGCGCGCATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTAAATGA 123

DB 592 GTTTCAGAGGCGCGCATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTAAATGA 123

QY 124 GCAATTCACCTGATCCCAAGTAATTAATTGGAGAGAGTGGGCAAAATCTTGAG 183

DB 652 GCAATTCACCTGATCCCAAGTAATTAATTGGAGAGAGTGGGCAAAATCTTGAG 183

QY 184 GCAATTCACCTGATCCCAAGTAATTAATTGGAGAGAGTGGGCAAAATCTTGAG 243

DB 712 GCAATTCACCTGATCCCAAGTAATTAATTGGAGAGAGTGGGCAAAATCTTGAG 243

QY 244 GGTACCAAGTGAATGTTCTTGAAGTGAATGAATCAATGATGGGCACTCTTAAG 303

DB 772 GGTACCAAGTGAATGTTCTTGAAGTGAATGAATCAATGATGGGCACTCTTAAG 303

QY 304 TACGTTAATGAACTGTCAAGCAACTTAA 332

DB 832 TACGTTAATGAACTGTCAAGCAACTTAA 332

QY 304 TACGTTAATGAACTGTCAAGCAACTTAA 332

DB 832 TACGTTAATGAACTGTCAAGCAACTTAA 332

QY 304 TACGTTAATGAACTGTCAAGCAACTTAA 332

DB 832 TACGTTAATGAACTGTCAAGCAACTTAA 332

QY 304 TACGTTAATGAACTGTCAAGCAACTTAA 332

DB 832 TACGTTAATGAACTGTCAAGCAACTTAA 332

QY 304 TACGTTAATGAACTGTCAAGCAACTTAA 332

DB 832 TACGTTAATGAACTGTCAAGCAACTTAA 332

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XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;  
KM gene; ds.  
XX  
OS Phytolacca americana.  
XX  
PH Key Location/Qualifiers  
FT 1..792  
FT /tag= a  
FT /product= "Mature PAP-S protein"  
FT primer_bind 1..29  
FT /tag= b  
FT /bound_moiety= "Primer PS1BP"  
FT primer_bind complement(436..462)  
FT /tag= c  
FT /bound_moiety= "Primer PS1SR"  
FT primer_bind 463..492  
FT /tag= d  
FT /bound_moiety= "Primer PS2BP"  
FT misc_feature 681..686  
FT /tag= e  
FT /note= "Sequence replacing removed XbaI site"  
FT primer_bind complement(765..792)  
FT /tag= f  
FT /bound_moiety= "Primer PS2SR"  
XX  
XX WO200233107-A2.  
XX  
XX 25-APR-2002.  
XX  
XX 15-OCT-2001; 2001WO-GB004593.  
XX  
XX 14-OCT-2000; 2000GB-00025217.  
XX  
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.  
XX Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;  
XX WPI; 2002-489891/52.  
XX P-PSDB; AAE25919.  
XX  
XX Inducing necrotic effect in specific cells of plant by transforming plant  
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter  
XX which acts in response to application of specific stimulus to plant.  
XX  
XX Claim 2; Page 76; 87pp; English.  
XX  
XX The invention relates to a method of inducing a necrotic effect in  
XX specific cells of a plant. The method involves transforming the plant  
XX with chimeric gene(s) which encodes a pokeweed antiviral protein namely  
XX PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts  
XX in response to the application of a specific stimulus to the plant so as  
XX to facilitate expression of the pokeweed antiviral protein in specific  
XX cells of the plant. The method is useful for inducing a necrotic effect  
XX in specific cells of a plant. The present sequence is pokeweed mature PAP  
XX -S protein encoding DNA  
XX  
SQ Sequence 792 BP; 268 A; 161 C; 151 G; 212 T; 0 U; 0 Other;  
Query Match 98.6%; Score 328.4; DB 6; Length 792;  
Best Local Similarity 99.7%; Pred. No. 2.2e-93;  
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 GGAGTTGATTCATCCCTGTAAGAGAGGCTTTTCTTACTGTAGCCATCAATG 63  
DB 463 GGAGTTGATTCATCCCTGTAAGAGAGGCTTTTCTTACTGTAGCCATCAATG 522  
QY 64 GTTTCAGAGCAGCGGATTCAGTACATAGAGAACCAAGTCAAGCTAATTATAG 123  
DB 523 GTTTCAGAGCAGCGGATTCAGTACATAGAGAACCAAGTCAAGCTAATTATAG 582  
QY 124 GCATTCTACCTGATCCCAAGTAATTAATTGGAGAGAGAGTGGGCAAAATCTCTGAG 183  
|||||
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DB 583 GCATTCTACCTGATCCCAAGTAATTAATTGGAGAGAGAGTGGGCAAAATCTCTGAG 642  
QY 184 GCAATTTCACCAATGCCAAGATGGGCTTTTACCAACCACTTAGCTAGTATGCCAA 243  
DB 643 GCAATTTCACCAATGCCAAGATGGGCTTTTACCAACCACTTAGCTAGTATGCCAA 702  
QY 244 GGTACCAAGTGAATAGTTCTTTAGAGTGAATCAATCGTAGTGGCACTCTTAAG 303  
DB 703 GGTACCAAGTGAATAGTTCTTTAGAGTGAATCAATCGTAGTGGCACTCTTAAG 762  
QY 304 TACGTTAATGGAACCTGTGAGCAACTTA 333  
DB 763 TACGTTAATGGAACCTGTGAGCAACTTA 792  
RESULT 4  
AAD42729  
ID AAD42729 standard; DNA; 1092 BP.  
XX  
XX AAD42729;  
AC  
XX 29-AUG-2003 (revised)  
DT 15-NOV-2002 (first entry)  
XX  
XX Pokeweed PAP-S/TEV PCS/rice cystatin delta D86 fusion DNA.  
XX  
XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;  
KM chimeric; rice; cystatin delta D86; N1A protease cleavage site; PCS; ds.  
XX  
XX Phytolacca americana.  
OS  
OS Oryza sativa.  
OS  
OS Tobacco; Etch virus.  
OS Chimeric.  
XX  
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FT 1..29  
FT /tag= a  
FT /bound_moiety= "Primer PS1BP"  
FT misc_feature 681..686  
FT /tag= b  
FT /note= "Modified XbaI site"  
FT primer_bind complement(742..786)  
FT /tag= c  
FT /bound_moiety= "Primer PCS-PAPSR"  
FT primer_bind 766..806  
FT /tag= d  
FT /bound_moiety= "Primer PCS-Delta86P"  
FT misc_feature 766..786  
FT /tag= e  
FT /note= "TEV N1A protease cleavage site"  
FT primer_bind complement(1066..1092)  
FT /tag= f  
FT /bound_moiety= "Primer SYNPOTdelta86P"  
XX  
XX WO200233107-A2.  
XX  
XX 25-APR-2002.  
XX  
XX 15-OCT-2001; 2001WO-GB004593.  
XX  
XX 14-OCT-2000; 2000GB-00025217.  
XX  
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.  
XX Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;  
XX WPI; 2002-489891/52.  
XX  
XX Inducing necrotic effect in specific cells of plant by transforming plant  
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter  
XX which acts in response to application of specific stimulus to plant.  
XX  
PS Disclosure; Page 83; 87pp; English.
```

XX The invention relates to a method of inducing a necrotic effect in
CC specific cells of a plant. The method involves transforming the plant
CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC PAP', PAP1 and PAP-8, where the gene(s) comprises a promoter which acts
CC in response to the application of a specific stimulus to the plant so as
CC to facilitate expression of the pokeweed antiviral protein in specific
CC cells of the plant. The method is useful for inducing a necrotic effect
CC in specific cells of a plant. The present sequence is a fusion DNA. This
CC sequence comprises pro-PAP-8 DNA, rice cytochrome delta D86 DNA
CC and Tobacco Etch virus (TEV) NTA protease cleavage site (PCS). (Updated
CC on 29-AUG-2003 to standardise OS field)

SO Sequence 1092 BP; 369 A; 195 C; 222 G; 306 T; 0 U; 0 Other;

Query Match 90.8%; Score 302.4; DB 6; Length 1092;
Best Local Similarity 99.7%; Pred. No. 4.2e-85;
Matches 303; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTAAGAACTGAGGCTTTTCTTACTGCTGAGCCTCAATG 63
DB 463 GGAGTTGATTCATTCCTGTAAGAACTGAGGCTTTTCTTACTGCTGAGCCTCAATG 522
QY 64 GTTTCAGAGGAGCGCGATTCATGATGAGAACCAAGTCAGACTAATTTTAAATGA 123
DB 523 GTTTCAGAGGAGCGCGATTCATGATGAGAACCAAGTCAGACTAATTTTAAATGA 582
QY 124 GCATTCACCTGATCCCAAGTAATTAATTGAGAGAAAGTGGGCAAAATCTCTGAG 183
DB 583 GCATTCACCTGATCCCAAGTAATTAATTGAGAGAAAGTGGGCAAAATCTCTGAG 642
QY 184 GCAATTCACAATGCCAAGATGAGGCTTTTACCAGAACCACTGAGCTAGTATGCCAA 243
DB 643 GCAATTCACAATGCCAAGATGAGGCTTTTACCAGAACCACTGAGCTAGTATGCCAA 702
QY 244 GGTAACCAAGTGAATGTTCTTGAAGTGAATCAATCGTATGTCGACTCTTTAAG 303
DB 703 GGTAACCAAGTGAATGTTCTTGAAGTGAATCAATCGTATGTCGACTCTTTAAG 762
QY 304 TACG 307
DB 763 TACG 766

RESULT 5
AAQ43967 standard; DNA; 2472 BP.

XX AAQ43967;
XX 09-NOV-1993 (first entry)
XX Pokeweed antiviral protein.
XX Pokeweed; ricin; protein synthesis inhibitor; cancer;
XX polymerase chain reaction; PCR; ss.
XX Phytolacca americana.

XX Key Location/Qualifiers
XX CAAT_signal 549..552
XX CAAT_signal 627..630
XX TATA_signal 845..850
XX sig_deptide 1014..1085
XX mat_deptide 1086..1868
XX polyA_signal 2130..2135
XX /tag= f

XX JP05137580-A.
XX 01-JUN-1993.
XX 20-NOV-1991; 91JP-00329672.
XX 20-NOV-1991; 91JP-00329672.
XX (NIBS) JAPAN TOBACCO INC.
XX WPI; 1993-211306/26.
XX P-PSDB; AAR37345.
XX New pokeweed antiviral protein (PAP) with similar activity to ricin -
XX used to treat cancer and as an agricultural chemical.

Claim 2; Page 11-13; 14pp; Japanese.

PAP has a similar activity to ricin, i.e. inhibits protein synthesis. The
protein may be obtained all year round by recombinant DNA techniques. PAP
can be used partic. against cancer and as an agricultural chemical. Total
mRNA, is extracted from the seeds, leaves and roots of pokeweed and used
to prepare cDNA using PCR. The resultant cDNA is used to prepare two DNA
fractions, which are introduced into a cloning vector EMBL3 and then into
host R.coli PLK-17 (P2) to produce PAP

Sequence 2472 BP; 864 A; 375 C; 463 G; 770 T; 0 U; 0 Other;

Query Match 73.8%; Score 245.8; DB 2; Length 2472;
Best Local Similarity 84.2%; Pred. No. 4.9e-67;
Matches 277; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTAAGAACTGAGGCTTTTCTTACTGCTGAGCCTCAATG 63
DB 1542 GGAGTTGATTCATTCCTGTAAGAACTGAGGCTTTTCTTACTGCTGAGCCTCAATG 1601
QY 64 GTTTCAGAGGAGCGCGATTCATGATGAGAACCAAGTCAGACTAATTTTAAATGA 123
DB 1602 GTTTCAGAGGAGCGCGATTCATGATGAGAACCAAGTCAGACTAATTTTAAATGA 1661
QY 124 GCATTCACCTGATCCCAAGTAATTAATTGAGAGAAAGTGGGCAAAATCTCTGAG 183
DB 1662 GCATTCACCTGATCCCAAGTAATTAATTGAGAGAAAGTGGGCAAAATCTCTGAG 1721
QY 184 GCAATTCACAATGCCAAGATGAGGCTTTTACCAGAACCACTGAGCTAGTATGCCAA 243
DB 1722 GCAATTCACAATGCCAAGATGAGGCTTTTACCAGAACCACTGAGCTAGTATGCCAA 1781
QY 244 GGTAACCAAGTGAATGTTCTTGAAGTGAATCAATCGTATGTCGACTCTTTAAG 303
DB 1782 GGTAACCAAGTGAATGTTCTTGAAGTGAATCAATCGTATGTCGACTCTTTAAG 1841
QY 304 TACGTTAATGGAACCTGTCAGACAACTTA 332
DB 1842 TACGTTAATGGAACCTGTCAGACAACTTA 1870

RESULT 6
AAQ56672 standard; cDNA; 1195 BP.

XX AAQ56672;
XX 16-OCT-2003 (revised)
XX 25-MAR-2003 (revised)
XX 04-SEP-1994 (first entry)
XX Sequence of Phytolacca antiviral protein (PAP) cDNA.
XX Antiviral protein; PAP; virus-resistance; transgenic plant; ss.
XX Phytolacca americana; L.

```

XX Key Location/Qualifiers
FH CDS 33..974
FT /tag= a
XX
XX PN BP585554-A1.
XX PD 09-MAR-1994.
XX PF 30-JUN-1993; 93BP-00110445.
XX PR 16-AUG-1992; 92KR-00014895.
XX (JINR-) JIN RO LTD.
XX PI Kim M, Lee K, Na B, Jeong H, Choi K, Moon Y, Jeon H;
XX P-PSDB; AAR48548.
XX DR WPI; 1994-076002/10.
XX PT Expression vector for phytoelacca antiviral protein - used for producing
XX transgenic virus-resistant plants and for producing the antiviral agent.
XX PS Disclosure; Fig 1; 15pp; English.
XX CC To isolate PAP gene, total cellular mRNA was purified from leaves of
XX Phytoelacca americana L. obtd. in Korea. A cDNA library was constructed.
XX The PAP gene was selected by immunoscreening employing anti-PAP antibody.
XX A deletion mutant was prepd. from the isolated PAP gene, and the DNA
XX sequence of the PAP gene was determined. (Updated on 25-MAR-2003 to
XX correct FN field.) (Updated on 16-OCT-2003 to standardise OS field)
XX SQ Sequence 1195 BP; 420 A; 201 C; 230 G; 344 T; 0 U; 0 Other;

Query Match 70.0%; Score 233; DB 2; Length 1195;
Best Local Similarity 81.8%; Pred. No. 4.2e-63;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAATTGATTCATTCCTGTAATAAAGTGGGCTTTTCTACGCTGACCAATG 63
Db 558 GGAATGATTCATTCCTGTAATAAAGTGGGCTTTTCTACGCTGACCAATG 617
QY 64 GTTTCAGAGGCGAGCGATTCAGATCAGATGAGAACCAAGTCAAGACTTAATTAAGA 123
Db 618 GTATCAGAGGCGAGCGATTCAGATCAGATGAGAACCAAGTCAAGACTTAATTAAGA 677
QY 124 GCAATTCACCTGATCCCAAGTAATTAATTTGAGAGAAAGTGGGCAAAATCTTGAG 183
Db 678 GCAATTCACCTGATCCCAAGTAATTTGAGAGAAAGTGGGCAAAATCTTGAG 737
QY 184 GCAATTCAGATGCGAAGATGGGGCTTTACCCAAACCACTTGAGCTAGTGAAGCCAA 243
Db 738 GCAATTCAGATGCGAAGATGGGGCTTTACCCAAACCACTTGAGCTAGTGAAGCCAGT 797
QY 244 GGTACCAAGTGAATGTTCTTAGAGTGAAGTAATCAATCGTATGAGCACTCTTAAG 303
Db 798 GGTACCAAGTGAATGTTCTTAGAGTGAAGTAATCAATCGTATGAGCACTCTTAAG 857
QY 304 TAGCTTAATGAACCTGTGACCAACTTA 332
Db 858 TAGCTTAATGAACCTGTGACCAACTTA 886

RESULT 7
AAQ81457 standard; cDNA, 1195 BP.
XX AAQ81457;
XX
XX 16-OCT-2003 (revised)
XX 25-AUG-1995 (first entry)
XX
XX Phytoelacca antiviral protein (PAP) cDNA.

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XX XX
XX Antiviral protein; vector pMJ12; KCCM 10037; PAP; ss.
XX KM Phytoelacca americana; L.
XX OS
XX PN AU9350642-A.
XX PD 19-JAN-1995.
XX PF 11-NOV-1993; 93AU-00050642.
XX PR 02-JUL-1993; 93KR-00012360.
XX (JINR-) JIN RO LTD.
XX PI Lee K, Choi K, Jeon H, Kim M, Moon Y;
XX P-PSDB; AAR48548.
XX DR WPI; 1995-067518/10.
XX PT Recombinant vector for producing Phytoelacca anti-viral protein - and
XX transformed E. coli useful for making immunocjugates for treatment of
XX AIDS.
XX PS Claim 1; Fig 1; 27pp; English.
XX CC Total cellular mRNA from leaves of P. americana was used to produce a
XX cDNA library and this screened with anti-PAP antibody raised in rabbits
XX against purified PAP. Inserts were isolated from 2 clones and sequenced
XX to identify a 1195 ORF (AAQ81457) that encodes a 313 AA PAP including a
XX 22 AA signal peptide. The mature PAP gene was suggested to PCR
XX amplification using primers AAQ81458 and AAQ81459. The amplification
XX product was cut with Hind III and inserted into the commercial FLAG (RTM)
XX vector cut with the same enzyme to form pMJ12. pMJ12 is deposited with
XX the Korean Collection of Culture and Microorganism (KCCM), an
XX International Depository Authority, on June 30 1993, ad deposition No.
XX KCCM 10037, and claimed. (Updated on 16-OCT-2003 to standardise OS field)
XX SQ Sequence 1195 BP; 420 A; 203 C; 229 G; 343 T; 0 U; 0 Other;

Query Match 70.0%; Score 233; DB 2; Length 1195;
Best Local Similarity 81.8%; Pred. No. 4.2e-63;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAATTGATTCATTCCTGTAATAAAGTGGGCTTTTCTACGCTGACCAATG 63
Db 558 GGAATGATTCATTCCTGTAATAAAGTGGGCTTTTCTACGCTGACCAATG 617
QY 64 GTTTCAGAGGCGAGCGATTCAGATCAGATGAGAACCAAGTCAAGACTTAATTAAGA 123
Db 618 GTATCAGAGGCGAGCGATTCAGATCAGATGAGAACCAAGTCAAGACTTAATTAAGA 677
QY 124 GCAATTCACCTGATCCCAAGTAATTAATTTGAGAGAAAGTGGGCAAAATCTTGAG 183
Db 678 GCAATTCACCTGATCCCAAGTAATTTGAGAGAAAGTGGGCAAAATCTTGAG 737
QY 184 GCAATTCAGATGCGAAGATGGGGCTTTACCCAAACCACTTGAGCTAGTGAAGCCAA 243
Db 738 GCAATTCAGATGCGAAGATGGGGCTTTACCCAAACCACTTGAGCTAGTGAAGCCAGT 797
QY 244 GGTACCAAGTGAATGTTCTTAGAGTGAAGTAATCAATCGTATGAGCACTCTTAAG 303
Db 798 GGTACCAAGTGAATGTTCTTAGAGTGAAGTAATCAATCGTATGAGCACTCTTAAG 857
QY 304 TAGCTTAATGAACCTGTGACCAACTTA 332
Db 858 TAGCTTAATGAACCTGTGACCAACTTA 886

RESULT 8
AAD42739 standard; DNA, 1378 BP.
XX AAD42739;
XX
XX

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XX 15-NOV-2002 (first entry)
DT
XX Pokeweed PAP' DNA #2.
DE
XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; ds.
KM
XX Phytolacca americana.
OS
XX Key Location/Qualifiers
FH mlec_feature 280..1076
FT /tag= a
FT /note= "Mature PAP' sequence"
XX
XX MO200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001MO-GB004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX Thomas CJR, McPherson MJ, Atkinson HJ, Neelam A;
PI Thomas CJR, McPherson MJ, Atkinson HJ, Neelam A;
XX
XX WPI; 2002-489891/52.
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
PT which acts in response to application of specific stimulus to plant.
XX
XX Claim 5; Page 86-87; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
XX specific cells of a plant. The method involves transforming the plant
XX with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
XX in response to the application of a specific stimulus to the plant so as
XX to facilitate expression of the pokeweed antiviral protein in specific
XX cells of the plant. The method is useful for inducing a necrotic effect
XX in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX
XX Sequence 1378 BP; 488 A; 234 C; 269 G; 387 T; 0 U; 0 Other;
SQ
Query Match 70.0%; Score 233; DB 6; Length 1378;
Best Local Similarity 81.8%; Pred. No. 4.4e-63;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
4 GAGATTGATTCATTCCTGTTAAACCTGAGGCTTTTCTACTGTGATGCAATCCAAATG 63
750 GAGATGATGTCATTCATCTGAGAAAACGAAATTCCTATTGTGATGCAATCAATG 809
64 GTTTCAGAGGAGGCGGATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTAATGA 123
810 GTATCAGAGGCGAGCAAGATTCAAGTACATAGAGAACGTAAGAAACTAATTTTAACGA 869
124 GCATTCTACCTGATCCCAAGATTAATTAATTTGAGAGGAAGTGGGGGCAAAATCTCTGAG 183
870 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAAGATTTCACA 929
184 GCAATTCAATGATCCCAAGATGGGCTTAACCAACCACTGAGCTAGTGATGCCAAA 243
930 GCAATTCAATGATCCCAAGATGGGCTTAACCAACCACTGAGCTAGTGATGCCAAAT 989
244 GGTACCAAGTGAATGTTCTTGAAGTGAATGAATCAATCGTGAATGCACTCTTAAAG 303
990 GGTGCCCAAGTGAATGTTCTTGAAGTGAATGAATCAAGCTGAATGCACTCTTAAAC 1049
304 TACGTTAATGAACCTGTGACAACTTA 332
1050 TACGTTGTTGGAGCTGTGACAACTTA 1078

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RESULT 9
ADG76061
ID ADG76061 standard; DNA; 1378 BP.
XX
XX ADG76061;
AC
XX 11-MAR-2004 (first entry)
DT
XX American pokeweed antiviral protein (PAP) DNA Seqid 1.
DE
XX gene; ds; pokeweed antiviral protein; PAP; HIV-1; anti-HIV; antiviral;
XX nucleoside analogue inhibitor; viral protease inhibitor; viral infection;
XX American pokeweed; retroviral.
XX
XX Phytolacca americana.
OS
XX MO2003106479-A2.
XX
XX 24-DEC-2003.
XX
XX 17-JUN-2003; 2003MO-US019141.
XX
XX 17-JUN-2002; 2002US-0389649P.
XX
XX (PARK-) PARKER HUGHES INST.
XX
XX Uckun FM;
PI WPI; 2004-082156/08.
XX
XX P-PSDB; ADG76064.
XX
XX Novel modified pokeweed antiviral protein useful for inhibiting viral
PT replication, for inducing depurination of viral RNA, or for treating
PT viral infection in subject.
XX
XX Example 2; SEQ ID NO 1; 62pp; English.
XX
XX This invention relates to novel modified pokeweed antiviral proteins
XX (PAPs). Specifically, it refers to modifications relative to wild-type
XX PAP that confer increased activity towards viral RNA, particularly
XX retroviral RNA such as HIV-1 and drug resistant HIV-1. Furthermore,
XX modified PAP also exhibits decreased activity towards ribosomal RNA
XX relative to wild-type PAP. The present invention describes a molecular
XX model of PAP-HIV RNA interactions that have been used for the rational
XX redesign of PAP mutants with potent anti-HIV activity, where
XX modifications have been introduced in regions other than the active site.
XX Accordingly, these mutants represent antiviral agents that can work as
XX nucleoside analogue inhibitors of reverse transcriptase, as well as viral
XX protease inhibitors that can be used for treating viral infections. As
XX such, they are useful for inhibiting viral replication and for
XX depurinating viral RNA. This polynucleotide sequence is the DNA encoding
XX the wild type American pokeweed antiviral protein (PAP) of the invention.
XX
XX Sequence 1378 BP; 487 A; 234 C; 268 G; 389 T; 0 U; 0 Other;
SQ
Query Match 70.0%; Score 233; DB 12; Length 1378;
Best Local Similarity 81.8%; Pred. No. 4.4e-63;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
4 GAGATTGATTCATTCCTGTTAAACCTGAGGCTTTTCTACTGTGATGCAATCCAAATG 63
749 GAGATGATGTCATTCATCTGAGAAAACGAAATTCCTATTGTGATGCAATCAATG 808
64 GTTTCAGAGGAGGCGGATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTAATGA 123
809 GTATCAGAGGCGAGCAAGATTCAAGTACATAGAGAACGTAAGAAACTAATTTTAACGA 868
124 GCATTCTACCTGATCCCAAGATTAATTAATTTGAGAGGAAGTGGGGGCAAAATCTCTGAG 183
869 GCAATTCAACCTTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAAGATTTCACA 928
184 GCAATTCAATGATCCCAAGATGGGCTTAACCAACCACTGAGCTAGTGATGCCAAA 243

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Db      929 GCAATTGATGATCCAGATGAGTTTACCCAACTCTGAGCTAGTGATGCACT 988
Qy      244 GGTACCAAGTGAATGTTCTTGAAGTGAATGAATCAATCGATGTGCACTCTTAA 303
Db      989 GGTGCAAGTGAATGTTCTTGAAGTGAATGAATCAATCGATGTGCACTCTTAA 1048
Qy      304 TACGTTAATGAACTGTGCAACAATT 332
Db      1049 TACGTTGCTGGAGCTGTGCAACAATT 1077

RESULT 10
AAZ45197 ID AAZ45197 standard; DNA; 1379 BP.
AAZ45197 AC AAZ45197;
Dl      29-FEB-2000 (first entry)
Dl      XX Wild-type pokeweed antiviral protein (PAP) nucleotide sequence.
Dl      XX
Dl      XX Pokeweed antiviral protein; PAP; PAP II; antifungal; transgenic plant;
Dl      XX ribosome inhibiting protein; RIP; cereal crop; viral resistance; PVX;
Dl      XX tomato yellow leaf curl virus; CMV; ss;
Dl      XX
Dl      XX Phytophthora americana.
Dl      XX
Dl      XX Key Location/Qualifiers
Dl      XX CDS 225..1166
Dl      XX /*tag= a
Dl      XX /product= "PAP"
Dl      XX /note= "Pokeweed antiviral protein"

PN      M09960843-A1.
XX      02-DEC-1999.
PD      21-MAY-1999; 99WO-US011301.
PF      22-MAY-1998; 98US-0086374P.
PR      (RUTP ) UNIV RUTGERS STATE NEW JERSEY.
PI      Turner NE, Wang P;
XX      WPI; 2000-062555/05.
DR      P-PDB; AAY58025.
XX      New antiviral DNA useful for generating transgenic plants resistant to
XX      viruses and/or fungi.
XX      Example; Page 4-5; 43pp; English.
XX      This is the pokeweed antiviral protein (PAP) nucleotide sequence. PAP is
XX      a type I ribosome-inhibiting protein (RIP) found in the cell walls of
XX      Phytophthora americana (pokeweed). It is a single polypeptide chain that
XX      catalytically removes a specific adenine residue from a highly conserved
XX      stem-loop structure in the 28S rRNA of eukaryotic ribosomes. The pokeweed
XX      antiviral protein II (PAP II) protein confers antiviral and or antifungal
XX      activities to plants. A DNA molecule encoding a PAP II protein with an
XX      intact catalytic active site amino acid residue (E172) is useful for
XX      generating transgenic plants. PAP II DNA is useful for generating
XX      transgenic plants (especially cereal crops) through transforming a
XX      protoplast or introducing the DNA directly into a plant part prior to
XX      regeneration. Cells and seeds which exhibit anti-viral and/or anti-fungal
XX      activity thus have increased resistance to viruses and/or fungi. Viruses
XX      include potato virus X (PVX), cucumber mosaic virus (CMV), and tomato
XX      yellow leaf curl virus, and fungi include Pythium, Phytophthora,
XX      Sclerotinia and Aspergillus. PAP II proteins also confer resistance to
XX      other plants pests including insects, bacteria and nematodes. PAP II DNA
XX      is also useful for identifying a PAP II protein having reduced

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CC      cytotoxicity. PAP II has a reduced cytotoxicity compared to PAP, so
CC      unlike PAP transgenic plants which are stunted and sterile, PAP II
CC      transgenic plants have a normal and fertile phenotype
XX      SQ      Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
Query Match      70.0%; Score 233; DB 3; Length 1379;
Beet Local Similarity 81.8%; Pred. No. 4.4e-63;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
Qy      4 GGAATGATGATTCCTCTGTAATAAAGTGAAGGCTTTTCTTCTAGTGTGATCCATCAATG 63
Db      750 GGAATGATGATTCCTCTGTAATAAAGTGAAGGCTTTTCTTCTAGTGTGATCCATCAATG 809
Qy      64 GTTTCAGAGGAGCGCGATTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 123
Db      810 GTATCAGAGGAGCGCGATTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 869
Qy      124 GCATTCTACCTGATCCCAAGTAAATTAATTTGAGAGGAGAGTGGGCAAAATCTGTAG 183
Db      870 GCATTCTACCTGATCCCAAGTAAATTAATTTGAGAGGAGAGTGGGCAAAATCTGTAG 929
Qy      184 GCAATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 243
Db      930 GCAATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 989
Qy      244 GGTACCAAGTGAATGTTCTTGAAGTGAATGAATCAATCGATGTGCACTCTTAA 303
Db      990 GGTGCAAGTGAATGTTCTTGAAGTGAATGAATCAATCGATGTGCACTCTTAA 1049
Qy      304 TACGTTAATGAACTGTGCAACAATT 332
Db      1050 TACGTTGCTGGAGCTGTGCAACAATT 1078

RESULT 11
AAZ59221 ID AAZ59221 standard; cDNA; 1379 BP.
AAZ59221 AC AAZ59221;
Dl      20-APR-2000 (first entry)
Dl      XX Variant pokeweed antiviral protein spring leaf form coding sequence.
Dl      XX
Dl      XX Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
Dl      XX resistance; potato virus X; potato virus Y; potato leaf roll virus;
Dl      XX tuber; ss.
Dl      XX
Dl      XX Phytophthora americana.
Dl      XX
Dl      XX US6015940-A.
Dl      XX PN 18-JAN-2000.
Dl      XX
Dl      XX 07-APR-1992; 92US-00865169.
Dl      XX PR 07-APR-1992; 92US-00865169.
Dl      XX (MONS ) MONGANTO CO.
Dl      XX PA
Dl      XX Kanielski WK, Turner NE, Lodge JK;
Dl      XX WPI; 2000-126326/11.
Dl      XX
Dl      XX Production of transgenic potato plants or tubers expressing pokeweed
Dl      XX antiviral protein which are resistant to potato virus X or Y.
Dl      XX Claim 7; Fig 5; 30pp; English.
Dl      XX
Dl      XX This is the coding sequence for a variant spring leaf form of the
Dl      XX pokeweed antiviral protein (PAP') which is used to generate transgenic
Dl      XX potato plants. PAP' is able to confer resistance to infection by potato

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virus X (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in the
CC the potato plant or tuber expressing PAP. PAP varies from PAP
CC (AA259220) by mutations 120R and Y49H
CC XX
SQ Sequence 1379 BP; 489 A; 234 C; 269 G; 387 T; 0 U; 0 Other;
Query Match 70.0%; Score 233; DB 3; Length 1379;
Best Local Similarity 81.8%; Pred. No. 4,4e-63;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 4 GGAGTTGATTCATTCCTGTAATAAAGCTTTTCTTACTGTGTAGCCATCCAAATG 63
DB 750 GGAGTGATGTCATTCCTGTAATAAAGCTTTTCTTACTGTGTAGCCATCCAAATG 809
QY 64 GTTTCAGAGCGGCGGATTCAGTACATAGAGAACCAAGTCAAGCTAATTTTAATAGA 123
DB 810 GTATCAGAGCGGCGGATTCAGTACATAGAGAACCAAGTCAAGCTAATTTTAATAGA 869
QY 124 GCATTCAACCTGATCCCAAGTAAATTTTGGAGAGAGATGGGGCAAAATCTCTGAG 183
DB 870 GCATTCAACCTGATCCCAAGTAAATTTTGGAGAGAGATGGGGCAAAATCTCTGAG 929
QY 184 GCATTCAACCTGATCCCAAGTAAATTTTGGAGAGAGATGGGGCAAAATCTCTGAG 243
DB 930 GCATTCAACCTGATCCCAAGTAAATTTTGGAGAGAGATGGGGCAAAATCTCTGAG 989
QY 244 GGTACCAAGTGATAGTCTTGAAGTGAATGAATCAATCGTATGTGGCACTCCTTAAG 303
DB 990 GGTACCAAGTGATAGTCTTGAAGTGAATGAATCAATCGTATGTGGCACTCCTTAAG 1049
QY 304 TACGTTAATGGAACCTGTCAACAACCTTA 332
DB 1050 TACGTTGATGGAGCTGTCAACAACCTTA 1078
RESULT 12
AA259220
ID AA259220 strand; cDNA; 1379 BP.
XX
AC AA259220;
XX
AC AA259220;
XX
DT 20-APR-2000 (first entry)
XX
DE Pokeweed antiviral protein coding sequence spring leaf form.
XX
XX Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
XX resistance; potato virus X; potato virus Y; potato leaf roll virus;
XX tuber; ss.
XX
OS Phytolacca americana.
XX
XX US6015940-A.
XX
XX 18-JAN-2000.
XX
XX 07-APR-1992; 92US-00865169.
XX
XX 07-APR-1992; 92US-00865169.
XX
XX (MONS) MONSANTO CO.
XX
XX (MONS) MONSANTO CO.
XX
XX Kaniewski WK, Turner NE, Lodge JK;
XX
XX WPI; 2000-126326/11.
XX
XX Production of transgenic potato plants or tubers expressing pokeweed
XX antiviral protein which are resistant to potato virus X or Y.
XX
XX Claim 6; Fig 4; 30pp; English.
XX
XX This is the coding sequence for the spring leaf form of the pokeweed
XX antiviral protein (PAP) which is used to generate transgenic potato
XX plants. PAP is able to confer resistance to infection by potato virus X
XX

(PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in the
CC potato plant or tuber expressing PAP
CC XX
SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
Query Match 70.0%; Score 233; DB 3; Length 1379;
Best Local Similarity 81.8%; Pred. No. 4,4e-63;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 4 GGAGTTGATTCATTCCTGTAATAAAGCTTTTCTTACTGTGTAGCCATCCAAATG 63
DB 750 GGAGTGATGTCATTCCTGTAATAAAGCTTTTCTTACTGTGTAGCCATCCAAATG 809
QY 64 GTTTCAGAGCGGCGGATTCAGTACATAGAGAACCAAGTCAAGCTAATTTTAATAGA 123
DB 810 GTATCAGAGCGGCGGATTCAGTACATAGAGAACCAAGTCAAGCTAATTTTAATAGA 869
QY 124 GCATTCAACCTGATCCCAAGTAAATTTTGGAGAGAGATGGGGCAAAATCTCTGAG 183
DB 870 GCATTCAACCTGATCCCAAGTAAATTTTGGAGAGAGATGGGGCAAAATCTCTGAG 929
QY 184 GCATTCAACCTGATCCCAAGTAAATTTTGGAGAGAGATGGGGCAAAATCTCTGAG 243
DB 930 GCATTCAACCTGATCCCAAGTAAATTTTGGAGAGAGATGGGGCAAAATCTCTGAG 989
QY 244 GGTACCAAGTGATAGTCTTGAAGTGAATGAATCAATCGTATGTGGCACTCCTTAAG 303
DB 990 GGTACCAAGTGATAGTCTTGAAGTGAATGAATCAATCGTATGTGGCACTCCTTAAG 1049
QY 304 TACGTTAATGGAACCTGTCAACAACCTTA 332
DB 1050 TACGTTGATGGAGCTGTCAACAACCTTA 1078
RESULT 13
AAD2738
ID AAD2738 strand; DNA; 1379 BP.
XX
AC AAD2738;
XX
AC AAD2738;
XX
DT 15-NOV-2002 (first entry)
XX
DE Pokeweed PAP' DNA #1.
XX
XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; db.
XX
XX Phytolacca americana.
XX
XX Key location/qualifiers
XX mISC_feature 290..1076
XX /tag= a
XX /note= "Mature PAP' sequence"
XX
XX WO200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-GB004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX Thomas CJR, McPherson MJ, Atkinson HJ, Neelam A;
XX
XX WPI; 2002-489891/52.
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX which acts in response to application of specific stimulus to plant.
XX
XX Claim 5; Page 86; 87pp; English.
XX

CC The invention relates to a method of inducing a necrotic effect in
CC specific cells of a plant. The method involves transforming the plant
CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
CC in response to the application of a specific stimulus to the plant so as
CC to facilitate expression of the pokeweed antiviral protein in specific
CC cells of the plant. The method is useful for inducing a necrotic effect
CC in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX
SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Query Match 70.0%; Score 233; DB 6; Length 1379;
Best Local Similarity 81.8%; Pred. No. 4.4e-63;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTGAATTCATTCCTGTAAGAACTGAGGGCTTTTCTCTAGTGCATCCAAATG 63
DB 750 GGAGTGAATTCATTCCTGTAAGAACTGAGGGCTTTTCTCTAGTGCATCCAAATG 809
QY 64 GTTTCAGAGGCGCGGATTCATCATAGAGAACCAAGTCAAGCTAATTTAATAGA 123
DB 810 GTTTCAGAGGCGCGGATTCATCATAGAGAACCAAGTCAAGCTAATTTAATAGA 869
QY 124 GCATTCACCTGATCCCAAGTAATTAATTGGAGAGAAAGTGGGCAAAATCTCTGAG 183
DB 870 GCATTCACCTGATCCCAAGTAATTAATTGGAGAGAAAGTGGGCAAAATCTCTGAG 929
QY 184 GCAATTCACCAATGCCAAGATGGGGCTTTACCCAAACCACTTGATGATGACCAAA 243
DB 930 GCAATTCACCAATGCCAAGATGGGGCTTTACCCAAACCACTTGATGATGACCAAA 989
QY 244 GGTACCAAGTGATAGTTCTTAGAGTGATGAATCAATCGATGTCACCTCTTAAAG 303
DB 990 GGTACCAAGTGATAGTTCTTAGAGTGATGAATCAATCGATGTCACCTCTTAAAG 1049
QY 304 TACGTTAATGGAACCTGTGACCAACTTA 332
DB 1050 TACGTTGATGGAGCTGTGACCAACTTA 1078

RESULT 14

AD105787
ID AD105787 standard; DNA; 1379 BP.

AC AD105787;

DT 15-APR-2004 (first entry)

XX DNA encoding the wild-type pokeweed antiviral protein.

XX ribosome depurination; antifungal; antiviral; viroinhibitor; anti-HIV;
XX cytoskeletal; immunosuppressive; agricultural biotechnology; pharmaceuticals;
XX medicine; cancer; AIDS; viral infection; autoimmune disease; T-cell;
XX B-cell; transgenic; plant; wild-type; pokeweed antiviral protein; gene;
XX ds.

XX Phytolacca americana.

XX Key Location/Qualifiers

XX CDS 225..1166

XX /tag= a

XX /product= "wild-type pokeweed antiviral protein"

XX W0200262952-A2.

XX 15-AUG-2002.

XX 01-FEB-2002; 2002WO-US002792.

XX 02-FEB-2001; 2001US-0266396P.
XX (RUTP) UNIV RUTGERS STATE NEW JERSEY.
XX

PI Turner NR, Hudak KA, Parikh B;

XX WPI; 2003-156656/15.
XX P-PsDB; AD105788.

XX New Pokeweed Antiviral Protein (PAP) mutant that is less toxic than wild-
XX type PAP, useful in agricultural biotechnology or in the fields of
XX pharmaceuticals and medicine, e.g. treating cancer, AIDS, viral infection
XX or autoimmune disease.

XX Disclosure; SEQ ID NO 1; S1DP; English.

XX The invention relates to a novel pokeweed Antiviral Protein (PAP) mutant
XX that is less toxic than wild-type PAP and exhibits ribosome depurination
XX activity, where the mutant is a central domain mutant or N-terminal
XX domain mutant. The PAP mutants have the following activities: antifungal,
XX antiviral, viroinhibitor, anti-HIV, cytoskeletal and immunosuppressive. The PAP
XX mutants are useful in agricultural biotechnology as well as in the fields
XX of pharmaceuticals and medicine. The PAP mutants and methods are useful in
XX treating mammals with cancer, AIDS, viral infection or autoimmune
XX diseases associated with proliferations of unwanted T-cells or B-cells.
XX The transgenic plants are useful in exhibiting resistance to a broad
XX spectrum of plant pests e.g. viruses and fungi. This polynucleotide
XX sequence represents the DNA encoding the wild-type pokeweed antiviral
XX protein of the invention.

SQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Query Match 70.0%; Score 233; DB 10; Length 1379;
Best Local Similarity 81.8%; Pred. No. 4.4e-63;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTGAATTCATTCCTGTAAGAACTGAGGGCTTTTCTCTAGTGCATCCAAATG 63
DB 750 GGAGTGAATTCATTCCTGTAAGAACTGAGGGCTTTTCTCTAGTGCATCCAAATG 809
QY 64 GTTTCAGAGGCGCGGATTCATCATAGAGAACCAAGTCAAGCTAATTTAATAGA 123
DB 810 GTTTCAGAGGCGCGGATTCATCATAGAGAACCAAGTCAAGCTAATTTAATAGA 869
QY 124 GCATTCACCTGATCCCAAGTAATTAATTGGAGAGAAAGTGGGCAAAATCTCTGAG 183
DB 870 GCATTCACCTGATCCCAAGTAATTAATTGGAGAGAAAGTGGGCAAAATCTCTGAG 929
QY 184 GCAATTCACCAATGCCAAGATGGGGCTTTACCCAAACCACTTGATGATGACCAAA 243
DB 930 GCAATTCACCAATGCCAAGATGGGGCTTTACCCAAACCACTTGATGATGACCAAA 989
QY 244 GGTACCAAGTGATAGTTCTTAGAGTGATGAATCAATCGATGTCACCTCTTAAAG 303
DB 990 GGTACCAAGTGATAGTTCTTAGAGTGATGAATCAATCGATGTCACCTCTTAAAG 1049
QY 304 TACGTTAATGGAACCTGTGACCAACTTA 332
DB 1050 TACGTTGATGGAGCTGTGACCAACTTA 1078

RESULT 15

AAC87929
ID AAC87929 standard; DNA; 1379 BP.

AC AAC87929;

DT 06-MAR-2001 (first entry)

XX P. americana pokeweed antiviral protein encoding DNA SEQ ID NO.1.

XX Phytolacca americana; pokeweed; pokeweed antiviral protein; PAP; cancer;
XX bioreproductive; fusion protein; immunosuppressive; mutant; cytoskeletal;
XX anti-HIV; human immunodeficiency virus; AIDS; leukemia; lymphoma;
XX brain tumour; neuroblastoma; soft tissue sarcoma; osteosarcoma; ss.
XX Phytolacca americana.
XX

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:25:18 ; Search time 1577.51 Seconds
(without alignments)
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Title: US-09-978-274A-7

Perfect score: 333

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hic.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_ges1.*
10: gb_ges2.*
11: gb_ges3.*

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	73.8	22.2	816	2	BR035038
C 2	73.8	22.2	993	2	BR035039
C 3	58.2	17.5	1033	2	BR035041
C 4	56.6	17.0	639	6	BR035041
C 5	56.6	17.0	649	6	BR035041
C 6	56.6	17.0	649	6	BR035041
C 7	56.6	17.0	649	6	BR035041
C 8	56.6	17.0	671	6	BR035041
C 9	56.6	17.0	689	6	BR035041
C 10	56.6	17.0	689	6	BR035041
C 11	52.4	15.7	405	8	BR035041
C 12	49.6	14.9	1038	2	BR035041
C 13	48.6	14.6	639	2	BR035041
C 14	46.4	13.9	829	2	BR035041
C 15	44.6	13.4	1021	2	BR035041
C 16	43	12.9	267	7	BR035041
C 17	41.6	12.5	571	7	BR035041
C 18	40	12.0	700	3	BR035041
C 19	40	12.0	715	3	BR035041
C 20	39.8	12.0	837	1	BR035041
C 21	39.6	11.9	614	7	BR035041
C 22	38.6	11.6	593	3	BR035041

C 23	38.6	11.6	669	7	CN848288
C 24	38.6	11.6	721	3	BM574953
C 25	38.2	11.5	791	7	CP998461
C 26	38	11.4	671	7	CN845973
C 27	37.8	11.4	627	8	CK043173
C 28	37.8	11.4	676	3	BM585966
C 29	37.8	11.4	1012	6	CA125924
C 30	37	11.1	749	7	CR530626
C 31	36.8	11.1	498	8	AJ281693
C 32	36.6	11.0	723	8	DR659480
C 33	36.6	11.0	841	8	DR803998
C 34	36.4	10.9	420	6	CP227009
C 35	36.4	10.9	557	2	BG450283
C 36	36.4	10.9	898	9	AZ676415
C 37	36	10.8	472	2	BG042437
C 38	36	10.8	612	2	AG341401
C 39	36	10.8	670	9	AQ343493
C 40	35.8	10.8	889	10	CZ951885
C 41	35.6	10.7	154	10	CR817274
C 42	35.6	10.7	595	5	BU549020
C 43	35.4	10.6	1465	10	CL643815
C 44	35	10.5	298	2	BM521963
C 45	35	10.5	391	6	CA148398

ALIGNMENTS

RESULT 1
LOCUS BR035038 816 bp mRNA linear EST 07-JUN-2000
DEFINITION MM02A01 MM Mesembryanthemum crystallinum cDNA 5' similar to
antiviral protein, mRNA sequence.

ACCESSION BR035038
VERSION BR035038.1 GI:8330047
KEYWORDS
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum

REFERENCE
AUTHORS Bohner, H., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
Ferreira, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
1 (bases 1 to 816)
Caryophyllales; Alzooceae; Mesembryanthemum.

TITLE Functional Genomics of Plant Stress Tolerance
JOURNAL Unpublished (2000)
COMMENT Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cdm@u.arizona.edu.

FEATURES

source
1. 816
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/cell_type="epidermal bladder cells"
/dev_stage="12 weeks old"
/clone_id="MM"
/notes="Vector: Bluescript SK+; Site 1: EcoRI; Site 2:
XhoI; Plants stressed 6 weeks in 500mM NaCl"

ORIGIN

Query Match 22.2%; Score 73.8; DB 2; Length 816;
Best Local Similarity 66.9%; Pred. No. 8.2e-11;
Matches 121; Conservative 0; Mismatches 57; Indels 3; Gaps 1;
DB 590 TCGATGGAAACATCGAGCCAAATCTTACTGATTCAGTCCAGATGCTTCAGAGCAG 531

QY 77 CGGATTCAGATCATAGAGAACCAAGT---CAGACTAAATTTTATAGAGCATTTACC 133
 DB 530 CAGGGTTCATTTATATGAGCTAAGGTGCCGAAAGTGGTGCATGGTTCTTCAAC 471
 QY 134 CTGATCCCAAGATTAATTAATTTGGAGAGAAAGTGGGCAAAATCTTGAGGCAATTCACA 193
 DB 470 CCGATCCGAAAGATTAATTAATTTGGAGAGAACTGGGGAAAGATTTCCGATGATGATCATA 411
 QY 194 A 194
 DB 410 A 410

RESULT 2
 BE035039/c 993 bp mRNA linear EST 07-JUN-2000
 LOCUS
 DEFINITION NM02A03 NM Mesembryanthemum crystallinum cDNA 5' similar to
 active viral protein, mRNA sequence.
 ACCESSION BE035039
 VERSION BE035039.1 GI:8330048
 KEYWORDS
 SOURCE Mesembryanthemum crystallinum (common iceplant)
 ORGANISM Mesembryanthemum crystallinum

REFERENCE
 AUTHORS Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
 Ferreira, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
 Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
 Functional Genomics of Plant Stress Tolerance
 Unpublished (2000)
 CONTACT: Michalowski, C.B.
 University of Arizona
 Bio Sciences West room 513, Tucson, AZ 85721, USA
 Tel: 520-621-7982
 Fax: 520-621-1697
 Email: cdm@u.arizona.edu
 Insert Length: 1 Std Error: 0.00.
 Location/Qualifiers
 1. 993
 /organism="Mesembryanthemum crystallinum"
 /mol_type="mRNA"
 /db_xref="taxon:3544"
 /cell_type="epidermal bladder cells"
 /dev_stage="12 weeks old"
 /clone_lib="MM"
 /note="Vector: Bluescript SK+; Site 1: EcoRI; Site 2:
 XhoI; Plants stressed 6 weeks in 500mM NaCl"

FEATURES
 source
 Query Match 22.2%; Score 73.8; DB 2; Length 993;
 Best Local Similarity 66.9%; Pred. No. 8.7e-11;
 Matches 121; Conservative 0; Mismatches 57; Indels 3; Gaps 1;

ORIGIN
 Query Match 22.2%; Score 73.8; DB 2; Length 993;
 Best Local Similarity 66.9%; Pred. No. 8.7e-11;
 Matches 121; Conservative 0; Mismatches 57; Indels 3; Gaps 1;
 QY 17 TCCCTGTAATAAAGTGAAGCTTTTCTTCTACTGTAGCATCAATGGTTTCAGAGGAG 76
 DB 591 TCGATGGGAAAGCTGAGGCCAAATTTCTTACTGATTCATCAATGGTTTCAAGAGAG 532
 QY 77 CGGATTCAGATCATAGAGAACCAAGT---CAGACTAAATTTTATAGAGCATTTACC 133
 DB 531 CACGGTTCATTTAATATGAGACTAAGGTGACCGAAAGTGGTCACTGGTTCTTCAAC 472
 QY 134 CTGATCCCAAGATTAATTAATTTGGAGAGAGAGTGGGCAAAATCTTGAGGCAATTCACA 193
 DB 471 CCGATCCGAAAGATTAATTAATTTGGAGAGAACTGGGGAAAGATTTCCGATGATGATCATA 412
 QY 194 A 194
 DB 411 A 411

RESULT 3

BE036541
 LOCUS 1033 bp mRNA linear EST 07-JUN-2000
 DEFINITION NM01B07 MP Mesembryanthemum crystallinum cDNA 5' similar to
 active viral protein, mRNA sequence.
 ACCESSION BE036541
 VERSION BE036541.1 GI:8331550
 KEYWORDS
 SOURCE Mesembryanthemum crystallinum (common iceplant)
 ORGANISM Mesembryanthemum crystallinum

REFERENCE
 AUTHORS Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
 Ferreira, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
 Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
 Functional Genomics of Plant Stress Tolerance
 Unpublished (2000)
 CONTACT: Michalowski, C.B.
 University of Arizona
 Bio Sciences West room 513, Tucson, AZ 85721, USA
 Tel: 520-621-7982
 Fax: 520-621-1697
 Email: cdm@u.arizona.edu
 An open reading frame exists.
 Location/Qualifiers
 1. 1033
 /organism="Mesembryanthemum crystallinum"
 /mol_type="mRNA"
 /db_xref="taxon:3544"
 /tissue_type="apical meristem and leaf primordia"
 /dev_stage="6 weeks"
 /clone_lib="MP"
 /note="3 d 500mM NaCl"

ORIGIN

Query Match 17.5%; Score 58.2; DB 2; Length 1033;
 Best Local Similarity 63.5%; Pred. No. 4.1e-06;
 Matches 106; Conservative 0; Mismatches 58; Indels 3; Gaps 1;
 QY 30 TGAGGCTTTTCTTCTACTGTATCCATCCAAATGGTTTCAGAGCGGGGATTCAGTA 89
 DB 298 TGAGGCCAAATTTCTTGATGATGCTATACCAATGGTTTCGAAAGCAGCAGGTTTAAGTA 357
 QY 90 CATAGAGAACCAAGTCA---AGACTAATTTTAATAGAGCATTTACCCGTATCCCAAGT 146
 DB 358 TATTGAAGATGATGATGACCCAAAGTGGTTTACATGCTCTTCAATACCGAACCGAAGT 417
 QY 147 AATTAAATTTGAGAGAGAGTGGGCAAAATCTTGAGGCAATTCACA 193
 DB 418 GCTGAGTTTGAAGAACAAATTTGGGGGAAGATTTGCGAAGATTCATA 464

RESULT 4
 CA835855
 LOCUS 639 bp mRNA linear EST 12-DEC-2002
 DEFINITION MCS004G12 161218 Ice Plant Lambda Uni-Zap XR expression library, 5
 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2
 AM). Mesembryanthemum crystallinum cDNA clone MCS004G12 5, mRNA
 sequence.
 ACCESSION CA835855
 VERSION CA835855.1 GI:26563620
 KEYWORDS
 SOURCE Mesembryanthemum crystallinum (common iceplant)
 ORGANISM Mesembryanthemum crystallinum

REFERENCE
 AUTHORS Cushman, J.C.
 TITLE An expressed sequence tag database for the common ice plant,
 Mesembryanthemum crystallinum
 JOURNAL Unpublished (1997)

COMMENT

Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

FEATURES

SOURCE

PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 004 row: G column: 12
Seq primer: T3 20mer
High quality sequence stop: 639.
Location/Qualifiers

1..639

/organism="Mesembryanthemum crystallinum"

/mol_type="mRNA"

/db_xref="taxon:3544"

/clone="MCS004G12"

/tissue_type="leaf"

/dev_stage="five-week-old"

/clone_lib="ice plant lambda Uni-Zap XR expression

library, 5 days 0.5 M NaCl treatment, Crassulacean acid

metabolism, phase I (2 AM)."

/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:

EcoRI; Site 2: XhoI; library construction was performed

according to Stratagene's recommended protocol for the

lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 17.0%; Score 56.6; DB 6; Length 639;
Best Local Similarity 62.4%; Pred. No. 1.1e-05;
Matches 108; Conservative 0; Mismatches 59; Indels 6; Gaps 1;

QY 25 AAACTGAGGCTTTTCTACTGTGATCCCAATGCTTTCAGAGCAGCGGATTC 84
DB 198 AGAATGAGGCAAAATTTCTGCTGATTCATACAGATGTTTCTGAAGCAGCAAGTTTC 257
QY 85 AAGTACATGAGAACCAAGTCAAGCTAATTT-----TAATAGACATTTACCTGAT 138
DB 258 AAGTATATGAGATGAGTGAACCAAGTCCGTTAGATTTGAACTCTTACCCGAC 317
QY 139 CCCAAGTAATTAATTTGAGAGAGAGTGGGCAAAATCTCTGAGCAATTC 191
DB 318 CCGAAATGCTGCTTTTGGAGACCAATGCGGGAAGATTTGCGAGGATTC 370

RESULT 5 649 bp mRNA linear EST 12-DEC-2002
CA838757 MCT020B02 167445 ice plant lambda Uni-Zap XR expression library, 5
LOCUS days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
DEFINITION (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT020B02 5,
mRNA sequence.

ACCESSION CA838757
VERSION CA838757.1 GI:26566522
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum

REFERENCE Baktayota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
TITLE Caryophyllales; Alzooaceae; Mesembryanthemum.
1 (bases 1 to 649)
Cushman, J.C.

COMMENT An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum

JOURNAL Unpublished (1997)
CONTACT: Cushman JC
DEPARTMENT OF BIOCHEMISTRY
UNIVERSITY OF NEVADA
MS200, Reno, NV 89557-0014, USA
TEL: 775-784-1918
FAX: 775-784-1650

Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 020 row: B column: 02
Seq primer: T3 20mer
High quality sequence stop: 649.
Location/Qualifiers

FEATURES

SOURCE

1..649

/organism="Mesembryanthemum crystallinum"

/mol_type="mRNA"

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/clone="MCT020B02"

/tissue_type="leaf"

/dev_stage="five-week-old"

/clone_lib="ice plant lambda Uni-Zap XR expression

library, 5 days 0.5 M NaCl treatment, Crassulacean acid

metabolism, phase IV (5:30 PM)."

/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:

EcoRI; Site 2: XhoI; library construction was performed

according to Stratagene's recommended protocol for the

lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 17.0%; Score 56.6; DB 6; Length 649;
Best Local Similarity 62.4%; Pred. No. 1.1e-05;
Matches 108; Conservative 0; Mismatches 59; Indels 6; Gaps 1;

QY 25 AAACTGAGGCTTTTCTACTGTGATCCCAATGCTTTCAGAGCAGCGGATTC 84
DB 187 AGAATGAGGCAAAATTTCTGCTGATTCATACAGATGTTTCTGAAGCAGCAAGTTTC 246
QY 85 AAGTACATGAGAACCAAGTCAAGCTAATTT-----TAATAGACATTTACCTGAT 138
DB 247 AAGTATATGAGATGAGTGAACCAAGTCCGTTAGATTTGAACTCTTACCCGAC 306
QY 139 CCCAAGTAATTAATTTGAGAGAGAGTGGGCAAAATCTCTGAGCAATTC 191
DB 307 CCGAAATGCTGCTTTTGGAGACCAATGCGGGAAGATTTGCGAGGATTC 359

RESULT 6 649 bp mRNA linear EST 12-DEC-2002
CA839330 MCT026C11 171755 ice plant lambda Uni-Zap XR expression library, 5
LOCUS days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
DEFINITION (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT026C11 5,
mRNA sequence.

ACCESSION CA839330
VERSION CA839330.1 GI:26567095
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum

REFERENCE Baktayota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
TITLE Caryophyllales; Alzooaceae; Mesembryanthemum.
1 (bases 1 to 649)
Cushman, J.C.

COMMENT An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum

JOURNAL Unpublished (1997)
CONTACT: Cushman JC
DEPARTMENT OF BIOCHEMISTRY
UNIVERSITY OF NEVADA
MS200, Reno, NV 89557-0014, USA
TEL: 775-784-1918
FAX: 775-784-1650
Email: jcushman@unr.edu

PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 026 row: C column: 11
Seq primer: T3 20mer

/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 17.0%; Score 56.6; DB 6; Length 671;
Best Local Similarity 62.4%; Pred. No. 1.1e-05;
Matches 108; Conservative 0; Mismatches 59; Indels 6; Gaps 1;

25 AAAAAGTGGCTTTTCTACTGTGATCCAAATGGTTTCAGAGCGCGGATTC 84
187 AGAATAGGCGCAAAATCTTGCTGATTCGCAATGATGTTTCGAAAGCAAGGTTTC 246
85 AAGTACATAGAGAACCAAGTCAAGCTAATTT-----TAATAGAGCATTTACCGTGAT 138
247 AAGTATATGAGATGAAGTGAACCAAGTCCGTTAGATTATGATCTTTTACCCGAC 306
Qy 139 CCCAAAGTAAATTTTGGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTC 191
Db 307 CCGAAATGCTGCTTTTGGAGACCAATGGGGGAAGATTTGCGAGGAGATTC 359

RESULT 9

LOCUS CA833333 689 bp mRNA linear EST 12-DEC-2002
DEFINITION MCS021A09 151944 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS021A09 5, mRNA sequence.

ACCESSION CA833333
VERSION CA833333.1 GI:26561098
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum

REFERENCE 1 (bases 1 to 689)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum

JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

PCR Primers
FORWARD: T7 20mer
BACKWARD: T7 21mer
Plate: 021 row: A column: 09
Seq primer: T3 20mer
High quality sequence stop: 689.

FEATURES

source

1. .689
location/Qualifiers

/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
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/clone="MCS021A09"
/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 17.0%; Score 56.6; DB 6; Length 689;
Best Local Similarity 62.4%; Pred. No. 1.1e-05;
Matches 108; Conservative 0; Mismatches 59; Indels 6; Gaps 1;

Qy 25 AAAAAGTGGCTTTTCTACTGTGATCCAAATGGTTTCAGAGCGCGGATTC 84
Db 198 AGAATAGGCGCAAAATCTTGCTGATTCGCAATGATGTTTCGAAAGCAAGGTTTC 257
Qy 85 AAGTACATAGAGAACCAAGTCAAGCTAATTT-----TAATAGAGCATTTACCGTGAT 138
Db 258 AAGTATATGAGATGAAGTGAACCAAGTCCGTTAGATTATGATCTTTTACCCGAC 317
Qy 139 CCCAAAGTAAATTTTGGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTC 191
Db 318 CCGAAATGCTGCTTTTGGAGACCAATGGGGGAAGATTTGCGAGGAGATTC 370

RESULT 10

LOCUS CA833383 689 bp mRNA linear EST 12-DEC-2002
DEFINITION MCS021F04 152044 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS021F04 5, mRNA sequence.

ACCESSION CA833383
VERSION CA833383.1 GI:26561148
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum

REFERENCE 1 (bases 1 to 689)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum

JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

PCR Primers
FORWARD: T7 20mer
BACKWARD: T7 21mer
Plate: 021 row: F column: 04
Seq primer: T3 20mer
High quality sequence stop: 689.

FEATURES

source

1. .689
location/Qualifiers

/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCS021F04"
/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 17.0%; Score 56.6; DB 6; Length 689;
Best Local Similarity 62.4%; Pred. No. 1.1e-05;
Matches 108; Conservative 0; Mismatches 59; Indels 6; Gaps 1;
Qy 25 AAAAAGTGGCTTTTCTACTGTGATCCAAATGGTTTCAGAGCGCGGATTC 84

Db 198 AGAATGAGCCAAATTTCTTGCTGATTCGATACAGATGGTTCTTGAGACGAGAGGTTTC 257

Qy 85 AAGTACATGAGAACCAAGTCAAGACTAATTT-----TATAGAGCATTTCTACCTGAT 138
|||||
Db 258 AAGTATATTGAGAGTGAAGTGAACCAAGGCGTTAGATATGATATGTTCTTACCGGAC 317

Qy 139 CCCAAGTATTAATTGAGGAGAAAGTGGGCAAAATCTCTGAGCAATTCA 191
|||||
Db 318 CCGAATAATGCTGCTTTGGAGACCATAATGGGGAGATTTCGACAGAGATTCA 370

RESULT 11
LOCUS T24255 405 bp mRNA linear EST 28-JUN-1995
DEFINITION csi1345 lambdaZAPST Ricinus communis cDNA clone pcsi1345, mRNA
sequence.
ACCESSION T24255
VERSION T24255.1 GI:689074
KEYWORDS EST.
SOURCE Ricinus communis (castor bean)
ORGANISM Ricinus communis
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Eukaryota; Magnoliophyta; eudicotyledons; core eudicotyledons;
TITLE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
JOURNAL rosids; eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae;
COMMENT Acalyphaceae; Ricinus.
1 (bases 1 to 405)
vandeloo,F.J., Turner,S. and Somerville,C.
Expressed sequence tags from developing castor seeds
Plant Physiol. 108, 1141-1150 (1995)
Contact: Somerville CR
Carnegie Institution
Carnegie Institution, 290 Panama St, Stanford, CA 94305
Tel: 4153251521
Email: crs@andrew.stanford.edu
Seq primer: T3.
Location/Qualifiers
1..405
/organism="Ricinus communis"
/mol_type="mRNA"
/strain="Baker 296"
/db_xref="taxon:3988"
/clone="pcsi1345"
/cclone_lib="lambdaZAPST"
/note="Vector: lambdaZAPIT; Site_1: EcoRI; Site_2: XhoI;
Poly(A)+ RNA was purified from developing stage III to
stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760,
1982) endosperm plus embryo of immature castor fruits.
cDNA was synthesized and cloned into lambdaZAPIT according
to the instructions of the manufacturer (Stratagene);
synthesis was primed from the poly(A) tail, and cloned
directionally into XhoI (3') and EcoRI (5') sites. In few
cases, sequence data indicated that this directionality
was reversed. Partial cDNA clones predominate."

ORIGIN
Query Match 15.7%; Score 52.4; DB 8; Length 405;
Best Local Similarity 59.2%; Fred. No. 0.00018;
Matches 125; Conservative 0; Mismatches 79; Indels 7; Gaps 2;

Db 262 ACCAAGAGCCTTGTGCTAGTCACATTCAACT 292

RESULT 12
LOCUS BE033546 1038 bp mRNA linear EST 07-JUN-2000
DEFINITION MF03A09 MF Mesembryanthemum crystallinum cDNA 5' similar to
ribosome-inactivating protein, mRNA sequence.
ACCESSION BE033546
VERSION BE033546.1 GI:8328555
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Eukaryota; Magnoliophyta; eudicotyledons; core eudicotyledons;
TITLE Caryophyllales; Aizoaceae; Mesembryanthemum.
JOURNAL 1 (bases 1 to 1038)
COMMENT Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M.,
Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
Functional genomes of plant stress tolerance
Unpublished (2000)
Contact: Michaelowski,C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cdmw@arizona.edu
An open reading frame exists.
Location/Qualifiers
1..1038
/organism="Mesembryanthemum crystallinum"
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/note="Vector: Bluescript SK+; Site_1: EcoRI; Site_2:
XhoI"

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Best Local Similarity 60.1%; Fred. No. 0.0016;
Matches 101; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

Qy 30 TGAGCCTTTTCTTACTGTGATGATCCAAATGTTTCGAGGACGGGATTCAGTA 89
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Db 391 TGAGGCCAAATCTTGCTGATGCTATACAGATGTTCTGAGACGACGCTTTAGTT 450

Qy 90 CATGAGAACCAAGTCA---AGACTAATTTTATATAGACATTTCTACCCCTGATCCAAAGT 146
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Db 451 TATTGAAGTAAAGTATGACCAAGATGATGATGCTGTTCAACCCGACCGAAAGT 510

Qy 147 AATTAAATTTGAGAGAGATGGGCAAAATCTCTGAGCAATTGACA 194
|||||
Db 511 GGTGAGTTCGGGTATCAATGAGTGAACATTTTCATGAGACTCATTA 558

RESULT 13
LOCUS BE037217 639 bp mRNA linear EST 07-JUN-2000
DEFINITION MP18B02 MP Mesembryanthemum crystallinum cDNA 5' similar to
ribosome-inactivating protein/antiviral protein, mRNA sequence.
ACCESSION BE037217
VERSION BE037217.1 GI:8332233
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Eukaryota; Magnoliophyta; eudicotyledons; core eudicotyledons;
TITLE Caryophyllales; Aizoaceae; Mesembryanthemum.
JOURNAL 1 (bases 1 to 639)
COMMENT Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M.,

Petrea, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cdm@u.arizona.edu.

FEATURES
SOURCE
1. 639
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/tissue_type="apical meristem and leaf primordia"
/dev_stage="6 weeks"
/clone_lib="MP"
/note="3 d 500mM NaCl"

ORIGIN

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DB 374 GATTAATGATGAAAGAGCTAGGCTACATTTCTTAGTGAGTCAATGTTTGT 433
QY 70 GAGGACGGGATTCAGTACATGAGAACCACT 104
DB 434 GAGGCTGACGGTCTCTACATACAGAGAGGT 468

RESULT 14
CN782289
LOCUS
DEFINITION
CN782289 829 bp mRNA linear EST 21-MAY-2004
EST00385 cgsed Chenopodium quinoa cDNA clone S02J22 5' similar to
antiviral ribosome-inactivating protein CAP30b [Chenopodium album],
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CN782289.1 GI:47561753
EST.
Chenopodium quinoa (quinoa)
Chenopodium quinoa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Chenopodium.
1 (bases 1 to 829)

REFERENCE
AUTHORS
1 Coles, N.D., Coleman, C.E., Christensen, S.A., Jellen, E.N.,
Stevens, M.R., Bonifacio, A., Rojas-Beltran, J.A., Fairbanks, D.J. and
Maughan, P.J.
Development and use of an expressed sequenced tag library in quinoa
(Chenopodium quinoa Willd.) for the discovery of single nucleotide
polymorphisms
Plant Sci. 168 (2), 439-447 (2005)
Contact: Coleman, Craig B.
Department of Plant and Animal Sciences
Brigham Young University
275 WIDB, Brigham Young University, Provo, UT 84602, USA
Tel: (801) 422-5145
Fax: (801) 422-0008
Email: craig.coleman@byu.edu
Plate: 02 row: J column: 22
Seq primer: M13 Forward
High quality sequence stop: 829.

JOURNAL
COMMENT
Location/Qualifiers
1. 829

FEATURES

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/organism="Chenopodium quinoa"
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/tissue_type="Developing Seed"
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Best Local Similarity 67.7%; Pred. No. 0.013;
Matches 65; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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DB 572 AAAAGTAAAGTGGTCTCTACTGATCGCATTAATGTTGAGAGCGCGATTC 631
QY 85 AAGTACATGAGAACCAAGTCAAGTCAATTTTAT 120
DB 632 AAGTACATGAGAACCAAGTCAAGTCAATTTTAT 667

RESULT 15

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LOCUS
DEFINITION
BE036639 1021 bp mRNA linear EST 07-JUN-2000
MP03B03 MP Mesembryanthemum crystallinum cDNA 5' similar to
ribosome-inactivating protein gelonin, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BE036639.1 GI:8331648
EST.
Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 1021)

REFERENCE
AUTHORS
1 Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
Petrea, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cdm@u.arizona.edu
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FEATURES

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Location/Qualifiers
1. 1021
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/tissue_type="apical meristem and leaf primordia"
/dev_stage="6 weeks"
/clone_lib="MP"
/note="3 d 500mM NaCl"

ORIGIN

Query Match 13.4%; Score 44.6; DB 2; Length 1021;
Best Local Similarity 58.9%; Pred. No. 0.049;
Matches 96; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

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DB 664 TGAAGCCAAATCTGCTATGCTATACAGATGTTTCAAGCGCGATTAAGTA 723
QY 90 CATAGAACCA--AGTCAAGCTAATTTATATAGCATCTACCCGATCCCAAGT 146
DB 724 TATTGAAGTAGTACCCAAAGTGTTACATGCTCTTAACCCGACCCGAAAGT 783
QY 147 AATTATTTGAGAGAGAGTGGGGCAAAATCTCTGAGGCAATT 189
DB 784 GCTGAGTTTGGGAGAACATGGGGAAAGATTTCCGAGAAATTT 826

Mon Apr 10 07:26:52 2006

us-09-978-274a-7.rst

Page 8

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Job time : 1581.51 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2006, 09:19:56 ; Search time 115.598 Seconds
(without alignments)
5120.590 Million cell updates/sec

Title: US-09-978-274A-7

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Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	233	70.0	1195	2	US-08-373-858-1
2	233	70.0	1195	2	US-08-343-786B-1
3	233	70.0	1379	2	US-08-500-611-1
4	233	70.0	1379	2	US-08-500-694-1
5	233	70.0	1379	3	US-07-865-169-1
6	233	70.0	1379	3	US-07-865-169-2
7	233	70.0	1379	3	US-07-865-169-1
8	233	70.0	1379	3	US-09-005-273-1
9	233	70.0	1379	6	PCT-US96-11546-1
10	231.4	69.5	1379	3	US-08-501-253A-1
11	221.8	66.6	918	2	US-08-138-636-1
12	221.8	66.6	918	2	US-08-319-622A-1
13	221.8	66.6	918	2	US-08-471-564-1
14	86	25.8	774	6	PCT-US91-05766-1
15	73.8	22.2	804	2	US-08-356-161-6
16	73.8	22.2	804	2	US-08-356-161-7
17	73.8	22.2	804	3	US-08-718-904-22
18	73.8	22.2	804	3	US-08-718-904-23
19	73.8	22.2	804	3	US-09-449-249-22
20	73.8	22.2	804	3	US-09-449-249-23
21	73.8	22.2	804	6	PCT-US93-05702-6
22	73.8	22.2	804	6	PCT-US93-05702-7
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26	72.6	21.8	1233	3	US-09-449-249-80	Sequence 80, Appl
27	72.4	21.7	813	2	US-07-901-707-11	Sequence 11, Appl
28	72.4	21.7	813	2	US-07-901-707-57	Sequence 57, Appl
29	72.4	21.7	813	2	US-07-988-430-11	Sequence 11, Appl
30	72.4	21.7	813	2	US-07-988-430-57	Sequence 57, Appl
31	72.4	21.7	813	2	US-08-425-336-11	Sequence 11, Appl
32	72.4	21.7	813	2	US-08-488-113B-11	Sequence 11, Appl
33	72.4	21.7	813	2	US-08-477-484B-11	Sequence 11, Appl
34	72.4	21.7	813	2	US-08-646-360-11	Sequence 11, Appl
35	72.4	21.7	813	2	US-08-621-803-246	Sequence 246, Appl
36	72.4	21.7	813	3	US-08-839-765-11	Sequence 11, Appl
37	72.4	21.7	813	3	US-09-136-389-11	Sequence 11, Appl
38	72.4	21.7	813	3	US-09-217-352-246	Sequence 246, Appl
39	72.4	21.7	813	3	US-09-610-838-11	Sequence 11, Appl
40	72.4	21.7	813	3	US-09-711-485-11	Sequence 11, Appl
41	72.4	21.7	813	6	PCT-US92-09487-11	Sequence 11, Appl
42	72.4	21.7	813	6	PCT-US92-09487-57	Sequence 57, Appl
43	72.4	21.7	955	2	US-08-621-803-258	Sequence 258, Appl
44	72.4	21.7	955	3	US-09-217-352-258	Sequence 258, Appl
45	72.4	21.7	1003	2	US-08-621-803-252	Sequence 252, Appl

ALIGNMENTS

RESULT 1
US-08-373-858-1
; Sequence 1, Application US/08373858
; Patent No. 5633155
; GENERAL INFORMATION:
; APPLICANT: Kim, Man-Keun
; APPLICANT: Lee, Kwan-Ho
; APPLICANT: Na, Byeong-Kook
; APPLICANT: Jeong, Han-Seung
; APPLICANT: Choi, Kyu-Whan
; APPLICANT: Moon, Young-Ho
; APPLICANT: Jeon, Hong-Seob
; TITLE OF INVENTION: Expression Vector for Phycolacca
; TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
; TITLE OF INVENTION: Plant Transformed Thereof.
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,858
; FILING DATE: 18-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0136/17986-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7770
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca americana
TISSUE TYPE: Leaf
US-08-373-858-1

Query Match 70.0%; Score 233; DB 2; Length 1195;
Best Local Similarity 81.8%; Pred. No. 8,8e-67;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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QY 124 GCATTCTACCTGATCCCAAGTAATTAATTGAGAGAAAGTGGGCGAAATCTCTGAG 183
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QY 184 GCAATTCAGATGCGAAGATGCGGCTTTACCCAAACCACTTGAGCTAGTATGCCAAA 243
DB 738 GCAATTCAGATGCGAAGATGCGGCTTTACCCAAACCTTGAGCTAGTATGCCAAA 797
QY 244 GGTACCAAGTGAATGTTCTTAGAGTGAATCAATCGTATGCGACTCTCTTAAAG 303
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RESULT 2
US-08-342-786B-1
Sequence 1, Application US/08342786B

PATENT NO. 5648234
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
APPLICANT: Choi, Kyu-Whan
APPLICANT: Lee, Kwan-Ho
APPLICANT: Kim, Man-Keun
TITLE OF INVENTION: A No. 5648234e1 Expression Vector for Phytolacca
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby
STREET: 805 Third Ave.
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,786B
FILING DATE: 21-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,024
FILING DATE: 01-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/08862-US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)527-7700
TELEFAX: (212)753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca americana L.
IMMEDIATE SOURCE:
CLONE: PAP

US-08-342-786B-1
Query Match 70.0%; Score 233; DB 2; Length 1195;
Best Local Similarity 81.8%; Pred. No. 8,8e-67;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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DB 558 GGAGTGTATTCATTCCTGTAATAAAGCTGAGGCTTTTCTACAGTACCAATG 617
QY 64 GTTTCAGAGGAGGCGATTCAGTACATAGAGAACCAAGTCAAGTCAATTTTAATGA 123
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QY 124 GCATTCTACCTGATCCCAAGTAATTAATTGAGAGAAAGTGGGCGAAATCTCTGAG 183
DB 678 GCATTCAACCTTAATCCAAAGTACTTAATTGCAAGACATGGGGTMAAGATTTCAACA 737
QY 184 GCAATTCAGATGCGAAGATGCGGCTTTACCCAAACCACTTGAGCTAGTATGCCAAA 243
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DB 858 TACGTTGTTGGAGCTGTGACCAACTTA 886

RESULT 3
US-08-500-611-1
Sequence 1, Application US/08500611

PATENT NO. 5756322
GENERAL INFORMATION:
APPLICANT: Turner, Nigun E.
TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,611
FILING DATE: 11-JUL-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.

REFERENCE/DOCKET NUMBER: OCIRS 3.0-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-611-1

Query Match 70.0%; Score 233; DB 2; Length 1379;
Best Local Similarity 81.8%; Pred. No. 9.4e-67;

Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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DB 930 GCAATTCATGATCCCAAGATGGGGCTTTAACCAACCACTTGAAGTGAATGCCAA 989
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DB 990 GGTACCAAGTGAATGTTCTTAGAGTGAATGAATGATGATGAGCACTCTTAAG 1049
QY 304 TACGTTAATGAACTGTGACACAATTA 332
DB 1050 TACGTTGATGAGGCTGTGACACAATTA 1078

RESULT 4
US-08-500-694-1
Sequence 1, Application US/08500694
Patent No. 5880329

GENERAL INFORMATION:
APPLICANT: Turner, Nijlun E.
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,694
FILING DATE: 11-JUL-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-694-1

Query Match 70.0%; Score 233; DB 2; Length 1379;
Best Local Similarity 81.8%; Pred. No. 9.4e-67;

Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GAGTTCATTCCTGTTAAACTGAGGCTTTTCTACTGTAGCCATCAATG 63
DB 750 GAGTTCATTCCTGTTAAACTGAGGCTTTTCTACTGTAGCCATCAATG 809
QY 64 GTTTCAGAGGAGGAGGATTCATGATGAGAGCAAGCAAGCAATTTTAAATGA 123
DB 810 GTTTCAGAGGAGGAGGATTCATGATGAGAGCAAGCAAGCAATTTTAAATGA 869
QY 124 GCAATTCACCTGATCCCAAGTAATTAATTTGAGAGAGAGTGGGCAAAATCTGAG 183
DB 870 GCAATTCACCTGATCCCAAGTAATTTGAGAGAGAGTGGGCAAAATCTGAG 929
QY 184 GCAATTCACATGCCAAGATGGGGCTTTAACCAACCACTTGAAGTGAATGCCAA 243
DB 930 GCAATTCATGATCCCAAGATGGGGCTTTAACCAACCACTTGAAGTGAATGCCAA 989
QY 244 GGTACCAAGTGAATGTTCTTAGAGTGAATGAATGATGATGAGCACTCTTAAG 303
DB 990 GGTACCAAGTGAATGTTCTTAGAGTGAATGAATGATGATGAGCACTCTTAAG 1049
QY 304 TACGTTAATGAACTGTGACACAATTA 332
DB 1050 TACGTTGATGAGGCTGTGACACAATTA 1078

RESULT 5
US-07-865-169-1
Sequence 1, Application US/07865169
Patent No. 6015940

GENERAL INFORMATION:
APPLICANT: Turner, Nijlun E.
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

ADDRESS: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
 STREET: 700 Chesterfield Parkway No. 6015940th
 CITY: St. Louis
 STATE: Missouri
 COUNTRY: USA
 ZIP: 63198
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/865,169
 FILING DATE: 19920407
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Hoerner Jr., Dennis R.
 REGISTRATION NUMBER: 30,914
 REFERENCE/DOCKET NUMBER: 38-21(10547)A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314)537-6099
 TELEFAX: (314)537-6047
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1379 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-07-865-169-1

Query Match 70.0%; Score 233; DB 3; Length 1379;
 Best Local Similarity 81.8%; Pred. No. 9,4e-67;
 Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

4 GGAGTTGATTCATTCCTGTAATAAAGCTGAGCTTTTCTACTGTCGATCCATCCAAATG 63
 750 GGAGGATGTCATTCCTGTAATAAAGCTGAGCTTTTCTACTGTCGATCCATCCAAATG 809
 64 GTTTCAGAGGAGCGGATTCAGTACATAGAGAACCAAGCTAACTAATTTAATAGA 123
 810 GTATCAGAGGAGCGGATTCAGTACATAGAGAACCAAGCTAACTAATTTAATAGA 869
 124 GCAATTCACCAATGCTGATCCCAAGTAAATTTGAGAGAGAGAGGAGGCAAAATCTCTGAG 183
 870 GCAATTCACCAATGCTGATCCCAAGTAAATTTGAGAGAGAGAGGAGGCAAAATCTCTGAG 929
 184 GCAATTCACCAATGCTGATCCCAAGTAAATTTGAGAGAGAGAGGAGGCAAAATCTCTGAG 243
 930 GCAATTCACCAATGCTGATCCCAAGTAAATTTGAGAGAGAGAGGAGGCAAAATCTCTGAG 989
 244 GGTACCAAGTGAATGATGTTCTTAAAGTGAATGAATCAATGATGTCGATGCTTAAAG 303
 990 GGTGCGCAAGTGAATGATGTTCTTAAAGTGAATGAATCAATGATGTCGATGCTTAAAG 1049
 304 TACGTTAATGGAACCTGTCAGACACTTA 332
 1050 TACGTTGATGAGAGCTGTCAGACACTTA 1078

RESULT 6
 US-07-865-169-2
 Sequence 2, Application US/07865169
 Patent No. 6015940
 GENERAL INFORMATION:
 APPLICANT: Turner, Nilgun E.
 APPLICANT: Lodge, Jennifer K.
 APPLICANT: Kaniewski, Wojciech K.
 TITLE OF INVENTION: Virus Resistant Potato Plants
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
 STREET: 700 Chesterfield Parkway No. 6015940th

CITY: St. Louis
 STATE: Missouri
 COUNTRY: USA
 ZIP: 63198
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/865,169
 FILING DATE: 19920407
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Hoerner Jr., Dennis R.
 REGISTRATION NUMBER: 30,914
 REFERENCE/DOCKET NUMBER: 38-21(10547)A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314)537-6099
 TELEFAX: (314)537-6047
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1379 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-07-865-169-2

Query Match 70.0%; Score 233; DB 3; Length 1379;
 Best Local Similarity 81.8%; Pred. No. 9,4e-67;
 Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

4 GGAGTTGATTCATTCCTGTAATAAAGCTGAGGCTTTTCTACTGTCGATCCATCCAAATG 63
 750 GGAGGATGTCATTCCTGTAATAAAGCTGAGGCTTTTCTACTGTCGATCCATCCAAATG 809
 64 GTTTCAGAGGAGCGGATTCAGTACATAGAGAACCAAGCTAACTAATTTAATAGA 123
 810 GTATCAGAGGAGCGGATTCAGTACATAGAGAACCAAGCTAACTAATTTAATAGA 869
 124 GCAATTCACCAATGCTGATCCCAAGTAAATTTGAGAGAGAGAGGAGGCAAAATCTCTGAG 183
 870 GCAATTCACCAATGCTGATCCCAAGTAAATTTGAGAGAGAGAGGAGGCAAAATCTCTGAG 929
 184 GCAATTCACCAATGCTGATCCCAAGTAAATTTGAGAGAGAGAGGAGGCAAAATCTCTGAG 243
 930 GCAATTCACCAATGCTGATCCCAAGTAAATTTGAGAGAGAGAGGAGGCAAAATCTCTGAG 989
 244 GGTACCAAGTGAATGATGTTCTTAAAGTGAATGAATCAATGATGTCGATGCTTAAAG 303
 990 GGTGCGCAAGTGAATGATGTTCTTAAAGTGAATGAATCAATGATGTCGATGCTTAAAG 1049
 304 TACGTTAATGGAACCTGTCAGACACTTA 332
 1050 TACGTTGATGAGAGCTGTCAGACACTTA 1078

RESULT 7
 US-09-005-273-1
 Sequence 1, Application US/09005273
 Patent No. 6137030
 GENERAL INFORMATION:
 APPLICANT: Turner, Nilgun E.
 TITLE OF INVENTION: PRC MUTANTS THAT EXHIBIT ANTI-VIRAL
 AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LEHNER, DAVID, LITTEMBERG, KRUMHOLTZ &
 STREET: 600 South, Avenue West
 CITY: Westfield
 STATE: New Jersey

```

COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,273
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/500,611
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE: 11-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 225..290
US-09-005-273-1

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Query Match 70.0%; Score 233; DB 3; Length 1379;
Best Local Similarity 81.8%; Pred. No. 9.4e-67;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTGAATTCATCCCTGTAAGAACTGAGGCTTTTCTACTGTGAGCCATCCAAATG 63
DB 750 GGAGTGAATTCATCCCTGTAAGAACTGAGGCTTTTCTACTGTGAGCCATCCAAATG 809
QY 64 GTTTCAGAGCAGCGGATTCAGATGATAGAAACCAAGTCAAGCTAATTTTAATGA 123
DB 810 GTTTCAGAGCAGCGGATTCAGATGATAGAAACCAAGTCAAGCTAATTTTAATGA 869
QY 124 GCATTCACCTGATCCCAAGTAATTATTGGAGAGAAAGTGGGCAAAATCTCTAG 183
DB 870 GCATTCACCTGATCCCAAGTAATTATTGGAGAGAAAGTGGGCAAAATCTCTAG 929
QY 184 GCAATTCACCAATGCCAAGATGGGGCTTTACCCCAACCACTTGAAGTATGCCAAA 243
DB 930 GCAATTCACCAATGCCAAGATGGGGCTTTACCCCAACCACTTGAAGTATGCCAAA 989
QY 244 GGTACCAAGTGAATGTTCTTAGAGTGAATCAATGATGATGAGGACTCCCTTAAG 303
DB 990 GGTACCAAGTGAATGTTCTTAGAGTGAATCAATGATGATGAGGACTCCCTTAAG 1049
QY 304 TACGTTAATGAACCTCTCAGACAACTTA 332
DB 1050 TACGTTAATGAACCTCTCAGACAACTTA 1078

```

RESULT 8
US-09-005-273-3

```

; Sequence 3, Application US/09005273
; Patent No. 6137030
; GENERAL INFORMATION:
; APPLICANT: Tumer, Nilgun E.
; TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
; TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: LERNER, DAVID, LITTEMBERG, KRUMHOLZ &
; ADDRESS: MENTILIK
; STREET: 600 South, Avenue West
; CITY: Westfield
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,273
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/500,611
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE: 11-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 225..290
US-09-005-273-3

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Query Match 70.0%; Score 233; DB 3; Length 1379;
Best Local Similarity 81.8%; Pred. No. 9.4e-67;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTGAATTCATCCCTGTAAGAACTGAGGCTTTTCTACTGTGAGCCATCCAAATG 63
DB 750 GGAGTGAATTCATCCCTGTAAGAACTGAGGCTTTTCTACTGTGAGCCATCCAAATG 809
QY 64 GTTTCAGAGCAGCGGATTCAGATGATAGAAACCAAGTCAAGCTAATTTTAATGA 123
DB 810 GTTTCAGAGCAGCGGATTCAGATGATAGAAACCAAGTCAAGCTAATTTTAATGA 869
QY 124 GCATTCACCTGATCCCAAGTAATTATTGGAGAGAAAGTGGGCAAAATCTCTAG 183
DB 870 GCATTCACCTGATCCCAAGTAATTATTGGAGAGAAAGTGGGCAAAATCTCTAG 929
QY 184 GCAATTCACCAATGCCAAGATGGGGCTTTACCCCAACCACTTGAAGTATGCCAAA 243

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Mon Apr 10 07:26:52 2006

us-09-978-274a-7.rnt

Db 930 GCAATTCATGATGCCAAGATGAGATTTTACCBAACCTCTGAGCTAGTGGATGCCAGT 989
Qy 244 GGTACCAAGTGAATGTTCTTGAAGTGAATGAATCATCGTGAATGGCACTCCCTTAAG 303
Db 990 GGTGCCAAGTGAATGTTCTTGAAGTGAATGAATCATCGTGAATGGCACTCCCTTAAG 1049
Qy 304 TACGTTAATGAACTCTGTCAGACACTTA 332
Db 1050 TACGTTGTTGGAGCTGTCTGACACACTTA 1078

RESULT 9
PCT-US96-11546-1
Sequence 1, Application PC/TUS9611546
GENERAL INFORMATION:
APPLICANT: Turner, Nilgun E.
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein
TITLE OF INVENTION: Mutants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littleberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
PCT-US96-11546-1

Query Match 70.0%; Score 233; DB 6; Length 1379;
Best Local Similarity 81.8%; Pred. No. 9.4e-67;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 4 GGAGTTGATTCATTCCTCTGTAATAACTGAGGCTTTTCTTACTGTAAGCAATCAATG 63
Db 750 GGAGTATGTCATTCATCACTGAGAAACCGAATTCCTATGTGTAGCCATACAAATG 809

Qy 64 GTTTCAGAGCGCGCATTCAGTACATAGAGAACCAAGTCACTAATTTTATAGA 123
Db 810 GTATCAGAGCGCGCATTCAGTACATAGAGAACCAAGTCACTAATTTTATAGA 869
Qy 124 GCATTCATCCTGATCCCAAGTATTAATTTGGAGAGAAATGGGCAAAATCTGTAG 183
Db 870 GCATTCATCCTGATCCCAAGTATTAATTTGGAGAGAAATGGGCAAAATCTGTAG 929
Qy 184 GCAATTCATGATGCCAAGATGAGATTTTACCBAACCTCTGAGCTAGTGGATGCCAGT 243
Db 930 GCAATTCATGATGCCAAGATGAGATTTTACCBAACCTCTGAGCTAGTGGATGCCAGT 989
Qy 244 GGTACCAAGTGAATGTTCTTGAAGTGAATGAATCATCGTGAATGGCACTCCCTTAAG 303
Db 990 GGTGCCAAGTGAATGTTCTTGAAGTGAATGAATCATCGTGAATGGCACTCCCTTAAG 1049
Qy 304 TACGTTAATGAACTCTGTCAGACACTTA 332
Db 1050 TACGTTGTTGGAGCTGTCTGACACACTTA 1078

RESULT 10
US-08-501-253A-1
Sequence 1, Application US/08501253A
Patent No. 6146628
GENERAL INFORMATION:
APPLICANT: Uckun, Fatih
TITLE OF INVENTION: Biotherapeutic Agents Comprising
TITLE OF INVENTION: Recombinant PAP and PAP Mutants
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 6146628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: US
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,253A
FILING DATE: 11-JUL-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kettlerberger, Denise M.
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 600.323US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
US-08-501-253A-1

Query Match 69.5%; Score 231.4; DB 3; Length 1379;
Best Local Similarity 81.5%; Pred. No. 3.2e-66;
Matches 268; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 4 GGAGTTGATTCATTCCTCTGTAATAACTGAGGCTTTTCTTACTGTAAGCAATCAATG 63
Db 750 GGAGTATGTCATTCATCACTGAGAAACCGAATTCCTATGTGTAGCCATACAAATG 809

QY 64 GTTTCAGAGCGACCGGATTCAAGTACATAGAGAACCAAGTCAGACTAATTTTATAGA 123
DB 810 GTATCAGAGCGACGAGATTCAGTACATAGAGAAATCAAGTGAATCTAATTTTAAACA 869
QY 124 GAATTCACCCGATGCCAAGTAATTAATTTGAGAGAAAGTGGGCAAAATCTGTGAG 183
DB 870 GCATTCACCCCTTAATCCCAAGTACTAATTTTGCAGAGAACATGGGGTAAGATTTCAACA 929
QY 184 GCAATTCACCAATGCCAAGAAATGGGGCTTTACCCAAACCACTTGAGCTAGTGAATGCCAA 243
DB 930 GCAATTCATGATGCCAAGATGAGATTTTACCCAAACCTCTGAGCTAGTGAATGCCAAT 989
QY 244 GTTACCAAGTGATAGTCTTGAAGTGAGTAATCAATCGATGTGCACTCCTTAAG 303
DB 990 GGTGCAAGTGATAGTGTGAGAGTGATGAATCAAGCTGATGTGCACTCTTAAC 1049
QY 304 TACGTTAATGGAACCTGTCAACAACCTTA 332
DB 1050 TACGTTGATGGAGCTGTCAACAACCTTA 1078

RESULT 11

US-08-138-636-1
Sequence 1, Application US/08138636

GENERAL INFORMATION:
PATENT NO. 5348865
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seoh
APPLICANT: Choi, Kyu-Whan
APPLICANT: Lee, Kwan Ho
APPLICANT: Kim, Man Keun
TITLE OF INVENTION: No. 5348865e1 Genome Coding PhytoIacca Antiviral
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: DARBY & DARBY
STREET: 805 THIRD AVE.
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,636
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/08818
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: PhytoIacca Insularis
IMMEDIATE SOURCE:
CLONE: antiviral protein (PIP)
US-08-138-636-1

Query Match 66.6%; Score 221.8; DB 2; Length 918;
Best Local Similarity 79.6%; Pred. No. 3,9e-63;
Matches 262; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 4 GAGATGATTCATTCCTCTGTAAATACTGAGCTTTTCTTACTGTAGCCATCCAAATG 63
DB 517 GAGATGAGTGTATTCATCTAGAGAAACGAGCTGAATTCCTACTGTAGCCATCCAAATG 576
QY 64 GTTTCAGAGCGACCGGATTCAAGTACATAGAGAACCAAGTCAGACTAATTTTATAGA 123
DB 577 GTATCAGAGCGACGAGATTCAGTACATAGAGAAATCAAGTGAATCTAATTTTAAACA 636
QY 124 GCATTCACCCGATGCCAAGTAATTAATTTGAGAGAAAGTGGGCAAAATCTGTGAG 183
DB 637 GCATTCACCCCTTAATCCCAAGTACTAATTTTGCAGAGAACATGGGGTAAGATTTCAACA 696
QY 184 GCAATTCACCAATGCCAAGAAATGGGGCTTTACCCAAACCACTTGAGCTAGTGAATGCCAA 243
DB 697 GCAATTCATGATGCCAAGATGAGATTTTACCCAAACCTCTGAGCTAGTGAATGCCAAT 756
QY 244 GTTACCAAGTGATAGTCTTGAAGTGAGTAATCAATCGATGTGCACTCCTTAAG 303
DB 757 GGTGCAAGTGATAGTGTGAGAGTGATGAATCAAGCTGATGTGCACTCTTAAC 816
QY 304 TACGTTAATGGAACCTGTCAACAACCTTA 332
DB 817 TACGTTGATGGAGCTGTCAACAACCTTA 845

RESULT 12

US-08-319-622A-1
Sequence 1, Application US/08319622A

PATENT NO. 5656466

GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Choi, Kyu-Whan
APPLICANT: Jeon, Hong-Seoh
APPLICANT: Kim, Chul-Hwan
APPLICANT: Kim, Man Keun
TITLE OF INVENTION: Process for Preparing Virus-Resistant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,622A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/04445
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca insularis Nakai
TISSUE TYPE: leaf
IMMEDIATE SOURCE:
CLONE: PIP
US-08-319-622a-1

Query Match 66.6%; Score 221.8; DB 2; Length 918;
Best Local Similarity 79.6%; Pred. No. 3.9e-63;
Matches 262; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTAATAAAGTGAAGGCTTTTCTTCTACTGTAGCCATCCAAATG 63
DB 517 GGAGTGACGTCAATCACTGAGAGAACCGAAGCTGAATTCCTACTGTAGCCATCAAAATG 576
QY 64 GTTTCAGAGGCGCGCATTCAGTACATAGAGAACCAAGTCAGACTTAATTTTAATGA 123
DB 577 GTATCAGAGGCGAGCAAGTTCAAGTACATAGAGATCAAGTGAAGAACTAATTTTAACGA 636
QY 124 GCATTTCACCTGATCCCAAGTAATTAATTTGGAGAGAGAGGCGCAAAATCTGTAG 183
DB 637 CCATTCAACCTTAATCCCAAGTACTTAATTTGCGAGACATGGGGTAAATTTCTTCA 696
QY 184 GCAATTCACATGCGCAAGATGGGGCTTTACCCCAACCACTTGAGCTAGTGAGTCCAAA 243
DB 697 GCAATTCATGGTCCAGAGATGAGTTTACCCCAATCCCTACAGCTAGTGATGCCAAT 756
QY 244 GTTTCAGAGGCGCGCATTCAGTACATAGAGAACCAAGTCAGACTTAATTTTAATGA 123
DB 757 GTATCAGAGGCGAGCAAGTTCAAGTACATAGAGATCAAGTGAAGAACTAATTTTAACGA 636
QY 304 TACGTTAATGGAACCTGTCAAGCACTTA 332
DB 817 TACGTTAATGGGAGCTGCCAGAACCTTA 845

RESULT 13
US-08-471-564-1
Sequence 1, Application US/08471564
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seoh
APPLICANT: Choi, Kyu-Whan
APPLICANT: Kim, Kwan Ho
APPLICANT: Kim, Man Keun
TITLE OF INVENTION: No. 5723326e1 Genome Coding Phytolacca Antiviral
TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 THIRD AVE.
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471.564
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/210,396
FILING DATE:
APPLICATION NUMBER: US 08/138,636
FILING DATE: 15-OCT-1993

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/18818US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca insularis
IMMEDIATE SOURCE:
CLONE: antiviral protein (PIP)
US-08-471-564-1

Query Match 66.6%; Score 221.8; DB 2; Length 918;
Best Local Similarity 79.6%; Pred. No. 3.9e-63;
Matches 262; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTAATAAAGTGAAGGCTTTTCTTCTACTGTAGCCATCCAAATG 63
DB 517 GGAGTGACGTCAATCACTGAGAGAACCGAAGCTGAATTCCTACTGTAGCCATCAAAATG 576
QY 64 GTTTCAGAGGCGCGCATTCAGTACATAGAGAACCAAGTCAGACTTAATTTTAATGA 123
DB 577 GTATCAGAGGCGAGCAAGTTCAAGTACATAGAGATCAAGTGAAGAACTAATTTTAACGA 636
QY 124 GCATTTCACCTGATCCCAAGTAATTAATTTGGAGAGAGAGGCGCAAAATCTGTAG 183
DB 637 CCATTCAACCTTAATCCCAAGTACTTAATTTGCGAGACATGGGGTAAATTTCTTCA 696
QY 184 GCAATTCACATGCGCAAGATGGGGCTTTACCCCAACCACTTGAGCTAGTGAGTCCAAA 243
DB 697 GCAATTCATGGTCCAGAGATGAGTTTACCCCAATCCCTACAGCTAGTGATGCCAAT 756
QY 244 GTTTCAGAGGCGCGCATTCAGTACATAGAGAACCAAGTCAGACTTAATTTTAATGA 123
DB 757 GTATCAGAGGCGAGCAAGTTCAAGTACATAGAGATCAAGTGAAGAACTAATTTTAACGA 636
QY 304 TACGTTAATGGAACCTGTCAAGCACTTA 332
DB 817 TACGTTAATGGGAGCTGCCAGAACCTTA 845

RESULT 14
PCT-US91-05766-1
Sequence 1, Application PC/TUS9105766
GENERAL INFORMATION:
APPLICANT: Rosenblum, Michael
APPLICANT: Kohr, William Jack
APPLICANT: Aggarwal, Bharat
TITLE OF INVENTION: Protein Structure of the Plant Toxin
TITLE OF INVENTION: Geloinin
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski Patent Department
STREET: 1301 McKinney #5100
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05766
FILING DATE: 19910814
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/567,220
FILING DATE: 14-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: launer, Charlene A.
REGISTRATION NUMBER: 33,035
REFERENCE/DOCKET NUMBER: D-5195 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 651-3634
TELEFAX: (713) 651-5246
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: YES
ORIGINAL SOURCE:
ORGANISM: Gelonium multiformum
DEVELOPMENTAL STAGE: Seed
TISSUE TYPE: Nut
FEATURE:
NAME/KEY: CDS
LOCATION: 1..774
PCT-US91-05766-1

Query Match 25.8%; Score 86; DB:6; Length 774;
Best Local Similarity 40.4%; Pred. No. 3.1e-18;
Matches 114; Conservative 49; Mismatches 116; Indels 3; Gaps 1;

QY 34 GCTTTTCTACTAGTCCATCCAAATGTTTTCAGAGCGGCGGATTCAGTACATA 93
DB 481 GGNWSMSWYTYTNTGNTGNATHCARATGNTWSGAGCGCGNCGNTTYATHT 540
QY 94 GAGAACCAAGTCAAGCTAATTTTATAGAGCATTTACCTGTATCCCAAGTAATTAAT 153
DB 541 GARAAYCARATMGNAAAYATTYCARCARMGNATMGNCCGNAAYAAVCMATHMSN 600
QY 154 TTGAGAGGAGAGTGGGGCAAAATCTCTGAGCAATTCACAAAATGCGGCT 210
DB 601 YTNGBAAATATGAGGAGAAATYTNMSNTTYCARATMGNACWNSGNCNAAYGAGATG 660
QY 211 TTACCAACCACTGAGCTAGTATGATGCAAGGATACCAAGTATGATTTCTTAGAGTG 270
DB 661 TTYWNGARAGCNGTNGARTYTNARAGNGCNAAYGNAAPAAATATATATGATNACNGCNGTN 720
QY 271 GATGAATCATCGTGTATGAGTGGCACTCTTAAATGATGTAAT 312
DB 721 GAYCARGTAAACCAABATGTCNTYTNATATYTGNGAY 762

RESULT 15
US-08-356-161-6
Sequence 6, Application US/08356161
Patent No. 5916772
GENERAL INFORMATION:
APPLICANT: Lapol, Douglas A.
APPLICANT: Barthelemy, Isabel
APPLICANT: Baird, J. Andrew
APPLICANT: Sosnowski, Barbara A.
TITLE OF INVENTION: RECOMBINANT PRODUCTION OF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: SEED and BERRY LLP
STREET: 701 Fifth Avenue, 6300 Columbia Center

CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,161
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,161
FILING DATE: 13-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: No. 5916772enhurg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.404US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..804
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..804
OTHER INFORMATION: /note="Nucleotide sequence
corresponding to the clone m13 mp18-G7 in Example 1.B.2."
FEATURE:
NAME/KEY: mat peptide
LOCATION: 46..804
OTHER INFORMATION: /product="Saporin"
US-08-356-161-6

Query Match 22.2%; Score 73.8; DB 2; Length 804;
Best Local Similarity 58.5%; Pred. No. 3.4e-14;
Matches 148; Conservative 0; Mismatches 102; Indels 3; Gaps 1;

QY 22 GTAAAACTGAGGCTTTTCTACTGATGATCCAAATGTTTTCAGAGCGGCGGA 81
DB 523 GTTAAAAAGAACTGATGATTCCTTATCGCTATTCAGATGAGCGCTGAGGCAACACA 582
QY 82 TTCAAGTACATAGAGAACTGATGATTTTATAGAGCATTTTACCTGATGCC 141
DB 583 TTAGGTACATACAAACTTGGTATCAAGAACTTCCCAACAACTGATCGGAAAC 642
QY 142 AAAGTAATTAATTTGAGAGAGAGTGGGGCAAAATCTCTGAGCAATTCAC---AATGCC 198
DB 643 AAAGTATTCAGTTGAGGTTTACCTGGAATAATTTCTACGCAATATACGGGGATGCC 702
QY 199 AAGATGGGGCTTTTACCAACCACTGATGATGATGCAAGGATACCAAGTATGATA 258
DB 703 AAAACGGCGGTGTTTAAATGAATTAATGATTCGGGTTTGAAAAAGTGAAGCAGGTAG 762
QY 259 GTCTTAGAGTG 271
DB 763 GACTTGCAATGG 775

Search completed: April 8, 2006, 09:48:55
Job time : 116.598 secs

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:31:27 ; Search time 384.756 Seconds
(without alignments)
7157.007 Million cell updates/sec

Title: US-09-978-274A-7

Perfect score: 333
Sequence: 1 atggagagtgatcattcc.....gaacctgcagacacttca 333

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA_Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	333	100.0	333	3	US-09-978-274A-7
2	329	98.8	945	3	US-09-978-274A-1
3	328.4	98.6	792	3	US-09-978-274A-3
4	302.4	90.8	1092	3	US-09-978-274A-19
5	233	70.0	1368	3	US-09-978-274A-31
6	233	70.0	1376	8	US-10-467-009-1
7	233	70.0	1379	3	US-09-978-274A-30
8	233	70.0	1379	10	US-11-106-187-1
9	78.8	23.7	2404	10	US-11-084-080-15
10	78.8	23.7	2404	10	US-11-084-080-19
11	78.8	23.7	2404	10	US-11-084-080-21
12	78.8	23.7	2404	10	US-11-084-080-23
13	78.8	23.7	2431	10	US-11-084-080-27
14	75.4	22.6	935	9	US-10-919-750-4
15	73.8	22.2	804	3	US-09-861-257-37
16	73.8	22.2	804	3	US-09-861-257-38
17	73.8	22.2	804	6	US-10-189-360-22
18	73.8	22.2	804	6	US-10-189-360-23
19	72.6	21.8	1233	3	US-09-861-257-24
20	72.6	21.8	1233	6	US-10-189-360-80
21	72.4	21.7	813	3	US-09-765-527-246
22	72.4	21.7	813	6	US-10-127-890-11
23	72.4	21.7	813	9	US-10-717-243-11

24	72.4	21.7	955	3	US-09-765-527-258	Sequence 258, App
25	72.4	21.7	1003	3	US-09-765-527-252	Sequence 252, App
26	72.4	21.7	1072	3	US-09-765-527-250	Sequence 250, App
27	72.4	21.7	1176	6	US-10-074-596-2	Sequence 2, App1
28	72.4	21.7	1500	9	US-10-964-195-12	Sequence 12, App1
29	72.4	21.7	1527	6	US-10-074-596-10	Sequence 10, App1
30	72.4	21.7	2407	10	US-11-084-080-25	Sequence 25, App1
31	70.6	21.2	855	10	US-11-06-187-20	Sequence 20, App1
32	70.6	21.2	934	3	US-09-978-274A-32	Sequence 32, App1
33	70.6	21.2	934	10	US-11-106-187-3	Sequence 3, App1
34	69	20.7	804	3	US-09-861-257-22	Sequence 22, App1
35	69	20.7	804	3	US-09-861-257-36	Sequence 36, App1
36	69	20.7	804	6	US-10-189-360-19	Sequence 19, App1
37	69	20.7	804	6	US-10-189-360-21	Sequence 21, App1
38	69	20.7	1230	6	US-10-189-360-53	Sequence 53, App1
39	69	20.7	1251	3	US-09-861-257-77	Sequence 77, App1
40	69	20.7	1251	6	US-10-189-360-74	Sequence 74, App1
41	69	20.7	1260	3	US-09-861-257-75	Sequence 75, App1
42	69	20.7	1260	6	US-10-189-360-72	Sequence 72, App1
43	69	20.7	1266	3	US-09-861-257-78	Sequence 78, App1
44	69	20.7	1266	6	US-10-189-360-75	Sequence 75, App1
45	69	20.7	1269	3	US-09-861-257-81	Sequence 81, App1

ALIGNMENTS

RESULT 1
US-09-978-274A-7
Sequence 7, Application US/0978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978, 274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225-4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 333
TYPE: DNA
ORGANISM: *Phytolacca americana*
US-09-978-274A-7

Query Match	100.0%;	Score 333;	DB 3;	Length 333;
Best Local Similarity	100.0%;	Pred. No. 4.6e-94;		
Matches 333;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGGAGTTGATTCATTCCTGTAATAAAGTGAAGCTTTTCTACTGTGACATCA	60	
DB	1	ATGGAGTTGATTCATTCCTGTAATAAAGTGAAGCTTTTCTACTGTGACATCA	60	
QY	61	ATGGAGTTGATTCATTCCTGTAATAAAGTGAAGCTTTTCTACTGTGACATCA	120	
DB	61	ATGGAGTTGATTCATTCCTGTAATAAAGTGAAGCTTTTCTACTGTGACATCA	120	
QY	121	AGAGCAATTCACCTGATCCCAAGTAATTAATTTGAGAGAGAGGCAAAATCTCT	180	
DB	121	AGAGCAATTCACCTGATCCCAAGTAATTAATTTGAGAGAGAGGCAAAATCTCT	180	
QY	181	GAGGCAATTCACCAATGCAAGAAATGGGGCTTAAACCAACCTTGAAGTATGATGCC	240	
DB	181	GAGGCAATTCACCAATGCAAGAAATGGGGCTTAAACCAACCTTGAAGTATGATGCC	240	
QY	241	AAAGTACCAAGTATGATTTCTTGAAGTATGATGAAATCATGATGATGCACTCTT	300	
DB	241	AAAGTACCAAGTATGATTTCTTGAAGTATGATGAAATCATGATGATGCACTCTT	300	

QY 301 AAGTACGTTAATGGAACCTGTGACAACTTAA 333
 Db 301 AAGTACGTTAATGGAACCTGTGACAACTTAA 333

RESULT 2
 US-09-978-274A-1
 ; Sequence 1, Application US/09978274A
 ; Patent No. US20020116737A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Christopher
 ; APPLICANT: McPherson, Michael
 ; APPLICANT: Atkinson, Howard
 ; APPLICANT: Neelam, Anil
 ; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
 ; FILE REFERENCE: 9341-028
 ; CURRENT APPLICATION NUMBER: US/09/978,274A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 0025225.4
 ; PRIOR FILING DATE: 2000-10-14
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 945
 ; TYPE: DNA
 ; ORGANISM: Phytiolacca americana
 ; US-09-978-274A-1

Query Match 98.8%; Score 329; DB 3; Length 945;
 Best Local Similarity 100.0%; Pred. No. 1.3e-92;
 Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTCTGTAAAACTGAGGCTTTTCTTCTGTCGTCATCCCAATG 63
 Db 532 GGAGTTGATTCATTCCTCTGTAAAACTGAGGCTTTTCTTCTGTCGTCATCCCAATG 591
 QY 64 GTTTCAGAGGACGCGGATTCAGTACATAGAGAAACCAAGTCAAGTAAATTTAATAGA 123
 Db 592 GTTTCAGAGGACGCGGATTCAGTACATAGAGAAACCAAGTCAAGTAAATTTAATAGA 651
 QY 124 GCATTTACCTGATCCCAAGTAAATTTGAGAGAGAGTGGGCAAAATCTCTGAG 183
 Db 652 GCATTTACCTGATCCCAAGTAAATTTGAGAGAGAGTGGGCAAAATCTCTGAG 711
 QY 184 GCAATTCACAATGCCAAGATGGGCTTTAACCACCACTTGAGCTAGTGAATGCCAAA 243
 Db 712 GCAATTCACAATGCCAAGATGGGCTTTAACCACCACTTGAGCTAGTGAATGCCAAA 771
 QY 244 GGTAACAAGTGAATGTTCTTAAGTGAATGAATCAATGATGATGCACTCTCTTAA 303
 Db 772 GGTAACAAGTGAATGTTCTTAAGTGAATGAATCAATGATGATGCACTCTCTTAA 831
 QY 304 TACGTTAATGGAACCTGTGACAACTTAA 332
 Db 832 TACGTTAATGGAACCTGTGACAACTTAA 860

RESULT 3
 US-09-978-274A-3
 ; Sequence 3, Application US/09978274A
 ; Patent No. US20020116737A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Christopher
 ; APPLICANT: McPherson, Michael
 ; APPLICANT: Atkinson, Howard
 ; APPLICANT: Neelam, Anil
 ; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
 ; FILE REFERENCE: 9341-028
 ; CURRENT APPLICATION NUMBER: US/09/978,274A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 0025225.4
 ; PRIOR FILING DATE: 2000-10-14

NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 792
 ; TYPE: DNA
 ; ORGANISM: Phytiolacca americana
 ; US-09-978-274A-3

Query Match 98.6%; Score 328.4; DB 3; Length 792;
 Best Local Similarity 99.7%; Pred. No. 1.9e-92;
 Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTCTGTAAAACTGAGGCTTTTCTTCTGTCGTCATCCCAATG 63
 Db 463 GGAGTTGATTCATTCCTCTGTAAAACTGAGGCTTTTCTTCTGTCGTCATCCCAATG 522
 QY 64 GTTTCAGAGGACGCGGATTCAGTACATAGAGAAACCAAGTCAAGTAAATTTAATAGA 123
 Db 523 GTTTCAGAGGACGCGGATTCAGTACATAGAGAAACCAAGTCAAGTAAATTTAATAGA 582
 QY 124 GCATTTACCTGATCCCAAGTAAATTTGAGAGAGAGTGGGCAAAATCTCTGAG 183
 Db 583 GCATTTACCTGATCCCAAGTAAATTTGAGAGAGAGTGGGCAAAATCTCTGAG 642
 QY 184 GCAATTCACAATGCCAAGATGGGCTTTAACCACCACTTGAGCTAGTGAATGCCAAA 243
 Db 643 GCAATTCACAATGCCAAGATGGGCTTTAACCACCACTTGAGCTAGTGAATGCCAAA 702
 QY 244 GGTAACAAGTGAATGTTCTTAAGTGAATGAATCAATGATGATGCACTCTCTTAA 303
 Db 703 GGTAACAAGTGAATGTTCTTAAGTGAATGAATCAATGATGATGCACTCTCTTAA 762
 QY 304 TACGTTAATGGAACCTGTGACAACTTAA 333
 Db 763 TACGTTAATGGAACCTGTGACAACTTAA 792

RESULT 4
 US-09-978-274A-19
 ; Sequence 19, Application US/09978274A
 ; Patent No. US20020116737A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Christopher
 ; APPLICANT: McPherson, Michael
 ; APPLICANT: Atkinson, Howard
 ; APPLICANT: Neelam, Anil
 ; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
 ; FILE REFERENCE: 9341-028
 ; CURRENT APPLICATION NUMBER: US/09/978,274A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 0025225.4
 ; PRIOR FILING DATE: 2000-10-14
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 19
 ; LENGTH: 1092
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: PAP-S/Cystatin fusion
 ; US-09-978-274A-19

Query Match 90.8%; Score 302.4; DB 3; Length 1092;
 Best Local Similarity 99.7%; Pred. No. 3.3e-84;
 Matches 303; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTCTGTAAAACTGAGGCTTTTCTTCTGTCGTCATCCCAATG 63
 Db 463 GGAGTTGATTCATTCCTCTGTAAAACTGAGGCTTTTCTTCTGTCGTCATCCCAATG 522
 QY 64 GTTTCAGAGGACGCGGATTCAGTACATAGAGAAACCAAGTCAAGTAAATTTAATAGA 123
 Db 523 GTTTCAGAGGACGCGGATTCAGTACATAGAGAAACCAAGTCAAGTAAATTTAATAGA 582

RESULT 6
US-10-467-009-1
; Sequence 1, Application US/10467009

Query Match 70.0%; Score 233; DB 3; Length 1379

Best Local Similarity 81.8%; Pred. No. 2.5e-62;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTAAGAACTGAGGCTTTTCTTCTAGCTAGCCATCCAAATG 63
DB 750 GGAGTATGTCATTCATCTGAGAAACCGAATTCCTATTTGGTAGCATATCAATG 809
QY 64 GTTTCAGAGGACGGGATTCAGTACATAGAGAACCAAGTCAAGATTAATTTTAAATGA 123
DB 810 GTATCAGAGGACGAGATTCAGTACATAGAGATGATGATGAACTTAATTTTAAACGA 869
QY 124 GCATTCATCCCTGATCCCAAGTAATTAATTTGGAGAGAAAGTGGGCAAAATCTCTAG 183
DB 870 GCATTCACCCCTATCCCAAGTAATTAATTTGGAGAGAAAGTGGGCAAAATCTCTAG 929
QY 184 GCATTCACATGCGCAAGAAATGGGCTTTTACCCAAACCTTGAAGCTAGTGCACCA 243
DB 930 GCATTCATGATCGCAAGAAATGGGCTTTTACCCAAACCTTGAAGCTAGTGCACCA 989
QY 244 GGTACCAAGTGAATGTTCTTAGAGTGAATCAATGATGATGATGCTCTTAAG 303
DB 990 GGTGCGCAAGTGAATGTTCTTAGAGTGAATCAATGATGATGATGCTCTTAAG 1049
QY 304 TACGTTAATGAACTGTGCAGACACTTA 332
DB 1050 TACGTTGTTGGAGCTGTGCAGACACTTA 1078

RESULT 8
US-11-106-187-1
; Sequence 1, Application US/11106187
; Publication No. US20050183162A1

; GENERAL INFORMATION:
; APPLICANT: TUMER, NIGUN E.
; APPLICANT: WANG, PINGER
; TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
; FILE REFERENCE: OCIRS 3.9-060 CONT
; CURRENT APPLICATION NUMBER: US/11/106,187
; PRIOR FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US/09/721,047
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: PCT/US99/11301
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/086,374
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: *Physiolacca americana*
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (225)..(1163)
US-11-106-187-1

Query Match 70.0%; Score 233; DB 10; Length 1379;
Best Local Similarity 81.8%; Pred. No. 2.5e-62;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GGAGTTGATTCATTCCTGTAAGAACTGAGGCTTTTCTTCTAGCTAGCCATCCAAATG 63
DB 750 GGAGTATGTCATTCATCTGAGAAACCGAATTCCTATTTGGTAGCATATCAATG 809
QY 64 GTTTCAGAGGACGGGATTCAGTACATAGAGAACCAAGTCAAGATTAATTTTAAATGA 123
DB 810 GTATCAGAGGACGAGATTCAGTACATAGAGATGATGATGAACTTAATTTTAAACGA 869
QY 124 GCATTCACCTGATCCCAAGTAATTAATTTGGAGAGAAAGTGGGCAAAATCTCTAG 183
DB 870 GCATTCACCTGATCCCAAGTAATTAATTTGGAGAGAAAGTGGGCAAAATCTCTAG 929
QY 184 GCATTCACCTGATCCCAAGTAATTAATTTGGAGAGAAAGTGGGCAAAATCTCTAG 243

DB 930 GCATTCATGATCCCAAGTAATGAGTTTAAACCAATCTCTCAGCTAGGATGCGCAGT 989

QY 244 GGTACCAAGTGAATGTTCTTGAAGTGAATCAATGATGATGCGCCTTAAG 303
DB 990 GGTGCGCAAGTGAATGTTCTTGAAGTGAATCAATGATGATGCGCCTTAAG 1049

QY 304 TACGTTAATGAACTGTGCAGACACTTA 332
DB 1050 TACGTTGTTGGAGCTGTGCAGACACTTA 1078

RESULT 9
US-11-084-080-15
; Sequence 15, Application US/11084080
; Publication No. US20050238642A1

; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARL, Francis J.
; APPLICANT: HELLENDORF, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSCH, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845
US-11-084-080-15

Query Match 23.7%; Score 78.8; DB 10; Length 2404;
Best Local Similarity 63.1%; Pred. No. 1e-13;
Matches 173; Conservative 0; Mismatches 92; Indels 9; Gaps 3;

QY 40 TTCTCTGTTAGCCATCCAAATGTTTCAAGGACGGGATTCAGATACATAGAGAC 99
DB 1287 TTCTTCTTATTTGTCATCCAAATGTTTCAAGGACGGGATTCAGATACATAGAGAC 1346
QY 100 CAAGTCAAGCTAAT---TTTAATAGAGCATTTCAACCTTAATTTTAAATTTTAA 156
DB 1347 GAGGTGTTGATTAAGATTAATAGATCAATCAACCTTAATTTTAAATTTTAACTTG 1406
QY 157 GAGGAGAAGTGGGCAAAATCTGTAGGCAATTCACA---ATGCCAAGATGGGCTTT 212
DB 1407 GAGGAGAAGTGGGCAAAATCTGTAGGCAATTCACA---ATGCCAAGATGGGCTTT 1466
QY 213 ACCCAAC--CACTTGAAGTGAATGCCAAGATGCCAAGATGAATGATTTCTTAAGTG 270
DB 1467 ATTATCCGCGCATCTTCAATGATTAAGCCCTCAATGACCCATGGTGTAAATTAAGTG 1526
QY 271 GATGAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 304
DB 1527 AGTCAATTAATGATCCGATGATGATGATGATGATGATGATGATGATGATGATG 1560

RESULT 10
US-11-084-080-19
; Sequence 19, Application US/11084080
; Publication No. US20050238642A1

GENERAL INFORMATION:
APPLICANT: BAKER, Matthew
APPLICANT: CARR, Francis J.
APPLICANT: HELLENDORF, Koen
APPLICANT: CIZEAU, Jeanmick
APPLICANT: MACDONALD, Glen Christopher
APPLICANT: ENTWISTLE, Joycelyn
APPLICANT: BOSC, Denis Georges
APPLICANT: GLOVER, Nicholas Ronald
TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
FILE REFERENCE: 10241-44
CURRENT APPLICATION NUMBER: US/11/084,080
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US 60/554,580
PRIOR FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: US 60/630,571
PRIOR FILING DATE: 2004-11-26
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.3
SEQ ID NO 19
LENGTH: 2404
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: VB6-845-CL-de-bouganin
US-11-084-080-19

Query Match 23.7%; Score 78.8; DB 10; Length 2404;
Best Local Similarity 63.1%; Pred. No. 1e-13;
Matches 173; Conservative 0; Mismatches 92; Indels 9; Gaps 3;

QY 40 TTCTACTGTTAGCCATCAATGGTTTCAGAGGAGGCGGCAATTCAGTACATAGAGAC 99
DB 2105 TTCTTTCTATGTCTATCCAAATGGTTTCAGAGGAGGCTCGGTTCAAAATATATAGACT 2164
QY 100 CAAGTCAAGACTAAT--TTAATAGAGCATTTCACTGATCCCAAGATTAATATTG 156
DB 2165 GAGGTGTTGATAGAGATTAATAGATCAATTCAAACCTAATTTAAAGTATGAACTTG 2224
QY 157 GAGGAGAAGTGGGCAAAATCTTGAGGCAATTCACA---ATGCCAAGATGGGGCTTT 212
DB 2225 GAGAACATTTGGGGGAGATCTTGATGCCATTCACAAATCATCCCAATGTACCACT 2284
QY 213 ACCCAAC--CACTTGAGCTAGTGATGCAAGGTACCAAGTATGTTCTTAGAGTG 270
DB 2285 ATTAATCCGACATTCAGTTGATTAAGCCCTCAATGACCCCAATGGGTTGAATTAAGTG 2344
QY 271 GATGAATCAATCGTATGATGGCACTCCTTAAGT 304
DB 2345 AGTCAATTAAGTCCGATATGGGTATCCTTAAGT 2378

RESULT 11
US-11-084-080-21
Sequence 21, Application US/11084080
Publication No. US20050238642a1
GENERAL INFORMATION:
APPLICANT: BAKER, Matthew
APPLICANT: CARR, Francis J.
APPLICANT: HELLENDORF, Koen
APPLICANT: CIZEAU, Jeanmick
APPLICANT: MACDONALD, Glen Christopher
APPLICANT: ENTWISTLE, Joycelyn
APPLICANT: BOSC, Denis Georges
APPLICANT: GLOVER, Nicholas Ronald
TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
FILE REFERENCE: 10241-44
CURRENT APPLICATION NUMBER: US/11/084,080
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US 60/554,580
PRIOR FILING DATE: 2004-03-19

PRIOR APPLICATION NUMBER: US 60/630,571
PRIOR FILING DATE: 2004-11-26
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.3
SEQ ID NO 21
LENGTH: 2404
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: VB6-845-NVL-de-bouganin
US-11-084-080-21

Query Match 23.7%; Score 78.8; DB 10; Length 2404;
Best Local Similarity 63.1%; Pred. No. 1e-13;
Matches 173; Conservative 0; Mismatches 92; Indels 9; Gaps 3;

QY 40 TTCTACTGTTAGCCATCAATGGTTTCAGAGGAGGCGGCAATTCAGTACATAGAGAC 99
DB 594 TTCTTTCTATGTCTATCCAAATGGTTTCAGAGGAGGCTCGGTTCAAAATATATAGACT 653
QY 100 CAAGTCAAGACTAAT--TTAATAGAGCATTTCACTGATCCCAAGATTAATATTG 156
DB 654 GAGGTGTTGATAGAGATTAATAGATCAATTCAAACCTAATTTAAAGTATGAACTTG 713
QY 157 GAGGAGAAGTGGGCAAAATCTTGAGGCAATTCACA---ATGCCAAGATGGGGCTTT 212
DB 714 GAGAACATTTGGGGGAGATCTTGATGCCATTCACAAATCATCCCAATGTACCACT 773
QY 213 ACCCAAC--CACTTGAGCTAGTGATGCAAGGTACCAAGTATGTTCTTAGAGTG 270
DB 774 ATTAATCCGACATTCAGTTGATTAAGCCCTCAATGACCCCAATGGGTTGAATTAAGTG 833
QY 271 GATGAATCAATCGTATGATGGCACTCCTTAAGT 304
DB 834 AGTCAATTAAGTCCGATATGGGTATCCTTAAGT 867

RESULT 12
US-11-084-080-23
Sequence 23, Application US/11084080
Publication No. US20050238642a1
GENERAL INFORMATION:
APPLICANT: BAKER, Matthew
APPLICANT: CARR, Francis J.
APPLICANT: HELLENDORF, Koen
APPLICANT: CIZEAU, Jeanmick
APPLICANT: MACDONALD, Glen Christopher
APPLICANT: ENTWISTLE, Joycelyn
APPLICANT: BOSC, Denis Georges
APPLICANT: GLOVER, Nicholas Ronald
TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
FILE REFERENCE: 10241-44
CURRENT APPLICATION NUMBER: US/11/084,080
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US 60/554,580
PRIOR FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: US 60/630,571
PRIOR FILING DATE: 2004-11-26
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.3
SEQ ID NO 23
LENGTH: 2404
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: VB6-845-NVL-de-bouganin
US-11-084-080-23

Query Match 23.7%; Score 78.8; DB 10; Length 2404;
Best Local Similarity 63.1%; Pred. No. 1e-13;
Matches 173; Conservative 0; Mismatches 92; Indels 9; Gaps 3;

QY 40 TTCTACTGAGGACCAATGTTTCAAGAGGAGGACGATTCAGATACATAGAGAC 99
DB 1412 TTCTTTTCTTATGTCATCCAAATGGTTTCAAGGACAGCTCGTTCCAAATATATGAGACT 1471
QY 100 CAAGTCAAGACTAAT---TTTAATAGACATTTCACTGATGCCAAAGTAATTAATTTG 156
DB 1472 GAGGTGTTGATAGAGATTATGATCATTTCAACTAATTTTAAAGTATGAACTTG 1531
QY 157 GAGGAGAAATGGGGCAAAATCTTGAGGCAATTCACA---ATGCCAAGATGGGGCTTT 212
DB 1532 GAGAACATTTGGGGCGACATCTTGATGCGCATTCACAAATCATCCCAATATGACACT 1591
QY 213 ACCCAAC--CACTGAGCTAGTGATGCGCAAGGTACCAAGTACGATAGTTCTTAGAGTG 270
DB 1592 ATTATCCGGCATCTCAGTTGATTAAGCCCTTCAATGACCATGGGTTGTAATTAAGTG 1651
QY 271 GATGAATCAATCGTATGATGCGCACTCCTTAAGT 304
DB 1652 AGTCAATTAGTCCCGAATGCGGATCCTTAAGT 1685

RESULT 13

US-11-084-080-27
; Sequence 27, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDORN, Koen
; APPLICANT: CIZEAU, Jeanick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSCH, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGAINVILLE PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THERMOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 2431
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-011
US-11-084-080-27

Query Match 23.7%; Score 78.8; DB 10; Length 2431;
Best Local Similarity 63.1%; Pred. No. 1e-13; Indels 9; Gaps 3;
Matches 173; Conservative 0; Mismatches 92;

QY 40 TTCTACTGAGGACCAATGTTTCAAGAGGAGGACGATTCAGATACATAGAGAC 99
DB 1314 TTCTTTTCTTATGTCATCCAAATGGTTTCAAGGACAGCTCGTTCCAAATATATGAGACT 1373
QY 100 CAAGTCAAGACTAAT---TTTAATAGACATTTCACTGATGCCAAAGTAATTAATTTG 156
DB 1374 GAGGTGTTGATAGAGATTATGATCATTTCAACTAATTTTAAAGTATGAACTTG 1433
QY 157 GAGGAGAAATGGGGCAAAATCTTGAGGCAATTCACA---ATGCCAAGATGGGGCTTT 212
DB 1434 GAGAACATTTGGGGGACATCTCTGATGCGCATTCACAAATCATCCCAATATGTAAGTACT 1493
QY 213 ACCCAAC--CACTTGAAGTATGATGCGCAAGGTACCAAGTACGATAGTTCTTAGAGTG 270
DB 1494 ATTATCCGGCATCTCAGTTGATTAAGCCCTTCAATGACCATGGGTTGTAATTAAGTG 1553

QY 271 GATGAATCAATCGTATGATGCGCACTCCTTAAGT 304
DB 1554 AGTCAATTAGTCCCGAATGCGGATGATCCTTAAGT 1587

RESULT 14

US-10-919-750-4
; Sequence 4, Application US/10919750
; Publication No. US20050120414A1
; GENERAL INFORMATION:
; APPLICANT: Diamond, Paul
; TITLE OF INVENTION: REGULATION OF POLYNUCLEIC ACID ACTIVITY AND EXPRESSION
; FILE REFERENCE: P1100-4US
; CURRENT APPLICATION NUMBER: US/10/919,750
; CURRENT FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: US 10/644,288
; PRIOR FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US 10/354,903
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US 60/352,705
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Microsoft Wordpad
; SEQ ID NO 4
; LENGTH: 935
; TYPE: DNA
; ORGANISM: Saponaria officinalis
US-10-919-750-4

Query Match 22.6%; Score 75.4; DB 9; Length 935;
Best Local Similarity 58.9%; Pred. No. 7.9e-13;
Matches 149; Conservative 0; Mismatches 101; Indels 3; Gaps 1;

QY 22 GTAAAACTGAGCTTTTCTTCTACTGTCGATCCCAATGTTTCAAGAGGACGCGCA 81
DB 634 GTTAAACACAGAGCTAGATTCCTTCTTATGCTATGATGATGACGCTGAGGACGCGCA 693
QY 82 TTCAAGTACATAGAGAACCAAGTCAATTTTAATGAGCATCTCACTGATCCC 141
DB 694 TTATGATCATCAAACTTGATATGAGAACTTCCCAAGTCAACTCGGAAAC 753
QY 142 AAATTAATTAATTTGAGAGAAAGTGGGCAAAATCTCTAGGCAATTCA--ATAGCC 198
DB 754 AAATGATTCAGTTTGAAGTTTAACTGAGAAATTTCTAGGCAATATAGGGGATGCC 813
QY 199 AAGATGGGCTTTACCAACCACTGAGCTAGTATGCAAGGTACCAAGTGCATA 258
DB 814 AAAACGCGCTTAAATTAAGATTATGATTCGCTTGGAAAGTTAGGCAAGTGAAG 873
QY 259 GTTCTTAGAGTGG 271
DB 874 GACTTGCAATGG 886

RESULT 15

US-09-861-257-37
; Sequence 37, Application US/09861257
; Publication No. US2003004096A1
; GENERAL INFORMATION:
; APPLICANT: Chandler, Lois Ann
; APPLICANT: Sosnowski, Barbara A.
; APPLICANT: Baird, J. Andrew
; TITLE OF INVENTION: TREATMENT OF TUMORS USING
; TITLE OF INVENTION: LIGAND-DIRECTED NUCLEIC ACID DELIVERY VEHICLES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESS: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/861,257
FILING DATE: 17-MAY-2001
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Christiansen Ph.D., William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 760100.423C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..804
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..804
OTHER INFORMATION: /note="Nucleotide sequence
OTHER INFORMATION: corresponding to the clone M13 mp18-G7"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 46..804
OTHER INFORMATION: /product="Saporin"
US-09-861-257-37

Query Match 22.2%; Score 73.8; DB 3; Length 804;
Best Local Similarity 58.5%; Pred. No. 2.4e-12;
Matches 148; Conservative 0; Mismatches 102; Indels 3; Gaps 1;

QY	22	GTAAAACTGAGGCTTTTCTCTGAGTACCAATGCTTTCAGAGGCAAGCGGA	81
DB	523	GTAAAAACGAAAGCTAGATTCCTTATCGTATTCAGATGACGCTGAGGCAAGCA	582
QY	82	TTCAAGTACATAGAGCAAGTCAAGCTAATTTTATAGCATTTCTACCTGATCCC	141
DB	583	TTTAGTACATACAAACTTGATATCAAGAACTTCCCAACAAGTCAACTCGGAAAC	642
QY	142	AAAGTAATTAATTGAGAGAGAGAGGAGGCAAAATCTCTGAGCAATTCAC--AATGCC	198
DB	643	AAAGTATTCAGTTGAGGTTAATCGAABAAAATTTCTACGCAATATACGGGATGCC	702
QY	199	AAGATGGGCTTACCAACCACTTGAGCTAGTGAATGCCAAGTACCAAGTGATTA	258
DB	703	AAAAACGCGGTGTTAATTAAGATTATGATTCGGGTTTGAAAAGTGAAGCAAGTGAAG	762
QY	259	GTCTTAGAGTGG	271
DB	763	GACTTGCAATGG	775

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OM nucleic - nucleic search, using SW model

Run on: April 9, 2006, 00:50:48 ; Search time 289.914 Seconds
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Perfect score: 333
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 18535810

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /SIDS5/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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10: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq3:*
11: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:*
12: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
13: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
14: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
15: /SIDS5/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	233	70.0	1360	14 US-11-010-795-19	Sequence 19, Appl
2	70.6	21.2	934	14 US-11-010-795-21	Sequence 21, Appl
3	63	18.9	1623	8 US-10-893-584-273	Sequence 273, Appl
4	61.4	18.4	807	14 US-11-010-795-23	Sequence 23, Appl
5	61.4	18.4	1807	8 US-10-893-584-196	Sequence 196, Appl
6	61.4	18.4	1810	8 US-10-893-584-168	Sequence 168, Appl
7	61.4	18.4	1813	8 US-10-893-584-245	Sequence 245, Appl
8	61.4	18.4	1819	8 US-10-893-584-238	Sequence 238, Appl
9	61.4	18.4	1822	8 US-10-893-584-175	Sequence 175, Appl
10	61.4	18.4	1822	8 US-10-893-584-182	Sequence 182, Appl
11	61.4	18.4	1825	8 US-10-893-584-231	Sequence 231, Appl
12	61.4	18.4	1828	8 US-10-893-584-210	Sequence 210, Appl
13	61.4	18.4	1831	8 US-10-893-584-161	Sequence 161, Appl
14	61.4	18.4	1834	8 US-10-893-584-203	Sequence 203, Appl
15	61.4	18.4	1834	8 US-10-893-584-154	Sequence 154, Appl
16	61.4	18.4	1837	8 US-10-893-584-266	Sequence 266, Appl
17	61.4	18.4	1843	8 US-10-893-584-259	Sequence 259, Appl
18	61.4	18.4	1849	8 US-10-893-584-252	Sequence 252, Appl

19	61.4	18.4	1855	8 US-10-893-584-3	Sequence 3, Appl
20	61.4	18.4	1855	8 US-10-893-584-5	Sequence 5, Appl
21	61.4	18.4	1855	8 US-10-893-584-7	Sequence 7, Appl
22	61.4	18.4	1855	8 US-10-893-584-9	Sequence 9, Appl
23	61.4	18.4	1855	8 US-10-893-584-13	Sequence 13, Appl
24	61.4	18.4	1855	8 US-10-893-584-15	Sequence 15, Appl
25	61.4	18.4	1855	8 US-10-893-584-17	Sequence 17, Appl
26	61.4	18.4	1855	8 US-10-893-584-19	Sequence 19, Appl
27	61.4	18.4	1855	8 US-10-893-584-21	Sequence 21, Appl
28	61.4	18.4	1855	8 US-10-893-584-23	Sequence 23, Appl
29	61.4	18.4	1855	8 US-10-893-584-25	Sequence 25, Appl
30	61.4	18.4	1855	8 US-10-893-584-27	Sequence 27, Appl
31	61.4	18.4	1855	8 US-10-893-584-29	Sequence 29, Appl
32	61.4	18.4	1855	8 US-10-893-584-31	Sequence 31, Appl
33	61.4	18.4	1855	8 US-10-893-584-33	Sequence 33, Appl
34	61.4	18.4	1855	8 US-10-893-584-35	Sequence 35, Appl
35	61.4	18.4	1855	8 US-10-893-584-37	Sequence 37, Appl
36	61.4	18.4	1855	8 US-10-893-584-39	Sequence 39, Appl
37	61.4	18.4	1855	8 US-10-893-584-48	Sequence 48, Appl
38	61.4	18.4	1855	8 US-10-893-584-50	Sequence 50, Appl
39	61.4	18.4	1855	8 US-10-893-584-52	Sequence 52, Appl
40	61.4	18.4	1855	8 US-10-893-584-54	Sequence 54, Appl
41	61.4	18.4	1855	8 US-10-893-584-74	Sequence 74, Appl
42	61.4	18.4	1855	8 US-10-893-584-77	Sequence 77, Appl
43	61.4	18.4	1855	8 US-10-893-584-80	Sequence 80, Appl
44	61.4	18.4	1855	8 US-10-893-584-83	Sequence 83, Appl
45	61.4	18.4	1855	8 US-10-893-584-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1
US-11-010-795-19
; Sequence 19, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NILDUN E.
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; TITLE OF INVENTION: RESISTANT TO TRICHOECHEMBE FUNGAL TOXINS
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010.795
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 19
; LENGTH: 1360
; TYPE: DNA
; ORGANISM: *Phytolacca americana*
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (207)..(1145)
US-11-010-795-19

Query Match 70.0%; Score 233; DB 14; Length 1360;
Best Local Similarity 81.8%; Pred. No. 2.1e-61;
Matches 269; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 4 GGAATTATTCATCCCTGTTAAACGAGGCTTTTCTACTGTTAGCATCAATG 63
DB 732 GGAATTATTCATTCATTCATGAAACCGAATTCCTATTGTTAGCATCAATG 791
QY 64 GTTTCAGAGGAGCGCATTCATGATAGATAGAACCAAGTCAAGATTAATTAATGA 123
DB 792 GTATCAAGGAGGAGCAATTCATGATAGATAGATAGATAGATTAATTAATGA 851
QY 124 GCATTTACCTTGATCCCAAGTAAATTAATTGGAGGAGAGTGGGCAAAATCTTGAG 183
DB 852 GCATTTACCTTGATCCCAAGTAAATTAATTGGAGGAGAGATGGGTAATTAATCAACA 911

QY 141 CAAGTAATTAATTGGAGAGAGAGGAGGCAAAATCTCTGAGCAATTCACAAATGCCAA 200
DB 609 TAGGTATTAATCACTTGGAGAAATAGTTGGGGGAGACTTTCACATGCAATTCAGAGCTTAA 668
QY 201 GAATGGGGCTTATCCCAACCACTGAGCTAGATGATGCCAAAGGTACCAAGTATGAT 260
DB 669 CCAAGAGGCTTGTGTAGTCCAAATTCACAGCAAGAGCTAATGTTCCAAATTCAGTGT 728
QY 261 TCTTAGAGTGATGAATCAATCGATGTGGCACTCCTTAAGTA 305
DB 729 GTAGATGTGAGTATTAATCCCTATCATAGCTCTCATGTGTA 773

RESULT 5
US-10-893-584-196
; Sequence 196, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OR INVENTION: Rich-Like Toxin Variants for Treatment of Cancer,
; TITLE OR INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 196
; LENGTH: 1807
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-196

Query Match 18.4%; Score 61.4; DB 8; Length 1807;
Best Local Similarity 53.7%; Pred. No. 2e-08;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 27 AACTGAGGCTTTTCTACTGTAGCCATCCAAATGTTTCAAGGAGGCGCATTCAA 86
DB 597 AACTGAGGCTTTTCTACTGTAGCCATCCAAATGTTTCAAGGAGGCGCATTCAA 656
QY 87 GTACATAGAGAACCAAGTCAAGACTAATTTT-----AATAGACATTCTACCTGATCC 140
DB 657 ATATATTGAGGAGAAATGGCGACGAAATTAAGTACACCGAGATCTGCACCAATCC 716
QY 141 CAAGTAATTAATTGGAGAGAGAGTGGGCAAAATCTCTGAGCAATTCACAAATGCCAA 200
DB 717 TAGGTATTAATCACTTGGAGAAATAGTTGGGGGAGACTTTCACATGCAATTCAGAGCTTAA 776
QY 201 GAATGGGGCTTATCCCAACCACTGAGCTAGATGATGCCAAAGGTACCAAGTATGAT 260
DB 777 CCAAGAGGCTTGTGTAGTCCAAATTCACAGCAAGAGCTAATGTTCCAAATTCAGTGT 836
QY 261 TCTTAGAGTGATGAATCAATCGATGTGGCACTCCTTAAGTA 305
DB 837 GTAGATGTGAGTATTAATCCCTATCATAGCTCTCATGTGTA 881

RESULT 6
US-10-893-584-168
; Sequence 168, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor

; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OR INVENTION: Rich-Like Toxin Variants for Treatment of Cancer,
; TITLE OR INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 168
; LENGTH: 1810
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-168

Query Match 18.4%; Score 61.4; DB 8; Length 1810;
Best Local Similarity 53.7%; Pred. No. 2e-08;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 27 AACTGAGGCTTTTCTACTGTAGCCATCCAAATGTTTCAAGGAGGCGCATTCAA 86
DB 597 AACTGAGGCTTTTCTACTGTAGCCATCCAAATGTTTCAAGGAGGCGCATTCAA 656
QY 87 GTACATAGAGAACCAAGTCAAGACTAATTTT-----AATAGACATTCTACCTGATCC 140
DB 657 ATATATTGAGGAGAAATGGCGACGAAATTAAGTACACCGAGATCTGCACCAATCC 716
QY 141 CAAGTAATTAATTGGAGAGAGAGTGGGCAAAATCTCTGAGCAATTCACAAATGCCAA 200
DB 717 TAGGTATTAATCACTTGGAGAAATAGTTGGGGGAGACTTTCACATGCAATTCAGAGCTTAA 776
QY 201 GAATGGGGCTTATCCCAACCACTGAGCTAGATGATGCCAAAGGTACCAAGTATGAT 260
DB 777 CCAAGAGGCTTGTGTAGTCCAAATTCACAGCAAGAGCTAATGTTCCAAATTCAGTGT 836
QY 261 TCTTAGAGTGATGAATCAATCGATGTGGCACTCCTTAAGTA 305
DB 837 GTAGATGTGAGTATTAATCCCTATCATAGCTCTCATGTGTA 881

RESULT 7
US-10-893-584-245
; Sequence 245, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OR INVENTION: Rich-Like Toxin Variants for Treatment of Cancer,
; TITLE OR INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 245
; LENGTH: 1813
; TYPE: DNA
; ORGANISM: E. coli

US-10-893-584-245

Query Match 18.4%; Score 61.4; DB 8; Length 1813;
Best Local Similarity 53.7%; Pred. No. 2e-08;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 27 AACTGAGGCTTTTCTTCTAGTGGAGCATCCAAATGTTTCAGAGGAGCGGATTCAA 86
DB 597 AACTGAGGCTTTTCTTCTTAAATTTGATCCAAATATTTTCAGAGGAGCGGATTCCA 656
QY 87 GTACATAGAGAACCAAGTCAAGCTAATTTT-----AATAGACATCTTACCTGATCC 140
DB 657 ATATATTGAGGAGAAATGGCGACGAAATTAGTACACCGAGATCTGACAGATCC 716
QY 141 CAAGTATTATTTTGGAGGAGAGTGGGCAAAATCTTGAGGCAATTCAAAATGCCAA 200
DB 717 TAGCGTAAATTAACCTTGAAGATAGTTGGGGAGACTTTCACCTGCAATTCAGAGTCAA 776
QY 201 GAATGGGCTTTACCCCAACCACTTGAGCTAGTGATGCCAAAGTCAAGTGATAGT 260
DB 777 CCAAGGAGCCTTGTCTGATCCAAATTCAGCAAAAGCGTAAATGTTCCAAATTCAGTGT 836
QY 261 TCTTAGAGTGAGTAATCAATCGTGAATGGCACTCCTTAAGTA 305
DB 837 GTACGATGTAGTAAATTAATCCCTATCATAGCTCTCATGTGTA 881

RESULT 8

US-10-893-584-238
; Sequence 238, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 238
; LENGTH: 1819
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-238

Query Match 18.4%; Score 61.4; DB 8; Length 1819;
Best Local Similarity 53.7%; Pred. No. 2e-08;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 27 AACTGAGGCTTTTCTTCTAGTGGAGCATCCAAATGTTTCAGAGGAGCGGATTCAA 86
DB 597 AACTGAGGCTTTTCTTCTTAAATTTGATCCAAATATTTTCAGAGGAGCGGATTCCA 656
QY 87 GTACATAGAGAACCAAGTCAAGCTAATTTT-----AATAGACATCTTACCTGATCC 140
DB 657 ATATATTGAGGAGAAATGGCGACGAAATTAGTACACCGAGATCTGACAGATCC 716
QY 141 CAAGTATTATTTTGGAGGAGAGTGGGCAAAATCTTGAGGCAATTCAAAATGCCAA 200
DB 717 TAGCGTAAATTAACCTTGAAGATAGTTGGGGAGACTTTCACCTGCAATTCAGAGTCAA 776
QY 201 GAATGGGCTTTACCCCAACCACTTGAGCTAGTGATGCCAAAGTCAAGTGATAGT 260

DB 777 CCAAGAGCCTTTGTAGTCCAAATTCAGCAAGAGCGTAATGTTCCAAATTCAGTGT 836

QY 261 TCTTAGAGTGAGTAATCAATCGTATGATGGCACTCTTAAGTA 305
DB 837 GTACGATGTAGTAAATTAATCCCTATCATAGCTCTCATGTGTA 881

RESULT 9

US-10-893-584-175
; Sequence 175, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 1822
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-175

Query Match 18.4%; Score 61.4; DB 8; Length 1822;
Best Local Similarity 53.7%; Pred. No. 2e-08;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 27 AACTGAGGCTTTTCTTCTAGTGGAGCATCCAAATGTTTCAGAGGAGCGGATTCAA 86
DB 597 AACTGAGGCTTTTCTTCTTAAATTTGATCCAAATATTTTCAGAGGAGCGGATTCCA 656
QY 87 GTACATAGAGAACCAAGTCAAGCTAATTTT-----AATAGACATCTTACCTGATCC 140
DB 657 ATATATTGAGGAGAAATGGCGACGAAATTAGTACACCGAGATCTGACAGATCC 716
QY 141 CAAGTATTATTTTGGAGGAGAGTGGGCAAAATCTTGAGGCAATTCAAAATGCCAA 200
DB 717 TAGCGTAAATTAACCTTGAAGATAGTTGGGGAGACTTTCACCTGCAATTCAGAGTCAA 776
QY 201 GAATGGGCTTTACCCCAACCACTTGAGCTAGTGATGCCAAAGTCAAGTGATAGT 260
DB 777 CCAAGGAGCCTTGTCTGATCCAAATTCAGCAAAAGCGTAAATGTTCCAAATTCAGTGT 836
QY 261 TCTTAGAGTGAGTAATCAATCGTGAATGGCACTCCTTAAGTA 305
DB 837 GTACGATGTAGTAAATTAATCCCTATCATAGCTCTCATGTGTA 881

RESULT 10

US-10-893-584-182
; Sequence 182, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584

CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 182
LENGTH: 1822
TYPE: DNA
ORGANISM: E. coli
US-10-893-584-182

Query Match 18.4%; Score 61.4; DB 8; Length 1822;
Best Local Similarity 53.7%; Pred. No. 2e-08; Indels 6; Gaps 1;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 27 AACTGAGCCTTTTCTACTGTAGCCATCCAAATGTTTCAGAGGAGCGCATTCAA 86
DB 597 AACTGAGCCTGCTTCCTTATTAATTGATCCAAATGTTTCAGAGGAGCAAGTTCCA 656
QY 87 GTACATAGAGAACCAAGTCAAGACTAATTTT-----AATAGACATTCTACCTGATCC 140
DB 657 ATATATTGAGGAGAAATGCGCACGAGATTAGGTACCAACCGAGATCTGCACCGATCC 716
QY 141 CAAGTATTAATTGAGGAGAAAGTGGGCAAAATCTGTAGAGCAATTCACATGCCAA 200
DB 717 TAGGTATTAATCACTTGAGATTAGTTGGGGAGACTTTCACCTGAATTCAGAGTTAA 776
QY 201 GAATGGGCTTTTACCCAAACCACTTGAGCTAGTGATGCCAAAGTACCAAGTGAATGT 260
DB 777 CCAAGAGCCTTTGCTGATGCAATTCACACTGCAAAAGCGTAATGTTCCAAATTCAGTGT 836
QY 261 TCTTAGAGTGATGAATCAATCGTATGTCGCACTCCTTAAGTA 305
DB 837 GTACGATGTGATATTAATCCCTATCATAGCTCTCATGTGTGA 881

RESULT 11
US-10-893-584-231
Sequence 231, Application US/10893584
Publication No. US20050272048A1
GENERAL INFORMATION:
APPLICANT: Borgford, Thor
APPLICANT: Braun, Curtis
APPLICANT: Purac, Admit
APPLICANT: Stoll, Dominik
TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
TITLE OF INVENTION: Viral or Parasitic Infections
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 231
LENGTH: 1825
TYPE: DNA
ORGANISM: E. coli
US-10-893-584-231

Query Match 18.4%; Score 61.4; DB 8; Length 1825;
Best Local Similarity 53.7%; Pred. No. 2e-08; Indels 6; Gaps 1;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;
QY 27 AACTGAGCCTTTTCTACTGTAGCCATCCAAATGTTTCAGAGGAGCGCATTCAA 86

DB 597 AACTGAGCCTGCTTCCTTATTAATTGATCCAAATGTTTCAGAGGAGCAAGTTCCA 656
QY 87 GTACATAGAGAACCAAGTCAAGACTAATTTT-----AATAGACATTCTACCTGATCC 140
DB 657 ATATATTGAGGAGAAATGCGCACGAGATTAGGTACCAACCGAGATCTGCACCGATCC 716
QY 141 CAAGTATTAATTGAGGAGAAAGTGGGCAAAATCTGTAGAGCAATTCACATGCCAA 200
DB 717 TAGGTATTAATCACTTGAGATTAGTTGGGGAGACTTTCACCTGAATTCAGAGTTAA 776
QY 201 GAATGGGCTTTTACCCAAACCACTTGAGCTAGTGATGCCAAAGTACCAAGTGAATGT 260
DB 777 CCAAGAGCCTTTGCTGATGCAATTCACACTGCAAAAGCGTAATGTTCCAAATTCAGTGT 836
QY 261 TCTTAGAGTGATGAATCAATCGTATGTCGCACTCCTTAAGTA 305
DB 837 GTACGATGTGATATTAATCCCTATCATAGCTCTCATGTGTGA 881

RESULT 12
US-10-893-584-210
Sequence 210, Application US/10893584
Publication No. US20050272048A1
GENERAL INFORMATION:
APPLICANT: Borgford, Thor
APPLICANT: Braun, Curtis
APPLICANT: Purac, Admit
APPLICANT: Stoll, Dominik
TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
TITLE OF INVENTION: Viral or Parasitic Infections
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 210
LENGTH: 1828
TYPE: DNA
ORGANISM: E. coli
US-10-893-584-210

Query Match 18.4%; Score 61.4; DB 8; Length 1828;
Best Local Similarity 53.7%; Pred. No. 2e-08; Indels 6; Gaps 1;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;
QY 27 AACTGAGCCTTTTCTACTGTAGCCATCCAAATGTTTCAGAGGAGCGCATTCAA 86
DB 597 AACTGAGCCTGCTTCCTTATTAATTGATCCAAATGTTTCAGAGGAGCAAGTTCCA 656
QY 87 GTACATAGAGAACCAAGTCAAGACTAATTTT-----AATAGACATTCTACCTGATCC 140
DB 657 ATATATTGAGGAGAAATGCGCACGAGATTAGGTACCAACCGAGATCTGCACCGATCC 716
QY 141 CAAGTATTAATTGAGGAGAAAGTGGGCAAAATCTGTAGAGCAATTCACATGCCAA 200
DB 717 TAGGTATTAATCACTTGAGATTAGTTGGGGAGACTTTCACCTGAATTCAGAGTTAA 776
QY 201 GAATGGGCTTTTACCCAAACCACTTGAGCTAGTGATGCCAAAGTACCAAGTGAATGT 260
DB 777 CCAAGAGCCTTTGCTGATGCAATTCACACTGCAAAAGCGTAATGTTCCAAATTCAGTGT 836
QY 261 TCTTAGAGTGATGAATCAATCGTATGTCGCACTCCTTAAGTA 305
DB 837 GTACGATGTGATATTAATCCCTATCATAGCTCTCATGTGTGA 881

RESULT 13
US-10-893-584-161
; Sequence 161, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Scoll, Dominik
; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 161
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-161

Query Match 18.4%; Score 61.4; DB 8; Length 1831;
Best Local Similarity 53.7%; Pred. No. 2e-08;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 27 AACTGAGGCTTTTCTTCTAGTGGATCCCAATGTTTCAGAGGAGCGGATTCAA 86
DB 597 AACTCGGCTCGTTCCTTTTAATTGATCCCAATGTTTCAGAGGAGCGGATTCCA 656
QY 87 GTACATRAGAGAACCAAGTCAAGTCTAATTTT-----AATAGACATTTCACTGATCC 140
DB 657 ATATATTGAGGAGAAATGGCGACGAGAAATTAGTACACCGGAGATCTGACAGATCC 716
QY 141 CAAAGTAAATTAATTGGAGAGAAAGTGGGCAAAATCTGAGGCAATTCAATGCCAA 200
DB 717 TAGCGTAATTACCTTGAGAAATGTTGGGAGACTTTCACATGCAATTCAAGAGTCTAA 776
QY 201 GAATGGGCTTTTACCCAAACCACTGAGCTAGTGATGCCAAAGTCAAGTGATAGT 260
DB 777 CCAAGAGCCTTTGCTGATGCTCAATTCACACTGCAAAAGCGTAAATGTTCCAAATTCAGTGT 836
QY 261 TCTTAGAGTGATGAATCAATCGTATGTCGATGTCGCACTCCTTAAGTA 305
DB 837 GTACGATGTGATATATTAATCCCTATCATAGCTCTCATGTGTGA 881

RESULT 14
US-10-893-584-203
; Sequence 203, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Scoll, Dominik
; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04

; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 203
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-203

Query Match 18.4%; Score 61.4; DB 8; Length 1831;
Best Local Similarity 53.7%; Pred. No. 2e-08;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 27 AACTGAGGCTTTTCTTCTAGTGGATCCCAATGTTTCAGAGGAGCGGATTCAA 86
DB 597 AACTCGGCTCGTTCCTTTTAATTGATCCCAATGTTTCAGAGGAGCGGATTCCA 656
QY 87 GTACATRAGAGAACCAAGTCAAGTCTAATTTT-----AATAGACATTTCACTGATCC 140
DB 657 ATATATTGAGGAGAAATGGCGACGAGAAATTAGTACACCGGAGATCTGACAGATCC 716
QY 141 CAAAGTAAATTAATTGGAGAGAAAGTGGGCAAAATCTGAGGCAATTCAATGCCAA 200
DB 717 TAGCGTAATTACCTTGAGAAATGTTGGGAGACTTTCACATGCAATTCAAGAGTCTAA 776
QY 201 GAATGGGCTTTTACCCAAACCACTGAGCTAGTGATGCCAAAGTCAAGTGATAGT 260
DB 777 CCAAGAGCCTTTGCTGATGCTCAATTCACACTGCAAAAGCGTAAATGTTCCAAATTCAGTGT 836
QY 261 TCTTAGAGTGATGAATCAATCGTATGTCGATGTCGCACTCCTTAAGTA 305
DB 837 GTACGATGTGATATATTAATCCCTATCATAGCTCTCATGTGTGA 881

RESULT 15
US-10-893-584-154
; Sequence 154, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Scoll, Dominik
; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 154
; LENGTH: 1834
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-154

Query Match 18.4%; Score 61.4; DB 8; Length 1834;
Best Local Similarity 53.7%; Pred. No. 2e-08;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 27 AACTGAGGCTTTTCTTCTAGTGGATCCCAATGTTTCAGAGGAGCGGATTCAA 86
DB 597 AACTCGGCTCGTTCCTTTTAATTGATCCCAATGTTTCAGAGGAGCGGATTCCA 656
QY 87 GTACATRAGAGAACCAAGTCAAGTCTAATTTT-----AATAGACATTTCACTGATCC 140
DB 657 ATATATTGAGGAGAAATGGCGACGAGAAATTAGTACACCGGAGATCTGACAGATCC 716

QY 141 CAAAGTAATTAATTTGGAGAGAGAGTGGGCAAAATCTCTGAGGCATTCACATGCCAA 200
 Db 717 TAGCCTAATTAACCTGAGAAATAGTTGGGGGAGACTTTCACCTGCAATTCAGAGGCTTA 776
 QY 201 GAATGGGGCTTTACCCAAACCACTTGAGCTAGTGAGATGCCAAGGTACCAAGTGATAGT 260
 Db 777 CCAGGAGGCTTTGCTAGTCAATTCACGCAAGAGCGTAATGGGTCCAAATTCAGGT 836
 QY 261 TCTTAGAGTGAGTAATCAATCGTAGTGGCACTCCTTAAGTA 305
 Db 837 GTACGATGTGAGTATTAATCCCTATCATAGCTCTCATGTGTA 881

Search completed: April 9, 2006, 04:47:48
 Job time : 289.914 secs

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GenCore version 5.1.7
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OM protein - nucleic search **using frame p2n model**

Run on: April 9, 2006, 01:20:32 ; Search time 2511.43 Seconds
(without alignments)
2489.732 Million cell updates/sec

Title: US-09-978-274A-8
Perfect score: 569
Sequence: 1 MGVDSPVKTAPFLVAIQ.....DEINRDVALLKYNGTCOTT 110

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Rgapop 6.0 , Rgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abses/ABSSWEB.spool/US09978274/rnat 07042006 173032 28388/app query.fasta.1
-DB=GenEmbl -OPMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=Dioum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pic -NOR=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abses04
-USER=US09978274 @CEN 1.1 5548 @rnat 07042006 173032 28388 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -RGAPOP=6 -RGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_dr:*
9: gb_to:*
10: gb_ste:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hlg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	569	100.0	333	6	AX427708	Sequence
2	564	99.1	792	6	AX427704	Sequence
3	564	99.1	945	6	AX427702	Sequence

4	564	99.1	1249	15	PAPASRIP	X98079 P.americana
5	559	98.2	786	15	AB071855	AB071855 PhytoIacc
6	519	91.2	1092	6	AX427720	AX427720 Sequence
7	457	80.3	2472	6	E05033	E05033 DNA encodin
8	457	80.3	2472	15	PTCAPAP	D10600 P. american
9	454	79.8	942	15	AY547315	AY547315 PhytoIacc
10	454	79.8	942	15	AY572976	AY572976 PhytoIacc
11	454	79.8	1114	15	AF533515	AF533515 PhytoIacc
12	454	79.8	1164	15	PAPAP	X55383 P.americana
13	454	79.8	1195	6	A36639	A36639 Sequence 1
14	454	79.8	1195	6	A42103	A42103 Sequence 1
15	454	79.8	1195	6	I43835	I43835 Sequence 1
16	454	79.8	1195	6	I55866	I55866 Sequence 1
17	454	79.8	1378	6	AX427732	AX427732 Sequence
18	454	79.8	1379	6	AR009535	AR009535 Sequence
19	454	79.8	1379	6	AR136704	AR136704 Sequence
20	454	79.8	1379	6	AR136705	AR136705 Sequence
21	454	79.8	1379	6	AX427731	AX427731 Sequence
22	451	79.3	1379	6	AR141172	AR141172 Sequence
23	449	78.9	1164	15	AY049785	AY049785 PhytoIacc
24	443	77.9	1052	15	AY137202	AY137202 PhytoIacc
25	440.5	77.4	939	15	AY327475	AY327475 PhytoIacc
26	439	77.2	882	6	A67183	A67183 Sequence 1
27	438	77.0	1113	15	AY071928	AY071928 PhytoIacc
28	437	76.8	951	6	A67185	A67185 Sequence 3
29	437	76.8	2369	15	AF141331	AF141331 PhytoIacc
30	429	75.4	783	15	AB071854	AB071854 PhytoIacc
31	399	70.1	918	6	A43003	A43003 Sequence 1
32	399	70.1	918	6	A48150	A48150 Sequence 1
33	399	70.1	918	6	I60482	I60482 Sequence 1
34	399	70.1	918	6	I89987	I89987 Sequence 1
35	356	62.6	714	15	AY603352	AY603352 PhytoIacc
36	355	62.4	711	15	AF338910	AF338910 PhytoIacc
37	353	62.0	711	15	AY603353	AY603353 PhytoIacc
38	352	61.9	714	15	AY603354	AY603354 PhytoIacc
39	302	53.1	1226	15	CAATIPR	X96474 C.aculeatum
40	302	53.1	1226	15	CAAV	AY491967 Beta vulg
41	215	37.8	926	15	BVBETAVUL	X85667 B.vulgaris
42	215	37.8	1080	15	AR003721	AR003721 Sequence
43	213.5	37.5	813	6	AR010057	AR010057 Sequence
44	213.5	37.5	813	6	AR055263	AR055263 Sequence
45	213.5	37.5	813	6	AR055263	AR055263 Sequence

ALIGNMENTS

RESULT 1
AX427708 333 bp DNA
DEFINITION Sequence 7 from Patent WO0233107.
ACCESSION AX427708
VERSION AX427708.1 GI:21537818

KEYWORDS
SOURCE
ORGANISM
Phytolacca americana (American pokeweed)

Phytolacca americana
Bakaryofa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.
TITLE Plant cell death system
JOURNAL Patient: WO 0233107-A 7 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)

FEATURES
Location/Qualifiers

source
1..333
/organism="Phytolacca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"

misc_feature
1..3
/note="Initiation codon added via PCR primer"
misc_feature
331..333
/note="Stop codon added via PCR primer"

ORIGIN

Alignment Scores:

Pred. No.: 2,18e-56 Length: 333
Score: 569.00 Matches: 110
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-8 (1-110) x AX427708 (1-333)

QY 1 MetGlyValAspSerPheProValIysThrGluAlaPhePheLeuValAlaIleGln 20
DB 1 ATGGGAGTGTATTCATTCCTGTAAAACTAGAGCTTTTCTTACTGTAAGCAATCCAA 60
QY 21 MetValSerGluAlaAlaArgPheIysTyrIleGluAsnGlnValIysThrAsnPheAsn 40
DB 61 ATGGTTTCAGAGCAGCGCATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTAAT 120
QY 41 ArgAlaPheTyrProAspProIysValIleAsnLeuGluGluIysTyrGlyIysIleSer 60
DB 121 AGAGCATTTTACCTGATCCCAAGTAAATTAATTTGGAGAGAAAGTGGGCAAAATCTCT 180
QY 61 GluAlaIleHisAsnAlaIysAsnGlyAlaLeuProIysProLeuGluLeuValAspAla 80
DB 181 GAGGCAATTCAACAATGCCAAGAAATGGGCTTTACCCAAACCACTTGAGCTAGTGATGCC 240
QY 81 LysGlyThrIysTyrPleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeu 100
DB 241 AAGGATCCAGTGGATAGTCTTCTAGAGTGAATCAATCATGCTGATGTGGCACTCTCT 300
QY 101 LysTyrValAsnGlyThrCysGlnThrThr 110
DB 301 AAGTACGTATATGGAACTGTCAAGACAAC 330

RESULT 2

AX427704 792 bp DNA linear PAT 20-JUN-2002
LOCUS AX427704
DEFINITION Sequence 3 from Patent WO0233107.
ACCESSION AX427704
VERSION AX427704.1 GI:21537816

KEYWORDS

SOURCE

Phytolacca americana (American pokeweed)
Phytolacca americana

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE

1 Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.
AUTHORS Plant cell death system
TITLE Patent: WO 0233107-A 3 25-APR-2002;
JOURNAL CAMBRIDGE ADVANCED TECH (GB)

FEATURES

Location/Qualifiers

1..792

/organism="Phytolacca americana"

/mol_type="unassigned DNA"

/db_xref="taxon:3527"

1..729

/note="Binding site for primer PS1BF"

1..3 /note="Initiation codon added via PCR primer"

/complement(436..462)

/note="Binding site for primer PS1SR"

463..492

/note="Binding site for primer PS2BF"

612 /note="Nucleotide change from published sequence"

681..686

/note="Sequence replacing removed XbaI site"

/complement(765..792)

/note="Binding site for primer PS2SR"

790..792

/note="Stop codon added via PCR primer"

ORIGIN

Alignment Scores:

Pred. No.: 2,13e-55 Length: 792
Score: 564.00 Matches: 109
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-8 (1-110) x AX427704 (1-792)

QY 2 GlyValAspSerPheProValIysThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 463 GAGGTGATTCAATTCCTGTAAAACTGAGGGCTTTTCTACTGTAGCATCCAAATG 522
QY 22 ValSerGluAlaAlaArgPheIysTyrIleGluAsnGlnValIysThrAsnPheAsnArg 41
DB 523 GTTCAGAGCGCGGATTCAGTACATAGAGAACCAAGTCAAGACTAATTTTAATAGA 582
QY 42 AlaPheTyrProAspProIysValIleAsnLeuGluGluIysTyrGlyIysIleSerGlu 61
DB 583 GCATTTCTACCTGATCCCAAGTAAATTAATTTGGAGAGAAAGTGGGCAAAATCTTGAG 642
QY 62 AlaIleHisAsnAlaIysAsnGlyAlaLeuProIysProLeuGluLeuValAspAlaIys 81
DB 643 GCATTCACAAATCCCAAGAAATGGGCTTTACCAAAACCACTTGAGCTAGTGATGCCAA 702
QY 82 GlyThrIysTyrPleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIys 101
DB 703 GTATCCAAAGTGAATGTTCTTAAAGTGAATGAATCAATGATGTGGCACTCTTAAAG 762
QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 763 TACGTTAATGAACTGTCAAGACAAC 789

RESULT 3

AX427702 945 bp DNA linear PAT 20-JUN-2002
LOCUS AX427702
DEFINITION Sequence 1 from Patent WO0233107.
ACCESSION AX427702
VERSION AX427702.1 GI:21537815

KEYWORDS

Phytolacca americana (American pokeweed)
Phytolacca americana

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE

1 Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.
AUTHORS Plant cell death system
TITLE Patent: WO 0233107-A 1 25-APR-2002;
JOURNAL CAMBRIDGE ADVANCED TECH (GB)

FEATURES

Location/Qualifiers

1..945

/organism="Phytolacca americana"

/mol_type="unassigned DNA"

/db_xref="taxon:3527"

1..724

/note="Binding site for primer PS1BF"

/complement(735..776)

/note="Binding site for primer PSXDR"

736..777

/note="Binding site for primer PSXDP"

750..759

/note="Sequence replacing removed XbaI site"

/complement(922..945)

/note="Binding site for primer PS2SR"

ORIGIN

Alignment Scores: 2,58e-55 Length: 945
Pred. No.: 564.00 Matches: 109
Score:

Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 99.1%
DB: 6
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-978-274A-8 (1-110) x AK427702 (1-945)

QY 2 GYVAlaSPSerPheProValIysThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
DB 532 GGAGTGTGATTCATCCCTGTAATAAAGCTGAGGCTTTTCTTCTGTTAGCCATCCAAAG 591
QY 22 ValSerGluAlaAlaArgPheIysTyrIleGluAsnGlnValIysThrAsnPhenArg 41
DB 592 GTTACAGAGGACGCGGATTCAGATGACATAGAGAACCAAGTCAAGCTAATTTTAATAGA 651
QY 42 AlaPheTyrProAspProIysValIleAsnLeuGluGluIysTyrGlyIysIleSerGlu 61
DB 652 GCATTCACCTCGATCCCAAGATGATTAATTTGGAGAGAGAGATGGGGCAAAATCTCTGAG 711
QY 62 AlaIleHisAsnAlaIysAsnGluValAlaLeuProIysProLeuGluLeuValAspAlaIys 81
DB 712 GCAATTCACAAATGCGCAAGATGGGGCTTTACCCAAACCACTTGAGCTAGTGCATGCCAA 771
QY 82 GlyThrIysTyrPheValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIys 101
DB 772 GTTACCAAGTGAATGATCTTGAAGTGAATCAATCGATGATGGCACTCCTTAAG 831
QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 832 TACGTTAATGCAACCTGTCAAGCAACT 858

RESULT 4
LOCUS PAPASRIP 1249 bp mRNA linear PLN 18-APR-2005
DEFINITION P. americana mRNA for pokeweed antiviral protein.
ACCESSION X98079.1 GI:1707648
VERSION X98079.1
KEYWORDS PAP-S gene; pokeweed antiviral protein (PAP); ribosome-inactivating protein.

SOURCE Phytoilaccea americana (American pokeweed)
ORGANISM Phytoilaccea americana

REFERENCE 1 Bukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE 2 Poyet, J.L. and Hoeveler, A.
AUTHORS Poyet, J.L.
TITLE cDNA cloning and expression of pokeweed antiviral protein from seeds in Escherichia coli and its inhibition of protein synthesis in vitro

JOURNAL FBS Lett. 406 (1-2), 97-100 (1997)
REFERENCE PUBMED 9109394
2 (bases 1 to 1249)

REFERENCE 3 Poyet, J.L.
AUTHORS Poyet, J.L.
TITLE Direct Submission
JOURNAL Submitted (22-MAY-1996) J.L. Poyet, Laboratoire de Biochimie-Biologie Molculaire, UFR Sciences et Techniques, 16 route de Gray, 25030 Besancon Cedex, FRANCE

REMARK FEATURES
FEATURES
source
location/qualifiers
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106..1050
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/notes="ribosome-inactivating protein type I"
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/protein_id="CAA66702.1"
/db_xref="GI:1707649"

/db_xref="GOA:P93444"
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/db_xref="UniProt/TREMBL:P93444"
/translation="MKVNLVVVTVLILAVLILAAPSTCAINTITPDAGNATINKATFEM
ESLRQADPKLKYGIPLMDPTNTPRYLVKIQGANLKITITMLRRNLLYVNGSD
PENGKRCRYHIFNDITSTERDVENTLCSSSSRVAMSINYSIPTMEKKAVNSRN
QVQGLIQLSDIDIKISGVDSFPVTEAFPLVLAIQVMSSEARFXYIENQVNTNRA
FYDPKVINLEBKWKISSEATHNMGALPKPLIYVDKGTWKVIYLRDEINRDVALL
KYVNTCCGTTTQNMFPQVITISTYINRMSNLGDLFEGP"
106..117
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178..1047
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1212..1217
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1235
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polyA_signal
polyA_site
ORIGIN

Alignment Scores:
Pred. No.: 3.5e-55 Length: 1249
Score: 564.00 Matches: 109
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatch: 0
Query Match: 99.1% Indels: 0
DB: 15 Gaps: 0

US-09-978-274A-8 (1-110) x PAPASRIP (1-1249)

QY 2 GYVAlaSPSerPheProValIysThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
DB 637 GGAGTGTGATTCATCCCTGTAATAAAGCTGAGGCTTTTCTTCTGTTAGCCATCCAAAG 696

QY 22 ValSerGluAlaAlaArgPheIysTyrIleGluAsnGlnValIysThrAsnPhenArg 41
DB 697 GTTACAGAGGACGCGGATTCAGATGACATAGAGAACCAAGTCAAGCTAATTTTAATAGA 756

QY 42 AlaPheTyrProAspProIysValIleAsnLeuGluGluIysTyrGlyIysIleSerGlu 61
DB 757 GCATTCACCTCGATCCCAAGATGATTAATTTGGAGAGAGAGTGGGGCAAAATCTCTGAG 816

QY 62 AlaIleHisAsnAlaIysAsnGluValAlaLeuProIysProLeuGluLeuValAspAlaIys 81
DB 817 GCAATTCACAAATGCGCAAGATGGGGCTTTACCCAAACCTTGAAGCTAGTGCATGCCAA 876

QY 82 GlyThrIysTyrPheValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIys 101
DB 877 GTTACCAAGTGAATGATCTTGAAGTGAATCAATCGATGATGGCACTCCTTAAG 936

QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 937 TACGTTAATGCAACCTGTCAAGCAACT 963

RESULT 5
LOCUS AB071855 786 bp DNA linear PLN 19-MAR-2002
DEFINITION Phytolacca americana paper2 gene for PAP-S2, partial cds.
ACCESSION AB071855
VERSION AB071855.1 GI:19570839
KEYWORDS Phytolacca americana (American pokeweed)
ORGANISM Phytolacca americana

REFERENCE 1 Bukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE 2 Honjo, B. and Watanabe, K.
AUTHORS Honjo, B. and Watanabe, K.
TITLE Cloning of genomic DNA encoding two types of pokeweed antiviral protein in seeds, PAP-S1 and PAP-S2, and functional comparison of their recombinant proteins with other PAP isoforms
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 786)

AUTHORS Watanabe,K. and Honjo,B.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2001) Keiichi Watanabe, Saga University,
Department of Applied Biological Sciences, Honjo-machi, Saga city,
Saga 840-8502, Japan (E-mail:watakei@cc.saga-u.ac.jp,
Tel:81-952-28-8774, Fax:81-952-28-8774)

FEATURES

source

1..786
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/protein_id="BAB86350.1"
/db_xref="GI:19570840"
/translation="INTPTDAGNSTINKYATMESHIRNAKDPKLCYIGIPMLPDTN
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KTEAPPLVAVIOWVSEARPKYIENOVKTPNPAFYDPPVIMLEEKMKISPAIHNA
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CDS

gene

ORIGIN

Alignment Scores:

Pred. No.: 7.94e-55 Length: 786
Score: 559.00 Matches: 108
Percent Similarity: 99.1% Conservative: 0
Best Local Similarity: 99.1% Mismatches: 1
Query Match: 98.2% Indels: 0
DB: 15 Gaps: 0

US-09-978-274A-8 (1-110) x AB071855 (1-786)

QY 2 GlyValAspSerPheProValIySerThcIuAlaPhePheLeuValAlaIleGlnMet 21

Db 460 GGAAGTTGATTCATTCCTCGTAAAAAATGAGAGCGCTTTTCTACCTGCTGACATCCAATG 519

QY 22 ValSerGluAlaIaAargPheIySerIleGluAsnValIySerThAspPheAsnArg 41

Db 520 GTTTCAGAGGAGCGCGATTCAAGACATAGAACCAAGTCACAGACTAATTTTATAGA 579

QY 42 AlaPheTyProAspProIyAsValIleAsnLeuGluGluIySTPGIlyIleSerGlu 61

Db 580 GCATTCTACCTGATCCCAAGTATTAATCTTGAGAGAGAGAGTGGGCAAAATCTCTGAG 639

QY 62 AlaIleHisAsnAlaIyAsnGluValAlaLeuProIyProLeuGluLeuValAspAlaIy 81

Db 640 GCAATTCACAATGCGCAAGATGGGGCTTTACCCAAACCTCTAGACCTGATGGATGCCAA 699

QY 82 GlyThrIySTPILeValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIy 101

Db 700 GGTACCAAGTGAATGTTCTTAGAGTGAATCAATCGTAGTGGCACTCTTAAG 759

QY 102 TyrValaAsnGlyThcYgeGlnThr 110

Db 760 TACGTTAATGGAACCTGTCAAGCCACT 786

RESULT 6 AX427720 1092 bp DNA linear PAT 20-JUN-2002

LOCUS AX427720

DEFINITION Sequence 19 from Patent WO0233107.

ACCESSION AX427720

VERSION AX427720.1 GI:21537829

KEYWORDS

SOURCE

ORGANISM synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE

1 Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.

TITLE Plant cell death system
JOURNAL Patent: WO 023107-A 19 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)

FEATURES

source

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PAP-6/Cystatin fusion"
1..29
/note="Binding site for primer PS18P"
681..686
/note="Modified XbaI site"
/note="complement(742..786)
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766..806
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complement(1066..1092)
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ORIGIN

Alignment Scores:

Pred. No.: 4.6e-50 Length: 1092
Score: 519.00 Matches: 101
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 91.2% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-8 (1-110) x AX427720 (1-1092)

QY 2 GlyValAspSerPheProValIySerThcIuAlaPhePheLeuValAlaIleGlnMet 21

Db 463 GGAAGTTGATTCATTCCTCGTAAAAAATGAGAGCGCTTTTCTACCTGCTGACATCCAATG 522

QY 22 ValSerGluAlaIaAargPheIySerIleGluAsnValIySerThAspPheAsnArg 41

Db 523 GTTTCAGAGGAGCGCGATTCAAGACATAGAACCAAGTCACAGACTAATTTTATAGA 582

QY 42 AlaPheTyProAspProIyAsValIleAsnLeuGluGluIySTPGIlyIleSerGlu 61

Db 583 GCATTCTACCTGATCCCAAGTATTAATCTTGAGAGAGAGAGTGGGCAAAATCTCTGAG 642

QY 62 AlaIleHisAsnAlaIyAsnGluValAlaLeuProIyProLeuGluLeuValAspAlaIy 81

Db 643 GCAATTCACAATGCGCAAGATGGGGCTTTACCCAAACCACTTGAGCTAGTGAATGCCAA 702

QY 82 GlyThrIySTPILeValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIy 101

Db 703 GGTACCAAGTGAATGTTCTTAGAGTGAATCAATCGTAGTGGCACTCTTAAG 762

QY 102 Tyr 102

Db 763 TAC 765

RESULT 7

E05033 2472 bp DNA linear PAT 29-SEP-1997

LOCUS E05033

DEFINITION DNA encoding antiviral protein.

ACCESSION E05033

VERSION E05033.1 GI:2173227

KEYWORDS

SOURCE

ORGANISM

Phytolacca americana (American pokeweed)
Phytolacca americana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE

1 (bases 1 to 2472) Katoaka,J., Habuka,N., Masuda,O., Miyano,M. and Koiwai,A.

AUTHORS

NEW PROTEIN AND GENE CAPABLE OF CODING THE SAME
TITLE Patent: JP 1993137580-A 1 01-JUN-1993;
JOURNAL

COMMENT	JAPAN TOBACCO INC	OS	Phytolacca americana	PN	JP 1993337580-A/1
PD	01-JUN-1993	PF	20-NOV-1991	JP 1991329672	
PI	KATOAKA JIRO, HABURA NORIYUKI, MASUDA OSAMU, MIYANO MASASHI,	PI	KOIMAI AKIRA		
PC	C12N15/29, C12N15/73, C12P21/02//C12N1/21, (C12P21/02, C12R1:19),	PC	(C12N1/21,		
PC	C12R1:19);	PC			
CC	strandedness: Double;	CC	topology: Linear;		
CC	hypochemical: No;	CC	anti-sense: No;		
CC	Feature is identified by similarity;	CC	Key		
FT	CAAT_signal	FT	549..552		
FT	CAAT_signal	FT	627..630		
FT	TATA_signal	FT	845..850		
FT	sig_peptide	FT	1014..1085		
FT	mat_peptide	FT	1086..1895		
FT	/product='antiviral protein'	FT	1014..1898		
FT	polya_site	FT	2130..2135.		
FEATURES	Location/Qualifiers				
SOURCE	1..2472				
ORIGIN	/organism="Phytolacca americana"				
Alignment Scores:	/mol_type="genomic DNA"				
Pred. No.:	/db_xref="taxon:3527"				
Score:	1.55e-42	Length:	2472		
Percent Similarity:	457.00	Matches:	90		
Best Local Similarity:	82.68	Conservative:	5		
Query Match:	80.38	Mismatches:	14		
DB:	6	Indels:	0		
	Gaps:		0		
US-09-978-274A-8 (1-110) x E05033 (1-2472)					
QY	2	GlyValAspSerPheProValIlyThrGluAlaPheIleLeuValAlaIleGlnMet	21		
DB	1542	GGAATGGATTCATTCACGTGAGAAAACCTGAAATCCGATTCTGTATAGTGCATCCAAATG	1601		
QY	22	ValSerGluAlaIlaArgPheIleThrIleGluAsnGlnValIlyThrAsnPheAsnArg	41		
DB	1602	GTTTCAGAGGAGGCGGGGTTCAGACACTGAAATAATCAGGTGAAGACATTAATTAATGA	1661		
QY	42	AlaPheTyrProAspProIlyValIleAsnLeuGluGlnIlySTPGLyIleSerGlu	61		
DB	1662	GCATTCACCTTAATGCAAGATCTTAACCTTGAGAGAGAGTGGGGTAAAGATCTTAACG	1721		
QY	62	AlaIleHisAsnAlaIlyAsnGlnIlyAlaLeuProIlySPProLeuGlnIlyValAspAlaIly	81		
DB	1722	GCGATTCACAAATGCGCAAGAAATGGGGCTTTAACAGCTCCTTAAGAGCTTAATAAATAAGCAAC	1781		
QY	82	GlyThrIlySTPPIleValIleLeuArgValAlaAspGluIleAsnArgAspValAlaLeuLeuIly	101		
DB	1782	GGTAGCAAGAGGAGATAGTGCAGAGATGATATCGAACCCTGATGTGGACCTCCTTAAG	1841		
QY	102	TyrValAsnGlnIlyThrCysGlnThrThr	110		
DB	1842	TATCTTAATGGACCTCGCAGGCAACT	1868		
RESULT 8					
PTCAPAP	PTCAPAP	2472 bp	DNA	linear	PLN 01-FEB-2000
LOCUS	P. americana	DNA	for alpha-PAP	(pokedweed antiviral protein),	
DEFINITION	complete cds				
ACCESSION	D10600.D90537				
VERSION	D10600.1 GI:218010				

KEYWORDS alpha-PAP: antiviral protein; pokeweed antiviral protein (PAP); ribosome-inactivating protein.

SOURCE *Phytolacca americana* (American pokeweed)

ORGANISM *Burkholderia gladii* (American pokeweed)

REFERENCE 1 (bases 1 to 2472)

AUTHORS Kataoka, J., Habuka, N., Maenaka, C., Miyano, M. and Koiwai, A.

TITLE Isolation and analysis of a genomic clone encoding a pokeweed antiviral protein

JOURNAL Plant Mol. Biol. 20 (5), 879-886 (1992)

PIRME 1281438

REFERENCE 2 (bases 1 to 2472)

AUTHORS Kataoka, J.

TITLE Direct Submission

JOURNAL Submitted (22-OCT-1991) Jiro Kataoka, Japan Tobacco Inc., Life Science Research Laboratory; 6-2 Umeagoka, Midori-ku, Yokohama, Kanagawa 227, Japan (Tel:045-972-5901, Fax:045-972-6205)

COMMENT Submitted (23-Oct-1991) to DDBJ by: Jiro Kataoka Life Science Research Laboratory Japan Tobacco Inc. 6-2 Umeagoka, Midori-ku Yokohama 227

FEATURES

source Japan Phone: 045-972-5901 Fax: 045-972-6205. Location/Qualifiers

1..2472

/organism="Phytolacca americana"

/mol_type="genomic DNA"

/db_xref="taxon:3527"

549..552

845..850

1014..1898

/codon_start=1

/product="alpha-PAP (pokeweed antiviral protein)"

/protein_id="BA001451.1"

/db_xref="GI:218011"

/translation="MKMMVVVVVMMMLSLKDPSTWAINITPDVGNATINRYATPM KSITHNOKDPTLKYCGIPMLPTNRLPKYLLVTLQDSLSKTTITLMLKRNLLYWGAD TNGSKRYHFKDISNTTERNDWTLICNPSSVGNINVDSTYPLKRVGPRGQ VQGIQILNSGIKIKYGVDSFTKTEAEFLVLAIQWSEARFXYINQVTFNRAFA YPAKAVLTLEESWGIKSTALIHNAKNGALTSPLEKNAKSGKVIARVDIEPDGLIK YNNGTCATATQASAMFPHL"

1014..1085

1086..1895

/product="alpha-PAP (pokeweed antiviral protein)"

2130..2135

ORIGIN polyA_signal

Alignment Scores:

Pred. No.: 1.55e-42

Score: 457.00

Percent Similarity: 87.2%

Best Local Similarity: 82.6%

Query Match: 80.3%

DB: 15 Gaps: 0

US-09-978-274A-8 (1-110) x PTCAPAP (1-2472)

QY 2 GIVaLaSerpPheProValIysTnTngLualAlaPhePheLeuDeuValAlaIleGlnMet 21

Db 1542 GAGGTGATTCATTCACCTGAGAAATCGAAGCCGAATTCCTGTAGTACCAATG 1601

QY 22 ValSerGluAlaAlaArgPheIysTyrIleGluAsnGlnValIysThrAsnPheAsnArg 41

Db 1602 GTTTCAGAGGACGCGGCTTCACAGTCACTPAGAAATCAAGTGAAAGACTAATTTAAATAGA 1661

QY 42 AlaPheTyrProAspProIysValIleAsnLeuGluGlnIulysTnTnIylsIleSerGlu 61

Db 1662 GCAATTCACCTTAAGCAAGTACTTAATCTGGAGAGAGATTGGGCTAGATCTTCACG 1721

Oy		62	A1A11EHBAENAlalyBaNGlYAlLeuProlySProLengluLeuValAsPaLaLyS	81
Db		1722	GCGATTACCAATGCGCAGAAAGGGGCTTTAACCACTCTCTTAGAGCTTAATAAATGCACAAC	1781
Oy		82	G1YhrytSPILeVallLeuArVaJaSpLuIleSaArGaPValAlaleuleuLyS	101
Db		1782	GCTGCAAGTGGATTCGTCTGAAGTGGAATATCATTCGAACCTGATGTGGACTCTTAAG	1841
Oy		102	TyrValaNgIyThrCyrgElNThr	110
Db		1842	TATGTATATGGACCTGCCAGCAACT	1868
Result_9				
AY547315				
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
PUBMED				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
FEATURES				
source				
mRNA				
CDS				
ORIGIN				
Alignment Scores:				
Pred. No.:				
Score:				
Percent Similarity:				
Best Local Similarity:				
Query Match:				
DB:				
US-09-978-274A-8	(1-110)	x	AY547315	(1-942)
Oy		2	G1yVala)aspSerPheBroValIyThrGuIua)aPhelLeuLeuValAlallegInwEt	21
Db		526	GGAGTATGTCATTCACTGAGAAAACCGAAGCCGAATTCCTATTGGTAGCCATACAAATG	585
Oy		22	valSerGUua)Ala)ArPheLyTyrtIlegIuaNgInValIyThrAnPheAnaNg	41
Db		586	GRATCGAGGCGCAAGATTCAAGTCAATAGAANAATCAGGTGAATACTAATTTTAAACA	645

OY		42	AAlpheYrPrCoApPProLySValIleAAsnLeGluIndUlySrTPGlYLvSiLesEgLu	61
Dd		646	GcATTCAACCTTATCCCAAGACTTAATTTCGAAGAACAATGGGGTTAAGATTTCACA	705
OY		62	AAlIeHIsEnAlALyVaSnGLyAlALeuPProLYsrProLengUlULeuVALASpAlALyE	81
Dd		706	GCAATTCAATCATGTGCCAAGAATGGAGTTTTACCMAACTCTCGAGCTTAGTGATGCCAGT	765
OY		82	GIYrhYvrSTPRileVAlleuArVaIAspGUlleAnrrAgAPValAlALEuleuLyE	101
Dd		766	GGTGCAGATGSAATNGTGTTCAGGTGAGTGAATCATAAGCTGATGACACTTTAAC	825
OY		102	TyrValasnGjYthrCYegIntHrThr	110
Dd		826	TACGTTGGTGGAGCTGTGCAGACAAC	852
RESULT 10				
AY572976		942 bp	mRNA	linear
LOCUS				PLN 05-APR-2004
DEFINITION				Phytoactase americana antiviral protein (PAV) mRNA, complete cds.
VERSION				AY572976
KEYWORDS				AY572976.1 GI:45826466
SOURCE				'
ORGANISM				Phytolacca americana (American pokeweed)
				Phytolacca americana
				Burayota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
				Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons;
				Caryophyllales; Phytolaccaceae; Phytolacca.
				1 (bases 1 to 942)
REFERENCE				Xiao,Z.A. and Jiang,Y.
AUTHORS				A gene encoding the pokeweed antivirus protein in the leaf of
TITLE				Phytolacca americana
JOURNAL				Unpublished
REFERENCES				2 (bases 1 to 942)
AUTHORS				Xiao,Z.A.
TITLE				Direct Submission
JOURNAL				Submitted (13-MAR-2004) College of Life Sciences, Beijing Normal University, No. 19 XinJiekouwai Street, Haidian District, Beijing 100875, China
FEATURES				
source				Location/Qualifiers
				1..942
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				/db_xref="taxon:3527"
				1..942
				/gene="PAV"
				1..942
				/gene="PAV"
				/codon_start=1
				/product="antiviral protein"
				/protein_id="AA577872.1"
				/translation="MKWLVVTISILIPASTFWAVNTIIYNVGSTTIISKAFELANI
				LANEKADPSLKICIGPMHPNNITPKYVLVELOSNNKTITLMIRBNLLYYMGSDPP
				EENKRKYHIENDISTGERQDVETTLCPANARSNSNIINPDRIYPLEBSAKCVKSQS
				QLGIDLSNIGIKSIGSVNFTEKTEAEFLVAIQVSSAANKFTIENGVKTNFRRAF
				PMPKIANTOETGWGKISTAIDAANGVELPKPELDVASGAKVIIVLRVDIKDVALNLN
				VGSQTYYNQNAAMPPLIMSTYYNYMVLIDLFEFGF"
ORIGIN				
Alignment Scores:				
Pred. No. :				1.19e-42
Score:				454.00
Percent Similarity:				87.2%
Best Local Similarity:				82.6%
Query Match:				79.8%
DB:				15
Gap:				0
US-09-978-274A-8 (1-110) X AY572976 (1-942)				
OY		2	GIYAALapSerPheprovalylgrhrgulaIphephelenuValAlalleglnmet	21

Db 526 GGAAGTATGTCATTCACTGAGAAAACCGAACCCGAAATTCCTATTGGTAGCCATACAAATG 585
Qy 22 ValSerGluAlaAlaArgPheLeuTyrIleGluGlnValIleThrAspPheAsnArg 41
Db 586 GTATCAGAGGCGAAGATTCAAGTACATAGAGATCAGGTAAAACTAATTTTAAACGA 645
Qy 42 AlaPheTyrProAspProLeuValIleAsnLeuGluGluTyrTPGILyLeIleSerGlu 61
Db 646 GCATTCAACCCCTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAAGATTCAACA 705
Qy 62 AlaIleHisAsnAlaIleAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLys 81
Db 706 GCAATTCATGATGCGCAAGATGAGATTTCACCAAACTCTCGAGCTAGTGATGCCAGT 765
Qy 82 GlyThrIleTyrPleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 101
Db 766 GTGCCAAGTGGATAGTGTGAGACTGATGAATCAAGCCGTGATGACTCTTAAAC 825
Qy 102 TyrValAsnGlyThrCysGlnThrThr 110
Db 826 TACGTGGTGGAGCTGCAGCAACT 852

RESULT 11

AF533515 1114 bp mRNA linear PLN 01-AUG-2005
LOCUS Phytoacca octandra anti-viral protein (pap) mRNA, partial cds.
DEFINITION
ACCESSION AF533515
VERSION AF533515.1 GI:3329822
KEYWORDS
SOURCE Phytoacca octandra
ORGANISM Phytoacca octandra
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS Lin, J.S. and McNally, K.P.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-2002) Reproductive Technologies, AgResearch
Wallaceville, Ward Street, Upper Hut, Wellington, New Zealand

FEATURES

source

1. 1114
/organism="Phytolacca octandra"
/mol_type="mRNA"
/db_xref="taxon:211655"
<1. 1114
/gene="pap"
<1. 920
/gene="pap"
/note="PAP"
/codon_start=3
/product="anti-viral protein"
/protein_id="AA010291.1"
/db_xref="GI:3329822"

gene
CDS

translation="ISVWLILAPSTMAVNTIIVNGSTTISKYTTSLDDLREANOP
NLKCYGIPMLPNTNPKYVLYVELQSNKRTITLMLRNMLYVWGYSDFPYNKCRH
IFNDISGTERODVETTLCPNPNRSVILKINIVDSRYPLIESRAGVSRQVGLQILD
SDIGKISGTVSFTKTEABFLVAIOMVSEARPKYENQKTNPNRAFPNPNVNL
EETWGIKSTAIHDANKGVLPKLEIVADSGAKMIVSVDEIKPDVALINTVSSGCTT
YNONAMPSQLIMSTYTYNMVNLGDLFEGP"

ORIGIN

Alignment Scores:

Pred. No.: 1.44e-42 Length: 1114
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conserved: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
Gaps: 0

US-09-978-274A-8 (1-110) x AF533515 (1-1114)

Qy 2 G|YValAspSerPheProValIleThrGluAlaPhePheLeuValAlaIleGlnMet 21

Db 504 GGAAGTATGTCATTCACTGAGAAAACCGAACCCGAAATTCCTACTGTAGCCATACAAATG 563
Qy 22 ValSerGluAlaAlaArgPheLeuTyrIleGluGlnValIleThrAspPheAsnArg 41
Db 584 GTATCAGAGGCGAAGATTCAAGTACATAGAGATCAGGTAAAACTAATTTTAAACGA 623
Qy 42 AlaPheTyrProAspProLeuValIleAsnLeuGluGluTyrTPGILyLeIleSerGlu 61
Db 624 GCATTCAACCCCTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAAGATTCTACA 683
Qy 62 AlaIleHisAsnAlaIleAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLys 81
Db 684 GCAATTCATGATGCGCAAGATGAGATTTCACCAAACTCTCGAAGTAGTGATGCCAGT 743
Qy 82 GlyThrIleTyrPleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 101
Db 744 GTGCCAAGTGGATAGTGTGAGACTGATGAATCAAGCCGTGATGACTCTTAAAC 803
Qy 102 TyrValAsnGlyThrCysGlnThrThr 110
Db 804 TACGTGGTGGAGCTGCAGCAACT 830

RESULT 12

PAPAP 1164 bp mRNA linear PLN 18-NOV-1991
LOCUS P. americana PAP gene for anti-viral protein.
DEFINITION
ACCESSION X55383
VERSION X55383.1 GI:20421
KEYWORDS
SOURCE Phytoacca americana (American pokeweed)
ORGANISM Phytoacca americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Phytolaccaceae; Phytolacca.

REFERENCE
AUTHORS Lin, J.S., Chen, Z.C., Antoniw, J.F. and White, R.F.
TITLE Isolation and characterization of a cDNA clone encoding the
anti-viral protein from Phytolacca americana
JOURNAL Plant Mol. Biol. 17 (4), 609-614 (1991)

1912488
2 (bases 1 to 1164)
REFERENCE
AUTHORS Antoniw, J.F.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-1990) Antoniw J.F., AFRC Inst of Arable Crops
Research, Dept. of Plant Pathology, Rothamsted Experimental
Station, Harpenden, Hert, AL5 2JQ, UK

FEATURES

1. 1164
/organism="Phytolacca americana"
/mol_type="mRNA"
/db_xref="taxon:3527"
/rlnsue_type="leaf"
/dev stage="vegetative"
1. 1164
/gene="PAP"
2. 943
/gene="PAP"
/codon_start=1
/product="anti-viral protein"
/protein_id="CA39054.1"
/db_xref="GI:20422"

gene
CDS

ORIGIN

Alignment Scores:

translation="MKSMVLVITISLWILILAPSTMAVNTIIVNGSTTISKYATPLND
LRNBAOPSLKCYGIPMLPNTNPKYVLYVELQSNKRTITLMLRNMLYVWGYSDF
ETKRCVHIFNDISGTERODVETTLCPNPNRSVILKINIVDSRYPLIESRAGVSRQV
OLGIIOLDSNIGKISGTVSFTKTEABFLVAIOMVSEARPKYENQKTNPNRAFPNPNVNL
PKNPVNLDETWKISTAIHDANKGVLPKLEIVADSGAKMIVSVDEIKPDVALINTV
VGSCCTTTNOMNMPOLIMSTYTYNMVNLGDLFEGP"

Pred. No.: 1,51e-42 Length: 1164
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
DB: 15 Gaps: 0

US-09-978-274a-8 (1-110) x PABAP (1-1164)

QY 2 GlyValAspSerPheProValIystrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 527 GGAGTATGATGATCTTCACTGAGAAACCGAAGCCGAATTCCTATTGGTAGCATACAAATG 586
QY 22 ValSerGluAlaAlaArgPheIystrIleGluBngInValIystrAenPheAsnArg 41
DB 587 GTATCAGAGGACCAAGATTCAAGTACATAGAGATCATGGTGAAGAACTTAATTTTAAACA 646
QY 42 AlaPheYrProAspProIystrValIleAsnLeuGluGluIystrPglYlserGlu 61
DB 647 GCATTCAACCCCTAATCCCAAGTACTTAATTGCAAGACATGGGGTAAAGATTTCACAA 706
QY 62 AlaIleHisAsnAlaIyAsnGluYAlaLeuProIystrProIystrGluLeuValAspAlaIy 81
DB 707 GCATTATGATGATGCAAGATGAGATTTCACCAACCTCTCGAGCTAGTGAGCCAGT 766
QY 82 GlyThrIystrPleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIy 101
DB 767 GGATCCAAAGTGAATGATGTTGAGAGATGATGATCAAGCTGATGATGACCTCTTAAC 826
QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 827 TACGTTGGTGGAGCTGTGACACAACT 853

RESULT 13

A36639 A36639 1195 bp DNA linear PAT 05-MAR-1997
LOCUS A36639
DEFINITION Sequence 1 from Patent EP0585554.
ACCESSION A36639
VERSION A36639.1 GI:2293943
KEYWORDS

SOURCE unidentified
ORGANISM unidentified

REFERENCE 1 (bases 1 to 1195)

AUTHORS Kim,M., Lee,K., Na,B., Jeong,H.S., Choi,K., Moon,Y. and Jeon,H.
TITLE Process for preparing a transgenic plant expressing phyto-lac-
cacin

JOURNAL JINRO LIMITED (KR)
PUBLISHED 1994-09-01

COMMENT Other publication JP 6078775 940322
Other publication KR 9512900 951023.
Location/Qualifiers

FEATURES

1..1195
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Alignment Scores:

Pred. No.: 1,55e-42 Length: 1195
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
DB: 6 Gaps: 0

US-09-978-274a-8 (1-110) x A36639 (1-1195)

QY 2 GlyValAspSerPheProValIystrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 558 GGAGTATGATGATCTTCACTGAGAAACCGAAGCCGAATTCCTATTGGTAGCATACAAATG 617
QY 22 ValSerGluAlaAlaArgPheIystrIleGluBngInValIystrAenPheAsnArg 41

DB 618 GTATCAGAGGACCAAGATTCAAGTACATAGAGATCAAGTGAAGAACTAATTTTACAGA 677
QY 42 AlaPheYrProAspProIystrValIleAsnLeuGluGluIystrPglYlserGlu 61
DB 678 GCATTCAACCCCTAATCCCAAGTACTTAATTGCAAGACATGGGGTAAAGATTTCACAA 737

QY 62 AlaIleHisAsnAlaIyAsnGluYAlaLeuProIystrProIystrGluLeuValAspAlaIy 81
DB 738 GCATTCAAGATGATGCAAGATGAGATTTCACCAACCTCTCGAGCTAGTGAGCCAGT 797

QY 82 GlyThrIystrPleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIy 101
DB 798 GGATCCAAAGTGAATGATGTTGAGAGATGATGAATCAAGCTGATGATGACCTCTTAAC 857

QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 858 TACGTTGGTGGAGCTGTGACACAACT 884

RESULT 14

A42103 A42103 1195 bp DNA linear PAT 05-MAR-1997
LOCUS A42103
DEFINITION Sequence 1 from Patent EP0637591.
ACCESSION A42103
VERSION A42103.1 GI:2297595
KEYWORDS

SOURCE Phyto-lacca americana (American pokeweed)

ORGANISM Phyto-lacca americana (American pokeweed)

REFERENCE 1 (bases 1 to 1195)

AUTHORS Moon,Y., Jeon,H., Choi,K., Lee,K. and Kim,M.
TITLE A novel expression vector for phyto-lacca antiviral protein

JOURNAL JINRO LIMITED (KR)
PUBLISHED 1995-08-01

COMMENT Other publication AU 662844 950914
Other publication JP 7067660 950314
Other publication CA 2102859 950103
Other publication AU 5064293 950119.
Location/Qualifiers

FEATURES

1..1195
/organism="Phyto-lacca americana"
/mol_type="unassigned DNA"
/db_xref="taxon:3527"

ORIGIN

Alignment Scores:

Pred. No.: 1,55e-42 Length: 1195
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
DB: 6 Gaps: 0

US-09-978-274a-8 (1-110) x A42103 (1-1195)

QY 2 GlyValAspSerPheProValIystrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 558 GGAGTATGATGATCTTCACTGAGAAACCGAAGCCGAATTCCTATTGGTAGCATACAAATG 617
QY 22 ValSerGluAlaAlaArgPheIystrIleGluBngInValIystrAenPheAsnArg 41
DB 618 GTATCAGAGGACCAAGATTCAAGTACATAGAGATCATGGTGAAGAACTAATTTTAAACA 677
QY 42 AlaPheYrProAspProIystrValIleAsnLeuGluGluIystrPglYlserGlu 61
DB 678 GCATTCAACCCCTAATCCCAAGTACTTAATTGCAAGACATGGGGTAAAGATTTCACAA 737
QY 62 AlaIleHisAsnAlaIyAsnGluYAlaLeuProIystrProIystrGluLeuValAspAlaIy 81
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 Db 858 TACGTTGGTGGAGCTGTCAAGCAACT 884
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RESULT 15

143835 1195 bp DNA linear PAT 07-OCT-1997
 LOCUS Sequence 1 from patent US 5633155.
 DEFINITION 143835
 ACCESSION 143835
 VERSION 143835.1 GI:2468933
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE

1 (bases 1 to 1195)
 Kim, M.-K., Lee, K.-H., Na, B.-K., Jeong, H.-S., Choi, K.-W., Moon, Y.-H.
 and Jeon, H.-S.

AUTHORS

TITLE

Expression vector for phytoelase antiviral protein and process for
 preparing transgenic plant transformed therewith
 Patent: US 5633155-A 1 27-MAY-1997;
 Location/Qualifiers

FEATURES

SOURCE

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ORIGIN

Alignment Scores:

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 Score: 454.00 Matches: 90
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 Best local Similarity: 82.6% Mismatches: 14
 Query Match: 79.8% Indels: 0
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US-09-978-274A-8 (1-110) x 143835 (1-1195)

QY 2 G|YValAspSerPheProValIySThrGluAlaPhePheLeuValAlaIleGlnMet 21
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 Db 558 GGAAGTATGTCATTCACCTGAGAAACCGAACCGAATTCCTATTGTGTAGCCATCAATG 617
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 QY 22 ValSerGluAlaIleArgPheIySThrIleGluAsnGluValIySThrAsnPheAsnArg 41
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 Db 618 GTATCAGAGGCGACGAATTCAGTACATAGAAATCGGTGAAACTAATTTTAACGA 677
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 Db 738 GCATTATCATATGCAAGAAATGAGTTTACCAACCTCTCGAGCTAGTGATGCCAGT 797
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 QY 82 G|YThrIySTP|IleValIleuArgValAspGluIleAsnArgAspValAlaIleuLeuLys 101
 |||||
 Db 798 GGTGCCAAGTGTGATGTGTGAGTGTGATGAAATCAAGCTGTAGTGAACCTTTAAAC 857
 |||||
 QY 102 TyrValaengIyThrCyGlnThrThr 110
 |||||
 Db 858 TACGTTGGTGGAGCTGTCAAGCAACT 884
 |||||

Search completed: April 9, 2006, 07:31:30
 Job time : 2513.43 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 9, 2006, 00:56:13 ; Search time 291.938 Seconds
(without alignments)
2511.204 Million cell updates/sec

Title: US-09-978-274A-8
Perfect score: 569
Sequence: 1 MGVDSPFKTEAPFLVAIQ.....DEINRDVALLKYNGTCQT 110

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Searched: 4996997 segs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	569	100.0	333	6	AAD42718 Pokewe
2	564	99.1	792	6	AAD42716 Pokewe
3	564	99.1	945	6	AAD42715 Pokewe
4	519	91.2	1092	6	AAD42729 Pokewe

5	457	80.3	2472	2	AAQ43967	Aa43967 Pokewe
6	454	79.8	1195	2	AAQ56672	Aa56672 Sequence
7	454	79.8	1195	2	AAQ81457	Aa81457 Phyto
8	454	79.8	1378	6	AAD42739	Aad42739 Pokewe
9	454	79.8	1379	3	AAZ45197	Aa45197 Wild-type
10	454	79.8	1379	3	AAZ59221	Aa59221 Variant p
11	454	79.8	1379	6	AAZ59220	Aa59220 Pokewe
12	454	79.8	1379	6	AAD42738	Aad42738 Pokewe
13	454	79.8	1379	10	AD105787	Ad105787 DNA encod
14	452	79.4	1378	12	ADG76061	Adg76061 American
15	451	79.3	1379	4	AAQ87929	Aa87929 P. americ
16	449	78.9	1164	11	ADM74751	Adm74751 HIV-1 inh
17	449	78.9	1164	11	ADM74765	Adm74765 HIV-1 inh
18	439	77.2	882	2	AAT99556	Aat99556 Phyto
19	437	76.8	2369	2	AAT99557	Aat99557 Phyto
20	437	76.8	2369	2	ABA96543	Ab96543 Phyto
21	399	70.1	918	2	AAQ64893	Aa64893 Antiviral
22	399	70.1	918	2	AAT04782	Aat04782 DNA pJMC2
23	213.5	37.5	813	2	AAQ48031	Aa48031 Encodes p
24	213.5	37.5	813	2	AAQ42222	Aa42222 Encodes p
25	213.5	37.5	813	2	AAQ75532	Aa75532 Type I r1
26	213.5	37.5	813	2	AAQ73242	Aa73242 Type I r1
27	213.5	37.5	1176	6	ABSS56021	Ab56021 CDNA enco
28	212.5	37.3	783	2	AAQ38041	Aa38041 Synthetic
29	212.5	37.3	955	2	AAT86336	Aat86336 BPI pepti
30	212.5	37.3	1003	2	AAT86341	Aat86341 BPI pepti
31	212.5	37.3	1072	2	AAT86332	Aat86332 BPI pepti
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34	200	35.1	934	6	AAZ45198	Aa45198 Wild-type
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37	200	35.1	1518	14	ABEB8724	Ab8724 scFv23-ge
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40	195.5	34.4	1813	5	AAI79929	Aai79929 Mutant pr
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ALIGNMENTS

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ID	AAD42718 standard; DNA; 333 BP.
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AC	AAD42718;
XX	
DT	15-NOV-2002 (first entry)
XX	
DE	Pokewe
XX	
KW	Neurotic effect; transgenic plant; antiviral protein; pokewe; gene;
XX	
OS	PAP-Sbeta; ds.
XX	
XX	Phytolacca americana.
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PH	Key
FT	CDS
FT	Location/Qualifiers
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FT	/*tag= a
FT	/product= "PAP-Sbeta protein"
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PN	WO200233107-A2.
XX	
PD	25-APR-2002.
XX	
PF	15-OCT-2001; 2001MO-GB004593.
XX	
PR	14-OCT-2000; 2000GB-00025217.
XX	

(ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
PA Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX WPI; 2002-489891/52.
XX P-PSDB; AAE25921.
PT Inducing necrotic effect in specific cells of plant by transforming plant
PT with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX which acts in response to application of specific stimulus to plant.
XX
XX Claim 4; Page 78; 87pp; English.
CC The invention relates to a method of inducing a necrotic effect in
CC specific cells of a plant. The method involves transforming the plant
CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
CC in response to the application of a specific stimulus to the plant so as
CC to facilitate expression of the pokeweed antiviral protein in specific
CC cells of the plant. The method is useful for inducing a necrotic effect
CC in specific cells of a plant. The present sequence is pokeweed PAP-Sbeta
CC protein encoding DNA
XX
XX SQ Sequence 333 BP; 106 A; 63 C; 76 G; 88 T; 0 U; 0 Other;
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XX Alignment Scores:
XX Pred. No.: 2,41e-67 Length: 333
XX Score: 569.00 Matches: 110
XX Percent Similarity: 100.0% Conservative: 0
XX Best Local Similarity: 100.0% Mismatches: 0
XX Query Match: 100.0% Indels: 0
XX DB: 6 Gaps: 0
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XX 1 ATGGAGATTATTCATTCCTCGTAAATACTGAGGCTTTTCTACGTGATGCAATCCAA 60
XX
XX Db 21 MetValSerGluAlaAlaArgPheLeuTyrlleGluAsnGlnValIyThrAsnPhaAsn 40
XX 61 ATGGTTTCAGAGGCGAGCGCATTCAGATACATAGAGAACCAAGTCAAGACTAATTTTAT 120
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XX QY 41 ArgAlaPheTyrrProAspProLyValIleAsnLeuGluGluTyrrPglYlyIleSer 60
XX 121 AGAGCATTCATCCCTGTATCCCAAGATATTAATTTGAGGAGAGAGTGGGGCAAAATCTCT 180
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XX QY 61 GluAlaIleHisAsnAlaLyAsnG1ValaLeuProLySProLeuGluLeuValAspAla 80
XX 181 GAGGCATTCACAAATGCCAAGAAATGGGGCTTTACCCAAACCACTTGAGCTAGTGATGCC 240
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XX Db 81 LyseG1YThrIySTP1IleValIleuArgValaSpGluIleAsnArgAspValAlaLeu 100
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XX QY 101 LyseTyValaAsnG1YThrCySgInThr 110
XX 301 AAGTACGTTATGAGAACCTGTCAAGACAACT 330
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XX RESULT 2
XX AAD42716
XX ID AAD42716 standard; DNA; 792 BP.
XX
XX AC AAD42716;
XX
XX DT 15-NOV-2002 (first entry)
XX
XX DE Pokeweed mature PAP-S protein encoding DNA.
XX
XX KS Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
XX gene; ds.
XX
XX OS Phytolacca americana.

XX
XX FH Key Location/Qualifiers
XX FT CDS 1..792
XX FT /tag= a
XX FT /product= "Mature PAP-S protein"
XX FT primer_bind /tag= b
XX FT 1..29
XX FT /bound_molecy= "Primer PS1BF"
XX FT complement(436..462)
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XX FT /bound_molecy= "Primer PS1SR"
XX FT 463..492
XX FT primer_bind /tag= d
XX FT /bound_molecy= "Primer PS2BF"
XX FT 681..686
XX FT misc_feature /tag= e
XX FT /note= "Sequence replacing removed XbaI site"
XX FT complement(765..792)
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XX PN W0200233107-A2.
XX
XX PD 25-APR-2002.
XX
XX PE 15-OCT-2001; 2001WO-GB004593.
XX
XX PF 14-OCT-2000; 2000GB-00025217.
XX
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX PA Thomas CJR, Mcpherson MJ, Atkinson HJ, Neelam A;
XX WPI; 2002-489891/52.
XX P-PSDB; AAE25919.
XX
XX DR Inducing necrotic effect in specific cells of plant by transforming plant
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX which acts in response to application of specific stimulus to plant.
XX
XX PS Claim 2; Page 76; 87pp; English.
XX
XX PS The invention relates to a method of inducing a necrotic effect in
XX specific cells of a plant. The method involves transforming the plant
XX with chimeric gene(s) which encodes a pokeweed antiviral protein namely
XX PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
XX in response to the application of a specific stimulus to the plant so as
XX to facilitate expression of the pokeweed antiviral protein in specific
XX cells of the plant. The method is useful for inducing a necrotic effect
XX in specific cells of a plant. The present sequence is pokeweed mature PAP
XX -S protein encoding DNA
XX
XX SQ Sequence 792 BP; 268 A; 161 C; 151 G; 212 T; 0 U; 0 Other;
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XX Alignment Scores:
XX Pred. No.: 3.6e-66 Length: 792
XX Score: 564.00 Matches: 109
XX Percent Similarity: 100.0% Conservative: 0
XX Best Local Similarity: 100.0% Mismatches: 0
XX Query Match: 99.1% Indels: 0
XX DB: 6 Gaps: 0
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XX 463 GAGTGTATTCATTCCTCGTAAATACTGAGGCTTTTCTACGTGATGCAATCCAAATG 522
XX
XX QY 22 ValSerGluAlaAlaArgPheLeuTyrlleGluAsnGlnValIyThrAsnPhaAsnArg 41
XX 523 GTTCAGAGCGAGCGCATTCAGATACATAGAGAACCAAGTCAAGACTAATTTTAAATGA 582
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XX Db 42 AlaPheTyrrProAspProLyValIleAsnLeuGluGluTyrrPglYlyIleSerGlu 61


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Qy 62 AAlaIleHsAsnAlaLyAsnGlyAlaLeuProLySProLeuGluLeuValAspAlaLyS 81
Db 643 GCATTTCACATGCCAGAAATCGGGCTTTACCCCAACCACTTGACCTAGTGATGCCAAA 702
Qy 82 GlyThrLySTrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLyS 101
Db 703 GGTACCAAGTGATGATGTTCTTAGAGTGATGAAATCAATCGATGTGGCACTCTTAG 762
Qy 102 TyrValAsnGlyThrCysGlnThrThr 110
Db 763 TACGTTAATGGAACCTGTCAGACAACT 789
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ID AAD42715 standard; DNA; 945 BP.
AC AAD42715;
XX 15-NOV-2002 (first entry)
DE Pokeweed pro-PAP-S protein encoding DNA.
KM Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
KW gene; ds.
OS Phytolacca americana.
XX
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FT /complement(735..776)
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XX W0200233107-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001MO-GB004593.
XX
XX 14-OCT-2000; 2000GB-00025217.
XX
XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
XX Thomas CJR, Mcpherson MJ, Atkinson HU, Neelam A;
XX P-PSDB; AAE25918.
XX
XX MPI; 2002-489891/52.
XX P-PSDB; AAE25918.
XX
XX Inducing necrotic effect in specific cells of plant by transforming plant
XX with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX which acts in response to application of specific stimulus to plant.
XX
XX Claim 24; Page 73-74; 87pp; English.
XX
XX The invention relates to a method of inducing a necrotic effect in
XX specific cells of a plant. The method involves transforming the plant
```

```
CC with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC PAP', PAP1 and PAP-S, where the gene(s) comprises a promoter which acts
CC in response to the application of a specific stimulus to the plant so as
CC to facilitate expression of the pokeweed antiviral protein in specific
CC cells of the plant. The method is useful for inducing a necrotic effect
CC in specific cells of a plant. The present sequence is pokeweed pro-PAP-S
CC protein encoding DNA
XX
SQ Sequence 945 BP; 307 A; 187 C; 180 G; 271 T; 0 U; 0 Other;
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Alignment Scores:
Pred. No.: 4,55e-66 Length: 945
Score: 564.00 Matches: 109
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: 6 Gaps: 0
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Qy 22 ValSerGluAlaAlaArgPheLySTrpIleGluAsnGlnValLySThrAsnPheAsnArg 41
Db 592 GTTTCAGAGCGCAGGCCAATTCAGTACATAGAGAACCAAGTCAGACTAATTTAATAGA 651
Qy 42 AlaPheTyrProAspProLySValIleAsnLeuGluLySTrpGlyLySileSerGlu 61
Db 652 GCATTTCACCTGATCCCAAGTAAATTTTGGAGAGAAAGTGGCGCAAAATCTCTGAG 711
Qy 62 AAlaIleHsAsnAlaLyAsnGlyAlaLeuProLySProLeuGluLeuValAspAlaLyS 81
Db 712 GCATTTCACCTGATCCCAAGTAAATTTTGGAGAGAAAGTGGCGCAAAATCTCTGAG 771
Qy 82 GlyThrLySTrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLyS 101
Db 772 GGTACCAAGTGATGATGTTCTTAGAGTGATGAAATCAATCGATGTGGCACTCTTAG 831
Qy 102 TyrValAsnGlyThrCysGlnThrThr 110
Db 832 TACGTTAATGGAACCTGTCAGACAACT 858
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AAD42729
ID AAD42729 standard; DNA; 1092 BP.
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XX AAD42729;
XX
XX 29-AUG-2003 (revised)
XX 15-NOV-2002 (first entry)
XX
XX Pokeweed PAP-S/TEV PCS/rice cystatin delta D86 fusion DNA.
XX
XX Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP-S;
XX chimeric; rice; cystatin delta D86; Nta protease cleavage site; PCS; ds.
XX
XX Phytolacca americana.
XX
XX Oryza sativa.
XX
XX Tobacco; Etch virus.
XX
XX Chimeric.
XX
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PP	15-OCT-2001; 2001WO-GB0045593.	
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PR	14-OCT-2000; 2000GB-00025217.	
XX		
PA	(ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.	
PI	Thomas CJR, Mcpherson MJ, Atkinson HU, Neelam A;	
XX		
XX	WPI; 2002-489891/52.	
DR		
XX		
PT	Inducing necrotic effect in specific cells of plant by transforming plant	
PT	with a chimeric gene encoding pokeweed antiviral protein and a promoter	
PT	which acts in response to application of specific stimulus to plant.	
XX		
PS	Disclosure; Page 83; 87pp; English.	
XX		
CC	The invention relates to a method of inducing a necrotic effect in	
CC	specific cells of a plant. The method involves transforming the plant	
CC	with chimeric gene(s) which encodes a pokeweed antiviral protein namely	
CC	PAP ¹ , PAPII and PAP-S, where the gene(s) comprises a promoter which acts	
CC	in response to the application of a specific stimulus to the plant so as	
CC	to facilitate expression of the pokeweed antiviral protein in specific	
CC	cells of the plant. The method is useful for inducing a necrotic effect	
CC	in specific cells of a plant. The present sequence is a fusion DNA. This	
CC	sequence comprises pokeweed pro-PAP-S DNA, rice cyatatin delta D6 DNA	
CC	and Tobacco Etch virus (TEV) N1A protease cleavage site (PCS). (Updated	
CC	on 29-AUG-2003 to standardise OS field)	
XX		
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	Score: 519.00 Matches: 101	
	Percent Similarity: 100.0% Conservative: 0	
	Best Local Similarity: 100.0% Mismatches: 0	
	Query Match: 91.2% Indels: 0	
	DB: 6 Gaps: 0	
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OY	22 ValserglunlaalaacgphelystryilgluhanglnVallystrhaenpheasnarg 41	
Db	523 GTTTCAGAAGGAGCGGCATTCACTACATGAAGAACCAAGTCAGACTAATTTAAATAGA 582	
OY	42 AlapheTyProasPProLySValIleAsnLeuglunlubystrpgilyslieserglu 61	
Db	583 GCATTTCACCTGATGCCAAGTAATTACTTGAGAGAGAAAGTGGGCAAAATCTCGAG 642	
OY	62 AlaIleHisenalalyseagilyAlaleupProLySProLeugluleuValaspaIalye 81	
Db	643 GCATTTCACAATGCCAAGAAATGGGGCTTTTACCNAACCACTTGAGCTAGTGGAGCCAAA 702	
OY	82 GlyThrlystrpIleValleuArgValAsngluilleamrAgspValAlaleuleuLyS 101	
Db	703 GGTGACCAAGTGAGTAATGTTTAGAGTGATATAATCAATCGTANAGTGCGACTCTTAG 766	

QY	102	Tyr 102
DB	763	TAC 765
RESULT 5		
ID	AAQ43967	standard; DNA; 2472 BP.
AC	AAQ43967	
XX	AAQ43967	
XX	09-NOV-1993	(first entry)
DT		
XX		
DE		Pokeweed antiviral protein.
XX		
KM		Pokeroot; ricin; protein synthesis inhibitor; cancer;
KW		polymerase chain reaction; PCR; 88.
XX		
OS		Phytolacca americana.
XX		
PH	Key	Location/Qualifiers
FT	CAAT_signal	549..552
FT		/*tag= a
FT	CAAT_signal	627..630
FT		/*tag= b
FT	TATA_signal	845..850
FT		/*tag= c
FT	sig_peptide	1014..1085
FT		/*tag= d
FT	mat_peptide	1086..1868
FT		/*tag= e
FT		/label= PAP
FT	polyA_signal	2130..2135
FT		/*tag= f
XX		
PN	JP05137580-A.	
PD	01-JUN-1993.	
XX		
PF	20-NOV-1991;	91JP-00329672.
XX		
PR	20-NOV-1991;	91JP-00329672.
XX		
PA	(NISR) JAPAN TOBACCO INC.	
XX		
DR	WPI; 1993-211306/26.	
XX	P-PSDB; AAR37345.	
PT		
PT	New pokeweed antiviral protein (PAP) with similar activity to ricin -	
PT	used to treat cancer and as an agricultural chemical.	
XX		
PS	Claim 2; Page 11-13; 14pp; Japanese.	
XX		
CC	PAP has a similar activity to ricin, i.e. inhibits protein synthesis. The	
CC	protein may be obtained all year round by recombinant DNA techniques. PAP	
CC	can be used partic. against cancer and as an agricultural chemical. Total	
CC	cdna, is extracted from the seeds, leaves and roots of pokeweed and used	
CC	to prepare cDNA using PCR. The resultant cDNA is used to prepare two DNA	
CC	fractions, which are introduced into a cloning vector EMBL3 and then into	
CC	host E.coli PLK-17 (P2) to produce PAP	
XX		
SQ	Sequence 2472 BP; 864 A; 375 C; 463 G; 770 T; 0 U; 0 Other;	
Alignment Scores:		
Pred. No.:	4.61e-51	Length: 2472
Score:	457.00	Matches: 90
Percent Similarity:	87.2%	Conservative: 5
Best Local Similarity:	82.6%	Mismatches: 14
Query Match:	80.3%	Indels: 0
DB:	2	Gaps: 0
US-09-978-274A-8 (1-110) x AAQ43967 (1-2472)		

```
QY      2 GlyValAspSerPheProValIleAsnLeuGluValAlaIleGlnMet 21
Db      1542 GGAGTGGATTCATTCACCTGAGAACTGAAAGCCGAATTCCTGTAGTCCATCCAAATG 1601
QY      22 ValSerGluAlaAlaArgPheIleTyrIleGluAsnGlnValIleThrAsnPheAsnArg 41
Db      1602 GTTACAGGGCAGCGGGTTCAAGTACATAGAAAATCAGGTGAACCTAAATTTATATGA 1661
QY      42 AlaPheTyrProAspProIleValIleAsnLeuGluIleTyrGlyIleSerGlu 61
Db      1662 GCATTCTACCTTAAGCCCAAGTACTTAACCTTGAGGAGAGTGGGGTAAAGTCTCTACG 1721
QY      62 AlaIleHisAsnAlaIleAsnGlyAlaLeuProIleProLeuGluLeuValAspAlaIle 81
Db      1722 GCGATTCAACAATGCGCAAGATGGGGCTTTAACCACTCTAGAGCTAAAAAATGCAAC 1781
QY      82 GlyThrIleTyrPheIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuIys 101
Db      1782 GGTGCGAAGTGATGATGCTGAGAGTGAATATCGAACCTGATGTGGACTCCTTAAG 1841
QY      102 TyrValAsnGlyThrCysGlnThrThr 110
Db      1842 TATGTATATGGGACCTGCCAGCAACT 1868
```

RESULT 6
AA056672
ID AA056672 standard; cDNA; 1195 BP.

XX AA056672;

XX 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 04-SEP-1994 (first entry)

XX Sequence of Phytolacca antiviral protein (PAP) cDNA.

XX Antiviral protein; PAP; virus-resistance; transgenic plant; ss.

XX Phytolacca americana; L.

XX Key Location/Qualifiers
FT 33..974
FT /*tag= a

XX EP585554-A1.

XX 09-MAR-1994.

XX 30-JUN-1993; 93EP-00110445.

XX 16-AUG-1992; 92KR-00014895.

XX (JINR-) JIN RO LTD.

XX Kim M, Lee K, Na B, Jeong H, Choi K, Moon Y, Jeon H;

XX WPI; 1994-076002/10.

XX P-PSDB; AAR48548.

XX Expression vector for phytolacca antiviral protein - used for producing
XX transgenic virus-resistant plants and for producing the antiviral agent.

XX Disclousure; Fig 1; 15pp; English.

XX To isolate PAP gene, total cellular mRNA was purified from leaves of
XX Phytolacca americana L. obd. in Korea. A cDNA library was constructed.
XX The PAP gene was selected by immunoscreening employing anti-PAP antibody.

XX A deletion mutant was prepd. from the isolated PAP gene, and the DNA
XX sequence of the PAP genome was determined. (Updated on 25-MAR-2003 to
XX correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 1195 BP; 420 A; 201 C; 230 G; 344 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,47e-51 Length: 1195
Score: 454.00 Matches: 90
Percent Simlarity: 87.2% Conservative: 5
Best Local Simlarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
DB: 2 Gaps: 0

US-09-978-274A-8 (1-110) x AA056672 (1-1195)

```
QY      2 GlyValAspSerPheProValIleAsnLeuGluValAlaIleGlnMet 21
Db      558 GGAGTGGATTCATTCACCTGAGAACTGAAAGCCGAATTCCTGTAGTCCATCCAAATG 617
QY      22 ValSerGluAlaAlaArgPheIleTyrIleGluAsnGlnValIleThrAsnPheAsnArg 41
Db      618 GTTACAGGGCAGCGGGTTCAAGTACATAGAAAATCAGGTGAACCTAAATTTATATGA 677
QY      42 AlaPheTyrProAspProIleValIleAsnLeuGluIleTyrGlyIleSerGlu 61
Db      678 GCATTCTACCTTAAGCCCAAGTACTTAACCTTGAGGAGAGATGGGGTAAAGTCTCTACG 737
QY      62 AlaIleHisAsnAlaIleAsnGlyAlaLeuProIleProLeuGluLeuValAspAlaIle 81
Db      738 GCAATTCATGATGCGCAAGATGGAGTATTACCCAAACCTCTGAGCTAGTGATGCCAGT 797
QY      82 GlyThrIleTyrPheIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuIys 101
Db      798 GGTGCGAAGTGATGATGCTGAGAGTGAATATCGAACCTGATGTGGACTCCTTAAG 857
QY      102 TyrValAsnGlyThrCysGlnThrThr 110
Db      858 TACGTGTGGTGGAGCTGTCAGCAACT 884
```

RESULT 7
AA081457
ID AA081457 standard; cDNA; 1195 BP.

XX AA081457;

XX 16-OCT-2003 (revised)
DT 25-AUG-1995 (first entry)

XX Phytolacca antiviral protein (PAP) cDNA.

XX Antiviral protein; vector pMJ12; KCCM 10037; PAP; ss.

XX Phytolacca americana; L.

XX AU9350642-A.

XX 19-JAN-1995.

XX 11-NOV-1993; 93AU-00050642.

XX 02-JUL-1993; 93KR-00012360.

XX (JINR-) JIN RO LTD.

XX Lee K, Choi K, Jeon H, Kim M, Moon Y;

XX WPI; 1995-067516/10.

XX Recombinant vector for producing Phytolacca anti-viral protein - and
XX transformed E. coli useful for making immunconjugates for treatment of
XX AIDS.

XX Claim 1; Fig 1; 27pp; English.

XX Total cellular mRNA from leaves of P. americana was used to produce a
XX cDNA library and this screened with anti-PAP antibody raised in rabbits
XX against purified PAP. Inserts were isolated from 2 clones and sequenced
XX to identify a 1195 ORF (AA081457) that encodes a 313 AA PAP including a

FT CDS 225..1166
FT /*tag= a
FT /product= "PAP"
FT /note= "Pokeweed antiviral protein"
PN W0960843-A1.
XX 02-DEC-1999.
XX 21-MAY-1999; 99WO-US011301.
XX 22-MAY-1998; 98US-0086374P.
XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX Turner NE, Wang P;
XX WPI: 2000-062555/05.
XX P-PSDB; MAY58025.
XX
XX New antiviral DNA useful for generating transgenic plants resistant to
XX viruses and/or fungi.
XX
XX Example; Page 4-5; 43pp; English.
XX
XX This is the Pokeweed antiviral protein (PAP) nucleotide sequence. PAP is
XX a type I ribosome-inhibiting protein (RIP) found in the cell walls of
XX Phytolacca americana (pokeweed). It is a single polypeptide chain that
XX catalytically removes a specific adenine residue from a highly conserved
XX stem-loop structure in the 28S rRNA of eukaryotic ribosomes. The pokeweed
XX antiviral protein II (PAP II) protein confers antiviral and or antifungal
XX activities to plants. A DNA molecule encoding a PAP II protein with an
XX intact catalytic active site amino acid residue (8172) is useful for
XX generating transgenic plants. PAP II DNA is useful for generating
XX transgenic plants (especially cereal crops) through transforming a
XX protoplast or introducing the DNA directly into a plant part prior to
XX regeneration. Cells and seeds which exhibit anti-viral and/or anti-fungal
XX activity thus have increased resistance to viruses and/or fungi. Viruses
XX include potato virus X (PVX), cucumber mosaic virus (CMV), and tomato
XX yellow leaf curl virus, and fungi include Pythium, Phytophthora,
XX Sclerotinia and Aspergillus. PAP II proteins also confer resistance to
XX other plants pests including insects, bacteria and nematodes. PAP II DNA
XX is also useful for identifying a PAP II protein having reduced
XX cytotoxicity. PAP II has a reduced cytotoxicity compared to PAP, so
XX unlike PAP transgenic plants which are stunted and sterile, PAP II
XX transgenic plants have a normal and fertile phenotype
XX
XX Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 5, 41e-51 Length: 1379
XX Score: 454.00 Matches: 90
XX Percent Similarity: 87.2% Conservative: 5
XX Best Local Similarity: 82.6% Mismatches: 14
XX Query Match: 79.8% Indels: 0
XX Gaps: 0
XX
XX US-09-978-274A-8 (1-110) x AAZ45197 (1-1379)
QY 2 G1VVA1aspserpHeProvallysrThrGluAlaPheHeuLeuValAla1leG1mEt 21
Db 750 GGAAGTATGTCATTCATCTGAGAAACCGAAGCCGAATTCCTATTGGTAGCATCAATG 809
QY 22 ValSerGluAlaAlaArgPheLystrTllegluAsnGlnVallysrThranPheAsnArg 41
Db 810 GTATCAGAGGACGAGAAATTCAGATCATAGAGATCAGGGAATCTAATTTTAAACAGA 869
QY 42 AlaPheTyrrProaspProlysValIleAsnLeuGluGlyLysTrpGlyLysIleSerGlu 61
Db 870 GCATTCACCTTATCCCAAGTACTTAAATTTCGAAGAGACATGGGTAAGATTTCACA 929
QY 62 AlaIleHisAsnAlaLysAsnGlyAlaLeuProlysTrpLeuGluLeuValAlaPalaLys 81

Db 930 GCAATTCATGATGCCAAGATGAGTTTACCAACCTCTCGAGTAGTGCAGTCCAGT 989
QY 82 G1YThrLystrPrlleValleuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 101
Db 990 GTGCCAAGTGGATGATGTTGATGATGATGAATAATCAAGCTGATGTAGCACTCTTAAAC 1049
QY 102 TyrValAsnGlyThrCysGlnThr-Thr 110
Db 1050 TACGTTGGTGGAGACTGTCAAGCAACT 1076
XX
XX RESULT 10
XX AAZ59221
XX ID AAZ59221 standard; cDNA; 1379 BP.
XX AC AAZ59221;
XX XX
XX 20-APR-2000 (first entry)
XX DE
XX Variant pokeweed antiviral protein spring leaf form coding sequence.
XX KW Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
XX resistance; potato virus X; potato virus Y; potato leaf roll virus;
XX tuber; ss.
XX KM
XX Phytolacca americana.
XX OS
XX US6015940-A.
XX PN 18-JAN-2000.
XX XX
XX 07-APR-1992; 92US-00865169.
XX PF
XX 07-APR-1992; 92US-00865169.
XX PR
XX (MONS) MONSANTO CO.
XX PA
XX KanlewsKI WK, Turner NE, Lodge JK;
XX PI
XX WPI: 2000-126326/11.
XX DR
XX Production of transgenic potato plants or tubers expressing pokeweed
XX antiviral protein which are resistant to potato virus X or Y.
XX FT
XX Claim 7; Fig 5; 30pp; English.
XX PS
XX This is the coding sequence for a variant spring leaf form of the
XX pokeweed antiviral protein (PAP') which is used to generate transgenic
XX potato plants. PAP' is able to confer resistance to infection by potato
XX virus X (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in
XX the potato plant or tuber expressing PAP'. PAP' varies from PAP
XX (AAZ59220) by mutations L20R and Y49H
XX CC
XX
XX Sequence 1379 BP; 489 A; 234 C; 269 G; 387 T; 0 U; 0 Other;
XX SQ
XX
XX Alignment Scores:
XX Pred. No.: 5, 41e-51 Length: 1379
XX Score: 454.00 Matches: 90
XX Percent Similarity: 87.2% Conservative: 5
XX Best Local Similarity: 82.6% Mismatches: 14
XX Query Match: 79.8% Indels: 0
XX Gaps: 0
XX
XX US-09-978-274A-8 (1-110) x AAZ59221 (1-1379)
QY 2 G1VVA1aspserpHeProvallysrThrGluAlaPheHeuLeuValAla1leG1mEt 21
Db 750 GGAAGTATGTCATTCATCTGAGAAACCGAAGCCGAATTCCTATTGGTAGCATCAATG 809
QY 22 ValSerGluAlaAlaArgPheLystrTllegluAsnGlnVallysrThranPheAsnArg 41
Db 810 GTATCAGAGGACGAGAAATTCAGATCATAGAGATCAGGGAATCTAATTTTAAACAGA 869
QY 42 AlaPheTyrrProaspProlysValIleAsnLeuGluGlyLysTrpGlyLysIleSerGlu 61

```
Db      870 GCATTACACCTTAATCCCAAGTACTTAATTGCAAGACATGGGTAAGATTCAACA 929
Qy      62 AAlIhIshAaAAlaYsAaNgIyAlaLeuProLySProlEuGluEuVaIaPaAlaYs 81
Db      930 GCATTACATGATCCCAAGATGAGTTTATCCCAACTCTCGAGCTAGTGCAGT 989
Qy      82 GLyThLySTrPlIeVAlleuAArgVaIaSPGluIlIeAaAArgAaPValaIaLeuLeuYs 101
Db      990 GGTGCCAAGTGAGTAGTGTGAGAGTGATGAATCAAGCTGATGACACTCTTAAC 1049
Qy      102 TyrVaIaAaNgIyThrCySGInThrThr 110
Db      1050 TACGTTGCTGGAGCTGTCAACACT 1076

RESULT 11
AAZ59220
ID      AAZ59220 standard; cDNA; 1379 BP.
XX
AC      AAZ59220;
XX
DT      20-APR-2000 (first entry)
XX
DE      Pokeweed antiviral protein coding sequence spring leaf form.
XX
KW      Pokeweed antiviral protein spring leaf form; PAP; transgenic plant;
KM      resistance; potato virus X; potato virus Y; potato leaf roll virus;
KW      tuber; 89.
XX
OS      Phytolacca americana.
XX
PN      US6015940-A.
XX
PD      18-JAN-2000.
XX
PF      07-APR-1992; 92US-00865169.
XX
PR      07-APR-1992; 92US-00865169.
XX
PA      (MONS ) MONSANTO CO.
XX
PI      KanlewsKI WK, Turner NE, Lodge JK;
XX
DR      WPI; 2000-126326/11.
XX
PT      Production of transgenic potato plants or tubers expressing pokeweed
XX      antiviral protein which are resistant to potato virus X or Y.
XX
PS      Claim 6; Fig 4; 30pp; English.
XX
CC      This is the coding sequence for the spring leaf form of the pokeweed
CC      antiviral protein (PAP) which is used to generate transgenic potato
CC      plants. PAP is able to confer resistance to infection by potato virus X
CC      (PVX) or potato virus Y (PVY) or potato leaf roll virus (PLRV) in the
CC      potato plant or tuber expressing PAP
XX
SQ      Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      5,41e-51      Length:      1379
Score:          454.00      Matches:      90
Percent Similarity: 87.2%      Conservative: 5
Best Local Similarity: 82.6%      Mismatches: 14
Query Match:    79.8%      Indels:      0
DB:             3      Gaps:      0

US-09-978-274a-8 (1-110) x AAZ59220 (1-1379)
Qy      2 GLyValaSPSerPheProVallySThrGluAlaPheLeuLeuValaIaIleGlnMet 21
Db      750 GGAGTGATGTCATTCACAGAAACCGAAGCCGAATTCCTATGTGTAGCCATCAAAATG 809
Qy      22 ValSerGluAlaAlaArgPheLeuTyrlIeGluAaNgInVallySThrAaPheAaAArg 41
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Db      810 GTATGAGGCGCAAGATTCAAGTACATAGAAATCAGGTGAATACTAATTTAACAG 869
Qy      42 AAlPheTyRProAaSProlYsValIlIeAaAeGluGluLySTrPlYsIlIeSArgLu 61
Db      870 GCATTACACCTTAATCCCAAGTACTTAATTGCAAGACATGGGTAAGATTCAACA 929
Qy      62 AAlIhIshAaAAlaYsAaNgIyAlaLeuProLySProlEuGluEuVaIaPaAlaYs 81
Db      930 GCATTACATGATCCCAAGATGAGTTTATCCCAACTCTCGAGCTAGTGCAGT 989
Qy      82 GLyThLySTrPlIeVAlleuAArgVaIaSPGluIlIeAaAArgAaPValaIaLeuLeuYs 101
Db      990 GGTGCCAAGTGAGTAGTGTGAGAGTGATGAATCAAGCTGATGACACTCTTAAC 1049
Qy      102 TyrVaIaAaNgIyThrCySGInThrThr 110
Db      1050 TACGTTGCTGGAGCTGTCAACACT 1076

RESULT 12
AAD42738
ID      AAD42738 standard; DNA; 1379 BP.
XX
AC      AAD42738;
XX
DT      15-NOV-2002 (first entry)
XX
DE      Pokeweed PAP' DNA #1.
XX
KW      Necrotic effect; transgenic plant; antiviral protein; pokeweed; PAP'; da.
XX
OS      Phytolacca americana.
XX
PN      WO200233107-A2.
XX
PD      25-APR-2002.
XX
PF      15-OCT-2001; 2001WO-GB004593.
XX
PR      14-OCT-2000; 2000GB-00025217.
XX
PA      (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
PI      Thomas CJR, Mcpherson MJ, Atkinson HD, Neelam A;
XX
DR      WPI; 2002-489891/52.
XX
PT      Inducing necrotic effect in specific cells of plant by transforming plant
XX      with a chimeric gene encoding pokeweed antiviral protein and a promoter
XX      which acts in response to application of specific stimulus to plant.
XX
PS      Claim 5; Page 86; 87pp; English.
XX
CC      The invention relates to a method of inducing a necrotic effect in
CC      specific cells of a plant. The method involves transforming the plant
CC      with chimeric gene(s) which encodes a pokeweed antiviral protein namely
CC      PAP', PAPII and PAP-S, where the gene(s) comprises a promoter which acts
CC      in response to the application of a specific stimulus to the plant so as
CC      to facilitate expression of the pokeweed antiviral protein in specific
CC      cells of the plant. The method is useful for inducing a necrotic effect
CC      in specific cells of a plant. The present sequence is pokeweed PAP' DNA
XX
SQ      Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      5,41e-51      Length:      1379
Score:          454.00      Matches:      90
Percent Similarity: 87.2%      Conservative: 5
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Best Local Similarity: 82.6% Mismatches: 14
 Query Match: 79.8% Indels: 0
 DB: 6 Gaps: 0

US-09-978-274A-8 (1-110) x AD42738 (1-1379)

QY 2 GlyValAspSerPheProValIyThrGluAlaPhePheLeuValAlaIleGlnMet 21
 DB 750 GGAGTGAATGTCATTCATGAGAAACCGAAGCCGAATTCCTATTGTTGTCATACAAATG 809
 QY 22 ValSerGluAlaAlaArgPheIleGluGlnValIyThrAsnPheAsnArg 41
 DB 810 GTATCAGAGCGCAGCAAGATTCAGATACATAGAGATCGGTGAAAACCTAATTTTAACGA 869
 QY 42 AlaPheTyProAspProLyValIleAsnLeuGluGluIySTPGIlyIleSerGlu 61
 DB 870 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGACATCGGGTAAAGTTTCAACA 929
 QY 62 AlaIleHisAsnAlaIyAsnGluValAlaLeuProLySProLeuGluLeuValAspAlaIyS 81
 DB 930 GCAATTCATGATGTCAGAAATGAGATGTTTACCCAAACCTCTGAGCTAGTGATGCCAGT 989
 QY 82 GlyThrIySTPILleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuIyS 101
 DB 990 GGTGCCAAGTGATAGTGTGAGAGTGATGAATCAAGCTGATGTAGCACTTTAAAC 1049
 QY 102 TyrValAsnGlyThrCysGlnThrThr 110
 DB 1050 TACGTTGGTGGAGCTGTCAACAACT 1076
 RESULT 13
 AD105787
 ID AD105787 standard; DNA; 1379 BP.
 AC AD105787;
 DT 15-APR-2004 (first entry)
 DE DNA encoding the wild-type pokeweed antiviral protein.
 XX
 KW ribosome depurination; antifungal; antiviral; virucide; anti-HIV;
 KW cytoskeletal; immunosuppressive; agricultural biotechnology; pharmaceuticals;
 KW medicine; cancer; AIDS; viral infection; autoimmune disease; T-cell;
 KW B-cell; transgenic; plant; wild-type; pokeweed antiviral protein; gene;
 KW de.
 XX
 OS Phytolacca americana.
 XX
 FH Key Location/Qualifiers
 FT CDS 225..1166
 FT /*tag=a
 FT /product="wild-type pokeweed antiviral protein"
 XX
 PN W0200262952-A2.
 XX 15-AUG-2002.
 PD
 XX 01-FEB-2002; 2002WO-US002792.
 PF
 XX 02-FEB-2001; 2001US-0266396P.
 PR
 XX (RUTP) UNIV RUTGERS STATE NEW JERSEY.
 XX
 PA Turner NB, Hudak KA, Parikh B;
 XX
 PI WPI; 2003-156656/15.
 DR P-PSDB; AD105788.
 XX
 XX New Pokeweed Antiviral Protein (PAP) mutant that is less toxic than wild-
 PT type PAP, useful in agricultural biotechnology or in the fields of
 PT pharmaceuticals and medicine, e.g. treating cancer, AIDS, viral infection
 PT or autoimmune disease.
 XX

PS Disclosure; SEQ ID NO 1; 51bp; English.

CC The invention relates to a novel pokeweed antiviral protein (PAP) mutant
 CC that is less toxic than wild-type PAP and exhibits ribosome depurination
 CC activity, where the mutant is a central domain mutant or N-terminal
 CC domain mutant. The PAP mutants have the following activities: antifungal,
 CC antiviral, virucide, anti-HIV, cytoskeletal and immunosuppressive. The PAP
 CC mutants are useful in agricultural biotechnology as well as in the fields
 CC of pharmaceuticals and medicine. The PAP mutants and methods are useful in
 CC treating mammals with cancer, AIDS, viral infection or autoimmune
 CC diseases associated with proliferations of unwanted T-cells or B-cells.
 CC The transgenic plants are useful in exhibiting resistance to a broad
 CC spectrum of plant pests e.g. viruses and fungi. This polynucleotide
 CC sequence represents the DNA encoding the wild-type pokeweed antiviral
 CC protein of the invention.

SEQ Sequence 1379 BP; 488 A; 233 C; 269 G; 389 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5,41e-51	Length:	1379
Score:	454.00	Matches:	90
Percent Similarity:	87.2%	Conservative:	5
Best Local Similarity:	82.6%	Mismatches:	14
Query Match:	79.8%	Indels:	0
DB:	10	Gaps:	0

US-09-978-274A-8 (1-110) x AD105787 (1-1379)

QY 2 GlyValAspSerPheProValIyThrGluAlaPhePheLeuValAlaIleGlnMet 21
 DB 750 GGAGTGAATGTCATTCATGAGAAACCGAAGCCGAATTCCTATTGTTGTCATACAAATG 809
 QY 22 ValSerGluAlaAlaArgPheIleGluGlnValIyThrAsnPheAsnArg 41
 DB 810 GTATCAGAGCGCAGCAAGATTCAGATACATAGAGATCGGTGAAAACCTAATTTTAACGA 869
 QY 42 AlaPheTyProAspProLyValIleAsnLeuGluGluIySTPGIlyIleSerGlu 61
 DB 870 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGACATCGGGTAAAGTTTCAACA 929
 QY 62 AlaIleHisAsnAlaIyAsnGluValAlaLeuProLySProLeuGluLeuValAspAlaIyS 81
 DB 930 GCAATTCATGATGTCAGAAATGAGATGTTTACCCAAACCTCTGAGCTAGTGATGCCAGT 989
 QY 82 GlyThrIySTPILleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuIyS 101
 DB 990 GGTGCCAAGTGATAGTGTGAGAGTGATGAATCAAGCTGATGTAGCACTTTAAAC 1049
 QY 102 TyrValAsnGlyThrCysGlnThrThr 110
 DB 1050 TACGTTGGTGGAGCTGTCAACAACT 1076
 RESULT 14
 ADG76061
 ID ADG76061 standard; DNA; 1378 BP.
 AC ADG76061;
 DT 11-MAR-2004 (first entry)
 DE American pokeweed antiviral protein (PAP) DNA Seqd 1.
 XX
 KW gene; ds; pokeweed antiviral protein; PAP; HIV-1; anti-HIV; antiviral;
 KW nucleoside analogue inhibitor; viral protease inhibitor; viral infection;
 KW american pokeweed; retroviral.
 XX
 OS Phytolacca americana.
 XX
 PN W02003106479-A2.
 XX
 PD 24-DEC-2003.
 XX
 PF 17-JUN-2003; 2003WO-US019141.

```

XX 17-JUN-2002; 2002US-0389649P.
XX
XX (PARK-) PARKER HUGHES INST.
XX
XX Uckun FM;
XX
XX WPI; 2004-082156/08.
XX P-PSDB; ADG76064.
XX
XX Novel modified pokeweed antiviral protein useful for inhibiting viral
XX replication, for inducing depurination of viral RNA, or for treating
XX viral infection in subject.
XX
XX Example 2; SEQ ID NO 1; 62pp; English.
XX
XX This invention relates to novel modified pokeweed antiviral proteins
XX (PAPs). Specifically, it refers to modifications relative to wild-type
XX PAP that confer increased activity towards viral RNA, particularly
XX retroviral RNA such as HIV-1 and drug resistant HIV-1. Furthermore,
XX modified PAP also exhibits decreased activity towards ribosomal RNA
XX relative to wild-type PAP. The present invention describes a molecular
XX model of PAP-HIV RNA interactions that have been used for the rational
XX redesign of PAP mutants with potent anti-HIV activity, where
XX modifications have been introduced in regions other than the active site.
XX Accordingly, these mutants represent antiviral agents that can work as
XX nucleoside analogue inhibitors of reverse transcriptase, as well as viral
XX protease inhibitors that can be used for treating viral infections. As
XX such, they are useful for inhibiting viral replication and for
XX depurinating viral RNA. This polynucleotide sequence is the DNA encoding
XX the wild type american pokeweed antiviral protein (PAP) of the invention.
XX
XX
XX Sequence 1378 BP; 487 A; 234 C; 268 G; 389 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 1.01e-50 Length: 1378
XX Score: 452.00 Matches: 90
XX Percent Similarity: 87.2% Conservative: 5
XX Best Local Similarity: 82.6% Mismatches: 14
XX Query Match: 79.4% Indels: 0
XX DB: 12 Gaps: 0
XX
XX US-09-978-274A-8 (1-110) x ADG76061 (1-1378)
XX
XX 2 GlyValAspSerPheProValIleThrGluAlaPheLeuLeuValAlaIleGlnMet 21
XX |||||
XX 749 GGAAGTATGTCATTCACCTGAGAAAACCGAACCCGAATTCCTATTGTGATGCAATG 808
XX
XX 22 ValSerGluAlaIleAspGlyPheIleGluAlaGlnValIleThrAsnPheAsnArg 41
XX |||||
XX 809 GTATCAGAGGACGACAGATTCAGTACATAGAGATCGGTGAAACTAATTTTAAACGA 868
XX
XX 42 AlaPheTyrProAspProIleValIleAsnLeuGluIleTyrGlyIleSerGlu 61
XX |||||
XX 869 GCATTCACCCCTATATCCCAAGTAACTTAATTCGAAGACATGGGGTAATATTCAACA 928
XX
XX 62 AlilIleHisAsnAlaIleAsnGlyAlaLeuProIleGluIleValAspAlaIle 81
XX |||||
XX 929 GCATTCATATGATGCCAAGATGAGTTTACCCAACTCTCGAGCTAGTGGATGCCAGT 988
XX
XX 82 GlyThrIleTyrIleValIleLeuArgValAspGluIleAsnArgValAlaLeuLeu 101
XX |||||
XX 989 GGTGCCAAGTGAATAGTGTGAGATGATGAATCAAGCTGATGTAGCACTCTTAAC 1048
XX
XX 102 TyrValAsnGlyTyrGlnThrThr 110
XX |||||
XX 1049 TACGTGTCTGGAGCTGTCAACAAC 1075
XX
XX
XX RESULT 15
XX AAC87929
XX ID AAC87929 standard; DNA; 1379 BP.
XX
XX AAC87929;

```

```

XX 06-MAR-2001 (first entry)
XX
XX P. americana pokeweed antiviral protein encoding DNA SEQ ID NO:1.
XX
XX PhytoIacca americana; pokeweed; pokeweed antiviral protein; PAP; cancer;
XX biotherapeutic; fusion protein; immunocjugate; mutant; cytostatic;
XX anti-HIV; human immunodeficiency virus; AIDS; leukaemia; lymphoma;
XX brain tumour; neuroblastoma; soft tissue sarcoma; osteosarcoma; B6.
XX
XX PhytoIacca americana.
XX
XX Key Location/Qualifiers
XX CDS 225..1166
XX FT /*tag= a
XX FT /product= "pokeweed antiviral protein (PAP)"
XX
XX US6146628-A.
XX
XX 14-NOV-2000.
XX
XX 11-JUL-1995; 95US-00501253.
XX
XX 11-JUL-1995; 95US-00501253.
XX
XX (MINU ) UNIV MINNESOTA & RUTGERS.
XX (UTNE-) UNIV STATE NEW JERSEY.
XX
XX Uckun FM, Turner NE;
XX
XX WPI; 2001-040422/05.
XX P-PSDB; AAB36500.
XX
XX Immunocjugates useful for treating cancer and acquired immunodeficiency
XX syndrome, comprises mutant pokeweed anti-viral protein and a targeting
XX moiety that binds a cell surface receptor.
XX
XX Disclosure; Col 47-50; 32pp; English.
XX
XX The present invention describes a fusion protein or an immunocjugate
XX (1), comprising mutant Pokeweed Anti-viral Protein (PAP) having an amino
XX acid substitution at residue 75, 97 or 176 of native PAP and a targeting
XX moiety that binds a cell surface receptor. (1) can have cytosstatic and
XX anti-HIV activities, and is an inhibitor of cellular RNA or protein
XX synthesis. (1) is useful for treating AIDS and cancers including
XX leukaemia, lymphoma, a brain tumour, neuroblastoma, osteosarcoma, soft
XX tissue sarcoma, breast, prostate, ovarian, testicular, melanoma, lung, or
XX colon cancer. Immunocjugates prepared using PAP mutants exhibit an
XX improved therapeutic index over immunocjugates containing either wild-
XX type PAP or variant PAP. The present sequence encodes the wild-type PAP,
XX which is given in the exemplification of the present invention
XX
XX
XX Sequence 1379 BP; 488 A; 234 C; 268 G; 389 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 1.37e-50 Length: 1379
XX Score: 451.00 Matches: 89
XX Percent Similarity: 87.2% Conservative: 6
XX Best Local Similarity: 81.7% Mismatches: 14
XX Query Match: 79.3% Indels: 0
XX DB: 4 Gaps: 0
XX
XX US-09-978-274A-8 (1-110) x AAC87929 (1-1379)
XX
XX 2 GlyValAspSerPheProValIleThrGluAlaPheLeuLeuValAlaIleGlnMet 21
XX |||||
XX 750 GGAAGTATGTCATTCACCTGAGAAAACCGAACCCGAATTCCTATTGTGATGCAATG 809
XX
XX 22 ValSerGluAlaIleAspGlyPheIleGluAlaGlnValIleThrAsnPheAsnArg 41
XX |||||
XX 810 GTATCAGAGGACGACAGATTCAGTACATAGAGATCGGTGAAACTAATTTTAAACGA 869
XX
XX 42 AlaPheTyrProAspProIleValIleAsnLeuGluIleTyrGlyIleSerGlu 61
XX |||||

```



```

Db      870 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGAGACATGGGTAAAGATTCAACA 929
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Db      930 GCAATTCAATGATGCCAAGATGAGATTTCACCAACCTCTGAGCTAGTGAATGCCAGT 989
Qy      82 GLyThrLySTPILeValIeUArgValaSpGIuIleasnaArgaSpValaIaIeUleUlyS 101
Db      990 GGTGCCAAGTGAATGATGTGAGAGTGAATCAAGCTGATGTAGCACTTTAAAC 1049
Qy      102 TyrValaenGIyThrCyasGIuThr 110
Db      1050 TACGTTGGTGGAGCTGTCAAGCAACT 1076

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 Job time : 295.938 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 9, 2006, 01:41:02 ; Search time 1999.23 Seconds
(without alignments)
2574.284 Million cell updates/sec

Title: US-09-978-274A-8
Perfect score: 569
Sequence: 1 MGVDSPFVKTAEPLVAIQ.....DEINRDVALLKYNGTCQT 110

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-UNITS=b1ts -START=1 -END=1 -MATRIX=bloum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=00 -THR SCORE=pcc -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=sbse07
-USER=US09978274 @CEN_1_1 9564 @runat_07042006_173034_28424 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -TSPELACK=100 -LONGLOG -DEV TIMEOUT=120
-MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

BST:
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsa1:*
10: gb_gsa2:*
11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	226	39.7	816	2	BE035038 MM02A01 M
C 2	226	39.7	993	2	BE035039 MM02A03 M
3	213.5	37.5	649	6	CA838757 MCT020B02
4	213.5	37.5	649	6	CA839330 MCT020B02
5	213.5	37.5	661	6	CA835532 MCT020B02
6	213.5	37.5	671	6	CA839511 MCT020B04
7	213.5	37.5	689	6	CA833333 MCT020B04

8	213.5	37.5	689	6	CA833383	CA833383 MCS021F04
9	200.5	35.2	639	6	CA835855	CA835855 MCS004G12
10	197	34.6	1033	7	BE035541	BE035541 MP01B07 M
11	157	27.6	829	7	CN782289	CN782289 EST00385
12	151	26.5	405	8	T24255	T24255 CRE1345 1am
13	140.5	24.7	1021	2	BE036639	BE036639 MP03B03 M
14	130	22.8	1038	2	BE033546	BE033546 MF03A09 M
15	121	21.3	267	1	AA856221	AA856221 L30-24273
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17	115.5	20.3	837	1	AM053634	AM053634 L30-1401T
18	115	20.2	649	7	CN948289	CN948289 020805A5B
19	112	19.7	1094	4	AY105813	AY105813 Zea mays
20	111	19.5	639	2	BE037217	BE037217 MP18B02 M
21	110	19.3	591	6	CA091595	CA091595 SCRTAM08
22	108	19.0	642	9	CC751502	CC751502 ZMBE013
23	107	18.8	299	2	BF704840	BF704840 FMI_52_B1
24	107	18.8	513	2	BF585775	BF585775 FMI_24_D0
25	107	18.8	587	2	BF704654	BF704654 FMI_49_G1
26	107	18.8	617	6	CA078731	CA078731 SCRTAM101
27	106	18.6	654	6	CA244111	CA244111 SCOGFL408
28	104	18.3	420	6	CP227009	CP227009 IH149 BUB
29	104	18.3	563	6	CA246414	CA246414 SCEZPL509
30	104	18.3	646	6	CA187396	CA187396 SCUTST309
31	104	18.3	719	6	CA206790	CA206790 SCACSB112
32	104	18.3	742	6	CA084039	CA084039 SCBPAM205
33	104	18.3	816	7	CO121195	CO121195 GR_Eb02E
34	103	18.1	641	6	CA077373	CA077373 SCOSAM103
35	103	18.1	628	6	CA184471	CA184471 SCRLST316
36	103	18.1	649	6	CA083619	CA083619 SCBPAM201
37	103	18.1	677	6	CA174183	CA174183 SCJFST100
38	103	18.1	698	6	CA221929	CA221929 SCGSLF403
39	103	18.1	759	6	CA074628	CA074628 SCEZAM108
40	102	17.9	653	6	CA260173	CA260173 SCRLRT303
41	102	17.9	680	6	CA198271	CA198271 SCCCF1300
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ALIGNMENTS

RESULT 1
LOCUS BE035038/c 816 bp mRNA linear EST 07-JUN-2000
DEFINITION MM02A01 M Mesembryanthemum crystallinum cDNA 5' similar to
ACCESSION BE035038
VERSION BE035038.1 GI:8330047
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
REFERENCE Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
Ferreira, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu

FEATURES
source
1..816
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/cell_type="epidermal bladder cells"

/dev_stage="12 weeks old"
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XhoI; Plants stressed 6 weeks in 500mM NaCl"

ORIGIN

Alignment Scores:

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Score:	226.00	Matches:	49
Percent Similarity:	64.7%	Conservative:	17
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Query Match:	39.7%	Indels:	8
DB:	2	Gaps:	2

US-09-978-274A-8 (1-110) x BE035038 (1-816)

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Qy 29 LyeTyrlleGluAengInVal---LyeThrAsnPhaAsnArgAlaPheTyProAspPro 47
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Db 522 CATTAATTCGAGACTAAGTGCCGGAAGTGCGTCAATGTTGTTCAAACTCCGATCCG 463
Qy 48 LyeValIleAsnLeuGluGluLysTyProGlyLysIleSerGluAlaIleHisAsnAlaLys 67
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|||
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Qy 81 LysGlyThyrLysTyrlleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeu 100
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Db 342 GATGTAACACAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 283
Qy 101 LyeTyTyr 102
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Db 282 AAGTTC 277

RESULT 2

BE035039/c 993 bp mRNA linear EST 07-JUN-2000
LOCUS M002A03 MM Mesembryanthemum crystallinum cDNA 5' similar to
DEFINITION anti-viral protein, mRNA sequence.

ACCESSION

BE035039
BE035039.1 GI:8330048

VERSION

EST.

KEYWORDS

Meesembryanthemum crystallinum (common iceplant)

ORGANISM

Meesembryanthemum crystallinum

REFERENCE

1 (bases 1 to 993)

AUTHORS

Bohner, H.J., Borchert, C., Brazille, S., Brooke, J., Eaton, M.,
Ferreira, H., Kawaeski, S., McCollough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.

TITLE

Functional Genomics of Plant Stress Tolerance

JOURNAL

Unpublished (2000)

COMMENT

Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: chm@u.arizona.edu
Insert Length: 1 Std Error: 0.00.

FEATURES

1..993
location/Qualifiers

/organism="Meesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/cell_type="epidermal bladder cells"
/dev_stage="12 weeks old"

/clone_1lb="MM"
/note="Vector: Bluescript SK+; Site_1: EcoRI; Site_2:
XhoI; Plants stressed 6 weeks in 500mM NaCl"

ORIGIN

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Best Local Similarity:	48.0%	Mismatches:	28
Query Match:	39.7%	Indels:	8
DB:	2	Gaps:	2

US-09-978-274A-8 (1-110) x BE035039 (1-993)

Qy 9 LyeThrgluAlaPheLeuLeuValAlaIleGlnMetValSerGluAlaIleAaArgPhe 28
|||
Db 583 AAACTCGAGGCCAAATCTTACTGATGTCCTCCAGTGTTCAGAGCAGCAGCGGTTCC 524
Qy 29 LyeTyrlleGluAengInVal---LyeThrAsnPhaAsnArgAlaPheTyProAspPro 47
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Db 523 CATTAATTCGAGACTAAGTGCCGGAAGTGCGTCAATGTTGTTCAAACTCCGATCCG 464
Qy 48 LyeValIleAsnLeuGluGluLysTyProGlyLysIleSerGluAlaIleHisAsnAlaLys 67
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Db 463 AAAGTGAATTAATCTTGAGAACCACTGGGGAAGATTCGAGTGAATTCATTAAGTCACTT 404
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|||
Db 403 ACGTCGAACACCTGCTAATTTGACGAACATTTCCCTCGGATTAATCAATCAATGCT 344
Qy 81 LysGlyThyrLysTyrlleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeu 100
|||
Db 343 GATGTAACACAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 284
Qy 101 LyeTyTyr 102
|||
Db 283 AAGTTC 278

RESULT 3

CA838757 649 bp mRNA linear EST 12-DEC-2002
LOCUS M07020B02.167445 Ice plant Lambda Uni-Zap XR expression library, 5
days 0.5 M NaCl treatment, Grasshopper acid metabolism, phase IV
(5:30 PM). Mesembryanthemum crystallinum cDNA clone M07020B02 5,
mRNA sequence.

ACCESSION

CA838757
CA838757.1 GI:2656522

VERSION

EST.

KEYWORDS

Meesembryanthemum crystallinum (common iceplant)

ORGANISM

Meesembryanthemum crystallinum

REFERENCE

1 (bases 1 to 649)

AUTHORS

Cushman, J.C.

TITLE

An expressed sequence tag database for the common ice plant.

JOURNAL

Unpublished (1997)

COMMENT

Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

FEATURES

1..993
location/Qualifiers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 020 row: B column: 02
Seq primer: T3 20mer
High quality sequence stop: 649.
location/Qualifiers

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/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT020B02"
/tissue_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:

Pred. No.:	2.16e-18	Length:	649
Score:	213.50	Matches:	50
Percent Similarity:	60.6%	Conservative:	16
Best Local Similarity:	45.9%	Mismatches:	34
Query Match:	37.5%	Indels:	9
DB:	6	Gaps:	3

US-09-978-274a-8 (1-110) x CA8393757 (1-649)

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Db 166 GGTAAAGCATCGACAGTCAGAGAAATGAGGCCAAATTCCTTGCTGATCCCATACAGATG 225
QY 22 ValSerGluAlaAlaArgPheLeuTyrlleGluAsnGlnValIleThrAsnPhe----- 39
Db 226 GTTCTGAGAGCAGCAGGTTCAAGTATATGAGTAAAGTAAACCAAGTGCCTTAGAT 285
QY 40 AsnArgAlaPheTyrrProAspProIleValIleAsnLeuGlnGluIleTyrlle 59
Db 286 TATGAATGCTCTTAACCGACCCGAAATGCTGCTTTGGAGACCAATTTGGGGAGATT 345
QY 60 SerGluAlaIleHisAsnAlaIleAsnGlnValAlaLeuPro-----Lys 73
Db 346 TCGCAGAGATTCATGAGAGTCT---GGGGCGAAACCTGCTGTGATGAATCTTCACT 402
QY 74 ProLeuGluLeuValAlaPheValysGlyThrIleTyrlleValIleuArgValAspGluIle 93
Db 403 CCGATTCCGTTAAAGAAACCAATGGTATCCATGACGCGTGAATAGTTGACACATATT 462
QY 94 AsnArgAspValAlaLeuLeuLeuTyrr 102
Db 463 AGACCTGAATAATGGGATATCTCAAGTTC 489

RESULT 4
CA839330 649 bp mRNA linear EST 12-DEC-2002
LOCUS MCT026C11.1171755 Ice plant Lambda Uni-Zap XR expression library, 5
days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
(5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT026C11.5,
mRNA sequence.

ACCESSION
VERSION CA839330.1 GI:26567095
KEYWORDS
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum

REFERENCE
AUTHORS Mesembryanthemum crystallinum
TITLE Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Astroceae; Mesembryanthemum.
1 (bases 1 to 649)
Cushman, J.C.

JOURNAL
COMMENT An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada

MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 026 row: C column: 11
Seq primer: T3 20mer
High quality sequence stop: 649.

FEATURES

SOURCE

1. 649

/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
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/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase IV (5:30 PM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:

Pred. No.:	2.16e-18	Length:	649
Score:	213.50	Matches:	50
Percent Similarity:	60.6%	Conservative:	16
Best Local Similarity:	45.9%	Mismatches:	34
Query Match:	37.5%	Indels:	9
DB:	6	Gaps:	3

US-09-978-274a-8 (1-110) x CA839330 (1-649)

QY 2 G1YValAspSerPheProValIleThrGluAlaPhePheLeuValAlaIleGluMet 21
Db 166 GGTAAAGCATCGACAGTCAGAGAAATGAGGCCAAATTCCTTGCTGATCCCATACAGATG 225
QY 22 ValSerGluAlaAlaArgPheLeuTyrlleGluAsnGlnValIleThrAsnPhe----- 39
Db 226 GTTCTGAGAGCAGCAGGTTCAAGTATATGAGTAAAGTAAACCAAGTGCCTTAGAT 285
QY 40 AsnArgAlaPheTyrrProAspProIleValIleAsnLeuGlnGluIleTyrlle 59
Db 286 TATGAATGCTCTTAACCGACCCGAAATGCTGCTTTGGAGACCAATTTGGGGAGATT 345
QY 60 SerGluAlaIleHisAsnAlaIleAsnGlnValAlaLeuPro-----Lys 73
Db 346 TCGCAGAGATTCATGAGAGTCT---GGGGCGAAACCTGCTGTGATGAATCTTCACT 402
QY 74 ProLeuGluLeuValAlaPheValysGlyThrIleTyrlleValIleuArgValAspGluIle 93
Db 403 CCGATTCCGTTAAAGAAACCAATGGTATCCATGACGCGTGAATAGTTGACACATATT 462
QY 94 AsnArgAspValAlaLeuLeuLeuTyrr 102
Db 463 AGACCTGAATAATGGGATATCTCAAGTTC 489

RESULT 5
CA835532 661 bp mRNA linear EST 12-DEC-2002
LOCUS MCS038A11.160572 Ice plant Lambda Uni-Zap XR expression library, 5
days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2
AM). Mesembryanthemum crystallinum cDNA clone MCS038A11.5, mRNA
sequence.

ACCESSION
VERSION CA835532
KEYWORDS
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
1 (bases 1 to 661)
Cushman, J.C.

REFERENCE
TITLE
An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum

JOURNAL
COMMENT
Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 038 row: A column: 11
Seq primer: T3 20mer
High quality sequence stop: 661.
Location/Qualifiers
1. .661

FEATURES
source
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCS038A11"
/rbase_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase I (2 AM) "
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Library construction was performed
according to Stratagene's recommended protocol for the
Lambda UnizapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:
Pred. No.: 2,22e-18 Length: 661
Score: 213.50 Matches: 50
Percent Similarity: 60.6% Conservative: 16
Best Local Similarity: 45.9% Mismatches: 34
Query Match: 37.5% Indels: 9
DB: Gaps: 3

US-09-978-274A-8 (1-110) x CA835532 (1-661)

QY 2 G|YValAspSerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
DB 177 GGTAAAGCATCGACAGTCAAGAAATGAGCCAAATCTTGCTGATGCGCATACAGATG 236
QY 22 ValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPh----- 39
DB 237 GTTCTGAAGCAGCAGGTTCAAGTATTTAGAGTAAAGTAAAGCAAAAGCGCTTAGAT 296
QY 40 AsnArgAlaPheTyrProAspProLysValIleAsnLeuGluGluLysTyrGlyLysIle 59
DB 297 TATGAATGCTTCTTAACCGACCGCAAAATGCTGCTTTGGAGACCAATTTGGGGGAAGATT 356
QY 60 SerGluAlaIleHisAsnAlaLysAsnGlyAlaLeuPro-----Lys 73
DB 357 TCGCAGGAGATTCAAGAGAGTGCCT--GGGGGAAACCTGCTGTATGAATCTTTACACT 413
QY 74 ProLeuGluLeuValAlaAspAlaLysGlyThrLysTyrIleValIleLeuArgValAspGluIle 93
DB 414 CCGATTCGCTTTAAAGAAACCAATGATCATCATGAGAGGATGAATAGGTTGACACTATT 473
QY 94 AsnArgAspValAlaLeuLeuLysTyr 102
DB 474 AGACCTGAATCGGGATCACTCAAGTTTC 500

RESULT 6

CA839511
LOCUS
DEFINITION
CA839511 671 bp mRNA linear EST 12-DEC-2002
MCT028D04 172117 Ice plant Lambda Uni-Zap XR expression library, 5
days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV
(5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT028D04 5,
mRNA sequence.

ACCESSION
VERSION
CA839511
GI:26567276

KEYWORDS
SOURCE
ORGANISM
Mesembryanthemum crystallinum (common iceplant)

REFERENCE
AUTHORS
TITLE
An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum

JOURNAL
COMMENT
Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 028 row: D column: 04
Seq primer: T3 20mer
High quality sequence stop: 671.
Location/Qualifiers
1. .671

FEATURES
source
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCT028D04"
/rbase_type="leaf"
/dev_stage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase IV (5:30 PM) "
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Library construction was performed
according to Stratagene's recommended protocol for the
Lambda UnizapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:
Pred. No.: 2,26e-18 Length: 671
Score: 213.50 Matches: 50
Percent Similarity: 60.6% Conservative: 16
Best Local Similarity: 45.9% Mismatches: 34
Query Match: 37.5% Indels: 9
DB: Gaps: 3

US-09-978-274A-8 (1-110) x CA839511 (1-671)

QY 2 G|YValAspSerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
DB 166 GGTAAAGCATCGACAGTCAAGAAATGAGCCAAATCTTGCTGATGCGCATACAGATG 225
QY 22 ValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPh----- 39
DB 226 GTTCTGAAGCAGCAGGTTCAAGTATTTAGAGTAAAGTAAAGCAAAAGCGCTTAGAT 285
QY 40 AsnArgAlaPheTyrProAspProLysValIleAsnLeuGluGluLysTyrGlyLysIle 59
DB 286 TATGAATGCTTCTTAACCGACCGCAAAATGCTGCTTTGGAGACCAATTTGGGGGAAGATT 345
QY 60 SerGluAlaIleHisAsnAlaLysAsnGlyAlaLeuPro-----Lys 73

Db 346 TCGCAGAGATTGATGAGTGTCT---GGGGCGAAACCTGCTGTATGATCTTTACCT 402
 Qy 74 ProleugluLeuValaAspAlaIysGlyThrIysTrpIleValaIleuArgValaAspGluIle 93
 Db 403 CGGATTCGCTTTAAAGAAACCAATATGATATCATGATGACGGTGAATGAAGTTGACACTATT 462
 Qy 94 AsnArgAspValaIalaLeuLeuIysTyr 102
 Db 463 AGACCTGAATGGGATGACTCAAGTTTC 489
 RESULT 7
 CA833333
 LOCUS
 DEFINITION MCS021A09.151944 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS021A09.5, mRNA sequence.
 ACCESSION CA833333
 VERSION CA833333.1 GI:26561098
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)
 ORGANISM Mesembryanthemum crystallinum
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
 REFERENCE 1 (bases 1 to 689)
 AUTHORS Cushman, J.C.
 TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
 JOURNAL Unpublished (1997)
 COMMENT Contact: Cushman JC
 Department of Biochemistry
 University of Nevada
 MS200, Reno, NV 89557-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu
 PCR PRIMERS
 FORWARD: T3 20mer
 BACKWARD: T7 21mer
 Plate: 021 row: A column: 09
 Seq primer: T3 20mer
 High quality sequence stop: 689.
 FEATURES
 source
 1. 689
 /organism="Mesembryanthemum crystallinum"
 /mol_type="mRNA"
 /db_xref="taxon:3544"
 /clone="MCS021A09"
 /issue_type="leaf"
 /dev_stage="five-week-old"
 /clone_lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM)."
 /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."
 ORIGIN
 Alignment Scores:
 Pred. No.: 2,34e-18 Length: 689
 Score: 213.50 Matches: 50
 Percent Similarity: 60.6% Conservative: 16
 Best Local Similarity: 45.9% Mismatches: 34
 Query Match: 37.5% Indels: 9
 DB: 6 Gaps: 3
 US-09-978-274a-8 (1-110) x CA833333 (1-689)
 Qy 2 G|YValaIspSerPheProValaIysThrGluAlaPheLeuLeuValaIalaIleGlnMet 21
 Db 177 GGTAAAGACATGACAGACTGAGAAATGAGGCAAAATTCCTGTGATTCATACATGATG 236

Qy 22 ValSerGluAlaIalaArgPheIysTrpIleGluAsnGlnValaIysThrAspHe----- 39
 Db 237 GTTCTGAAGCAGCAGAGTTCAAGATATATATAGATAGAGGAAACCAAGTGCCTTAGAT 296
 Qy 40 AsnArgAlaPheTyrProAspProIysValIleAsnLeuGluGluIysTrpGlyIysIle 59
 Db 297 TATGATGCTTCTTACCAGACCCGAAATGCTGCTTTGGAGACCAATGGGGGAAGATT 356
 Qy 60 SerGluAlaIleHisAsnAlaIysAsnGlyAlaLeuPro-----Lys 73
 Db 357 TCGCAGAGATTGATGAGTGTCT---GGGGCGAAACCTGCTGTATGATCTTTACCT 413
 Qy 74 ProleugluLeuValaAspAlaIysGlyThrIysTrpIleValaIleuArgValaAspGluIle 93
 Db 414 CGGATTCGCTTTAAAGAAACCAATATGATATCATGATGACGGTGAATGAAGTTGACACTATT 473
 Qy 94 AsnArgAspValaIalaLeuLeuIysTyr 102
 Db 474 AGACCTGAATGGGATGACTCAAGTTTC 500
 RESULT 8
 CA833383
 LOCUS
 DEFINITION MCS021F04.152044 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS021F04.5, mRNA sequence.
 ACCESSION CA833383
 VERSION CA833383.1 GI:26561148
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)
 ORGANISM Mesembryanthemum crystallinum
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Alzooceae; Mesembryanthemum.
 REFERENCE 1 (bases 1 to 689)
 AUTHORS Cushman, J.C.
 TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
 JOURNAL Unpublished (1997)
 COMMENT Contact: Cushman JC
 Department of Biochemistry
 University of Nevada
 MS200, Reno, NV 89557-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu
 PCR PRIMERS
 FORWARD: T3 20mer
 BACKWARD: T7 21mer
 Plate: 021 row: F column: 04
 Seq primer: T3 20mer
 High quality sequence stop: 689.
 FEATURES
 source
 1. 689
 /organism="Mesembryanthemum crystallinum"
 /mol_type="mRNA"
 /db_xref="taxon:3544"
 /clone="MCS021F04"
 /issue_type="leaf"
 /dev_stage="five-week-old"
 /clone_lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM)."
 /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.34e-18 Length: 689

Score: 213.50 Matches: 50
 Percent Similarity: 60.6% Conservative: 16
 Best Local Similarity: 45.9% Mismatches: 34
 Query Match: 37.5% Indels: 9
 DB: 6 Gaps: 3

US-09-978-274A-8 (1-110) x CA835855 (1-689)

QY 2 G1ValAspSerPheProValIysThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
 Db 177 GGTAAAGCATCGACCACTCAGCAAAATGAGCCAAATCTTGCTGATGCTCATACAGATG 236
 QY 22 ValSerGluAlaIleAaGpPheIysTyrIleGluAsnGlnValIysThrAspPhe----- 39
 Db 237 GTTCTGACAGCAGCAAGTTCAGTATATTAAGGTAAAGGTAAACCAAGTGGCTTAGAT 296
 QY 40 AsnArgAlaPheTyrProAspProIysValIleAsnLeuGluGluIysTyrGlyIysIle 59
 Db 297 TATGAATCGTTCTTACCGACCCGAAATGCTGCTTTGGAGACCAATGGGGAGATT 356
 QY 60 SerGluAlaIleHisAsnAlaIysAsnGlyAlaLeuPro-----Lys 73
 Db 357 TCGCAGAGATTCATGAGAGTGTCT---GGGGCGAAACCTGCTGTATGAACTTTCACT 413
 QY 74 ProLeuGluLeuValAlaPheIleGlyThrIysTyrIleValLeuArgValAspGluIle 93
 Db 414 CCGATTCGCTTAAAGAAACCAATGTCATGACGCTGATTAAGGTGACACTAT 473
 QY 94 AsnArgAspValAlaLeuLeuIysTyr 102
 Db 474 AGACCTGAATGGGATACCTCAAGTTC 500

RESULT 9 639 bp mRNA linear EST 12-DEC-2002
 LOCUS CA835855
 DEFINITION MGS004G12.161218 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crasulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MGS004G12.5, mRNA sequence.

ACCESSION CA835855
 VERSION CA835855.1 GI:26563620
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)

ORGANISM Mesembryanthemum crystallinum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.

REFERENCE 1 (bases 1 to 639)

AUTHORS Cushman, J.C.
 TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
 JOURNAL COMMENT Unpublished (1997)

CONTACT: Cushman JC
 Department of Biochemistry
 University of Nevada
 MS200, Reno, NV 89557-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu

PCR PRIMERS
 FORWARD: T3 20mer
 BACKWARD: T7 21mer
 Plate: 004 row: G column: 12
 Seq primer: T3 20mer
 High quality sequence scop: 639.

FEATURES
 SOURCE location/Qualifiers

1..639
 /organism="Mesembryanthemum crystallinum"
 /mol_type="mRNA"
 /db_xref="taxon:3544"
 /clone="MGS004G12"
 /feature_type="leaf"
 /dev_stage="five-week-old"

ORIGIN

Alignment Scores:

Pred. No.: 1.28e-16 Length: 639
 Score: 200.50 Matches: 50
 Percent Similarity: 60.0% Conservative: 16
 Best Local Similarity: 45.5% Mismatches: 34
 Query Match: 35.2% Indels: 10
 DB: 6 Gaps: 3

US-09-978-274A-8 (1-110) x CA835855 (1-639)

QY 2 G1ValAspSerPheProValIysThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
 Db 177 GGTAAAGCATCGACCACTCAGCAAAATGAGCCAAATCTTGCTGATGCTCATACAGATG 236
 QY 22 ValSerGluAlaIleAaGpPheIysTyrIleGluAsnGlnValIysThrAspPhe----- 39
 Db 237 GTTCTGACAGCAGCAAGTTCAGTATATTAAGGTAAAGGTAAACCAAGTGGCTTAGAT 296
 QY 40 AsnArgAlaPheTyrProAspProIysValIleAsnLeuGluGluIysTyrGlyIysIle 59
 Db 297 TATGAATCGTTCTTACCGACCCGAAATGCTGCTTTGGAGACCAATGGGGAGATT 356
 QY 60 SerGluAlaIleHisAsnAlaIysAsnGlyAlaLeuPro-----Lys 73
 Db 357 TCGCAGAGATTCATGAGAGTGTCT---GGGGCGAAACCTGCTGTATGAACTTTCACT 413
 QY 74 ProLeuGluLeuValAlaPheIleGlyThrIysTyrIleValLeu-ArgValAspGluIle 93
 Db 414 CCGATTCGCTTAAAGAAACCAATGTCATGACGCTGATTAAGGTGACACTAT 473
 QY 93 AsnArgAspValAlaLeuLeuIysTyr 102
 Db 474 TAGACCTGAATGGGATACCTCAAGTTC 501

RESULT 10

BE036541 1033 bp mRNA linear EST 07-JUN-2000
 LOCUS BE036541
 DEFINITION MP01B07 MP Mesembryanthemum crystallinum cDNA 5' similar to antiviral protein, mRNA sequence.

ACCESSION BE036541
 VERSION BE036541.1 GI:8331550
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)

ORGANISM Mesembryanthemum crystallinum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Aizoaceae; Mesembryanthemum.

REFERENCE 1 (bases 1 to 1033)
 AUTHORS Bohnert, H.J., Borchert, C., Brazille, S., Brooke, J., Eaton, M., Ferreira, H., Kawaasaki, S., McColough, A., Michalowski, C.B., Palacio, C., Scarpa, G., Wheeler, M. and Zepeda, G.R.
 TITLE Functional Genomics of Plant Stress Tolerance
 JOURNAL COMMENT Unpublished (2000)

CONTACT: Michalowski, C.B.
 University of Arizona
 Bio Sciences West room 513, Tucson, AZ 85721, USA
 Tel: 520-621-7982
 Fax: 520-621-1697
 Email: cbm@u.arizona.edu

FEATURES

SOURCE location/Qualifiers
 1..1033
 /organism="Mesembryanthemum crystallinum"
 /mol_type="mRNA"

/clone.lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crasulacean acid metabolism, phase I (2 AM)."
 /note="vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

/db_xref="taxon:3988"
/clone="pct81345"
/note="Vector: lambdaZAP1; site_1: EcoRI, site_2: XhoI;
stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760,
1982) endosperm plus embryo of immature castor fruits.
cDNA was synthesized and cloned into lambdaZAP1 according
to the instructions of the manufacturer (Stratagene).
Synthesis was primed from the poly(A) tail, and cloned
directionally into XhoI (3') and EcoRI (5') sites. In few
cases, sequence data indicated that this directionality
was reversed. Partial cDNA clones predominate."

ORIGIN

Alignment Scores:

Pred. No.: 4,16e-10 Length: 405
Score: 151.00 Matches: 33
Percent Similarity: 61.6% Conservative: 12
Best Local Similarity: 45.2% Mismatches: 25
Query Match: 26.5% Indels: 3
DB: 8 Gaps: 1

US-09-978-274A-8 (1-110) x T24255 (1-405)

QY 8 VallyrThrGluAlaPhePheLeuValAlaIleGlnMetValSerGluAlaAlaArg 27
Db 77 ATTCAACTGCTGCTCTTCTTATGCTTGCATCCAAATGATTTCAGAGCGACAGGA 136
QY 28 PheleTyrlleGluAenGlnVallyrThr-----AenPheAenArgAlaPheTyPro 45
Db 137 TTCAGATCACTGAGGAGAAATCGCAGCATTTAGTCAACCGAATCTGCACCA 196
QY 46 AspProLyValIleAenLeuGlnLyTyPglyTylleSerGluAlaIleHisAs 65
Db 197 GATCTAGCGTAAATTATACCTTNAAGATAGTTGGGGAGACTTCCACATTCAGGA 256
QY 65 nAlaLyAenGlnValLeuProLyProLeuGlnLeu 77
Db 257 GTCTAACCAAGAGCCTTTGCTAGTCCANTTCACTG 293

RESULT 13
BE036639 1021 bp mRNA linear EST 07-JUN-2000
LOCUS BE036639 MP Mesembryanthemum crystallinum cDNA 5' similar to
DEFINITION ribosome-inactivating protein gelonh, mRNA sequence.
ACCESSION BE036639
VERSION BE036639.1 GI:8331648
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzaceae; Mesembryanthemum.
1 (bases 1 to 1021)

REFERENCE Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
Ferreira, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Palacio, C., Scarpa, G., Wheeler, M. and Zepeda, G.R.,
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
CONTACT: Michalowski, C.B.
UNIVERSITY OF ARIZONA
BIO SCIENCES WEST ROOM 513, TUCSON, AZ 85721, USA
TEL: 520-621-7982
FAX: 520-621-1697
EMAIL: chm@u.arizona.edu
AN OPEN READING FRAME EXISTS.
INSERT LENGTH: 1 Std Error: 0.00.
LOCATION/QUALIFIERS

FEATURES
Source
1..1021
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"

/issue_type="apical meristem and leaf primordia"
/dev_stage="6 weeks"
/clone_lib="MP"
/note="3 d 500mM NaCl"

ORIGIN

Alignment Scores:

Pred. No.: 3.87e-08 Length: 1021
Score: 140.50 Matches: 41
Percent Similarity: 61.9% Conservative: 11
Best Local Similarity: 48.8% Mismatches: 28
Query Match: 24.7% Indels: 5
DB: 2 Gaps: 3

US-09-978-274A-8 (1-110) x BE036639 (1-1021)

QY 11 GluAlaPhePheLeuValAlaIleGlnMetValSerGluAlaAlaArgPheTyTr 30
Db 665 GAGGCCAAATCTTGCTGATGCTATACAGATGTTCTGAGACGACGCGTTAAGTAT 724
QY 31 IleGluAenGln---VallyrThrAenPheAenArgAlaPheTyProAspProLyVal 49
Db 725 ATTGAAGTGTGAGACCCAAAGCTGTACATGCTCTCCAAACCCGACCGAAAGTG 784
QY 50 IleAenLeuGlnLyTyPglyTylleSer---GluAlaIleHisAenAlaAen 68
Db 785 CTGAGTTGGAGAGACAAATTGGGAGATTTCCAGAAATTAAGACAGTCGCCGAA 844
QY 69 GlnAlaLeuProLy-----ProLeuGlnLeuValAenAlaLySerGlyThrLyTyP 86
Db 845 AACTGTTTGTTC-AAATATTCACCGCGCATCTTCCAAATGTGATGATTACATGAG 903
QY 87 ValLeuArgVal 90
Db 904 GTGATTAAGGGTG 915

RESULT 14
BE033546 1038 bp mRNA linear EST 07-JUN-2000
LOCUS BE033546 MP Mesembryanthemum crystallinum cDNA 5' similar to
DEFINITION ribosome-inactivating protein, mRNA sequence.
ACCESSION BE033546
VERSION BE033546.1 GI:8328555
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Alzaceae; Mesembryanthemum.
1 (bases 1 to 1038)

REFERENCE Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
Ferreira, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Palacio, C., Scarpa, G., Wheeler, M. and Zepeda, G.R.,
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
CONTACT: Michalowski, C.B.
UNIVERSITY OF ARIZONA
BIO SCIENCES WEST ROOM 513, TUCSON, AZ 85721, USA
TEL: 520-621-7982
FAX: 520-621-1697
EMAIL: chm@u.arizona.edu
AN OPEN READING FRAME EXISTS.
LOCATION/QUALIFIERS

FEATURES
Source
1..1038
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/issue_type="Root"
/dev_stage="5-6 weeks old"
/clone_lib="MP"
/note="Vector: Bluescript SK+, Site_1: EcoRI, Site_2:
XhoI"

ORIGIN

Alignment Scores:

Pred. No.:	1.08e-06	Length:	1038
Score:	130.00	Matches:	31
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Best Local Similarity:	46.3%	Mismatches:	22
Query Match:	22.8%	Indels:	4
DB:	2	Gaps:	2

US-09-978-274A-8 (1-110) x BE033546 (1-1038)

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DB 386 CAGGTGAGGCCAATCTGCTGATTCCTATACAGATGCTCCGAGACGACGCTTT 445
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 29 LysTyrIleGluAsnGlnVal---LysThrAsnPheAsnArgAlaPheTyrProAspPro 47
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DB 446 AAGTTATTGAAAGTAAAGTAAACCCAAAGTGGTGTACATGCTGTTCAAAACCCGACCCG 505
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QY 48 LysValIleAsnLeuGluGluLysTyrPqlLysIleSerGluAlaIleHisAsnAlaLys 67
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DB 506 AAGTGGCGAGTTGGGTGTACATTTGGGTGAACATT-----TTCCATGAGACTCAT 556
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QY 68 AsnGlyAlaLeuProLysPro 74
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DB 557 AAGACAGCCGCGTCAAAACT 577
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RESULT 15

AA856221

LOCUS

L30-242T3 Ice plant Lambda Uni-Zap XR expression library, 30 hours

DEFINITION

NaCl treatment Mesembryanthemum crystallinum cDNA clone L30-242 5' similar to Ribosome inactivating protein precursor (antiviral protein), mRNA sequence.

AA856221 GI:2944523

VERSION

AA856221.1

KEYWORDS

Mesembryanthemum crystallinum (common iceplant)

Mesembryanthemum crystallinum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

Caryophyllales; Alzooceae; Mesembryanthemum.

1 (bases 1 to 267)

Cushman, J.C.

An expressed sequence tag database for the common ice plant.

Mesembryanthemum crystallinum

Unpublished (1997)

Contact: Cushman JC

Department of Biochemistry

University of Nevada

MS200, Reno, NV 89557-0014, USA

Tel: 775-784-1918

Fax: 775-784-1650

Email: jcushman@unr.edu

PCR Primers

FORWARD: T7

REVERSE: T3

BACKWARD: T3

Plate: L30-3

Seq primer: T3

High quality sequence stop: 230.

Location/Qualifiers

1. 267

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/mol_type="mRNA"

/db_xref="taxon:3544"

/clone="L30-242"

/issue_type="Leaf, 30 h 0.4M NaCl"

/dev_stage="Six week old"

/clone_lib="Ice plant Lambda Uni-Zap XR expression

library, 30 hours NaCl treatment"

/note="Vector: Lambda Uni-Zap XR, Bluescript SK-, Site_1:

EcoRI, Site_2: XhoI"

Alignment Scores:

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Percent Similarity:	68.5%	Conservative:	8
Best Local Similarity:	53.7%	Mismatches:	15
Query Match:	21.3%	Indels:	2
DB:	1	Gaps:	1

US-09-978-274A-8 (1-110) x AA856221 (1-267)

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DB 104 GGTAAAGCATGACAGACAGAAAGAGGCGCAATTCCTGCTGATTCCTATACAGATG 163
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QY 22 ValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPhe----- 39
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 164 GTTCTGAGAGCAGCAGAGTTCAAGTATATTGAGAGTGAAGTGAACCAAGTGCCTTAGAT 223
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 40 AsnArgAlaPheTyrProAspProLysValIleAsnLeuGlu 53
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 224 TATGAATGCTCTTAACCGACCCGAAATGCTGCTTTGGAG 265
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Search completed: April 9, 2006, 06:20:23
Job time : 2001.23 secs

FEATURES

source

ORIGIN

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 8, 2006, 13:04:24 ; Search time 120.071 Seconds
(without alignments)
1628.463 Million cell updates/sec

Title: US-09-978-274A-8

Perfect score: 569

Sequence: 1 MGVDSPVKTAEAFLLVAIQ.....DEINRDVALLKYVNGTCQTT 110

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents NA -OPMT=fastap -SUFFIX=p2n.rtf -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Issued Patents NA:

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2: /cgn2_6/ptodata/1/ina/5.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	454	79.8	1195	2	US-08-373-858-1
2	454	79.8	1195	2	US-08-342-786B-1
3	454	79.8	1195	2	US-08-500-511-1
4	454	79.8	1195	2	US-08-500-594-1
5	454	79.8	1195	3	US-07-865-169-1
6	454	79.8	1195	3	US-07-865-169-2
7	454	79.8	1195	3	US-09-005-273-1
8	454	79.8	1195	3	US-09-005-273-2
9	454	79.8	1195	6	PCT-US96-11546-1

10	451	79.3	1379	3	US-08-501-253A-1	Sequence 1, Appl1
11	399	70.1	918	2	US-08-138-636-1	Sequence 1, Appl1
12	399	70.1	918	2	US-08-319-622A-1	Sequence 1, Appl1
13	399	70.1	918	2	US-08-471-564-1	Sequence 1, Appl1
14	213.5	37.5	813	2	US-07-901-707-11	Sequence 11, Appl1
15	213.5	37.5	813	2	US-07-901-707-57	Sequence 57, Appl1
16	213.5	37.5	813	2	US-07-988-430-11	Sequence 11, Appl1
17	213.5	37.5	813	2	US-07-988-430-57	Sequence 57, Appl1
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19	213.5	37.5	813	2	US-08-488-113B-11	Sequence 11, Appl1
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21	213.5	37.5	813	2	US-08-646-360-11	Sequence 11, Appl1
22	213.5	37.5	813	2	US-08-621-803-246	Sequence 246, App
23	213.5	37.5	813	3	US-08-839-765-11	Sequence 11, Appl1
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25	213.5	37.5	813	3	US-09-217-352-246	Sequence 246, App
26	213.5	37.5	813	3	US-09-610-838-11	Sequence 11, Appl1
27	213.5	37.5	813	3	US-09-711-485-11	Sequence 11, Appl1
28	213.5	37.5	813	6	PCT-US92-09487-11	Sequence 11, Appl1
29	213.5	37.5	813	6	PCT-US92-09487-57	Sequence 57, Appl1
30	212.5	37.3	783	2	US-08-327-440-1	Sequence 1, Appl1
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32	212.5	37.3	955	2	US-09-217-352-258	Sequence 258, App
33	212.5	37.3	1003	2	US-08-621-803-252	Sequence 252, App
34	212.5	37.3	1003	2	US-09-217-352-252	Sequence 252, App
35	212.5	37.3	1072	2	US-08-621-803-250	Sequence 250, App
36	212.5	37.3	1072	2	US-09-217-352-250	Sequence 250, App
37	196.5	34.5	1855	3	US-09-403-752A-35	Sequence 35, Appl1
38	196.5	34.5	1855	3	US-09-551-151A-35	Sequence 35, Appl1
39	192	33.7	1855	2	US-08-356-786-7	Sequence 7, Appl1
40	192	33.7	1140	2	US-08-218-303-15	Sequence 15, Appl1
41	192	33.7	1140	2	US-08-338-793D-60	Sequence 60, Appl1
42	192	33.7	1605	2	US-08-356-786-9	Sequence 9, Appl1
43	192	33.7	1698	2	US-09-785-921A-1	Sequence 1, Appl1
44	192	33.7	1731	3	US-09-785-921A-2	Sequence 2, Appl1
45	192	33.7	1731	3	US-09-785-921A-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-373-858-1
Sequence 1, Application US/08373858
Patent No. 5633155
GENERAL INFORMATION:
APPLICANT: Kim, Man-Keun
APPLICANT: Lee, Kwan-Ho
APPLICANT: Na, Byeong-Kook
APPLICANT: Jeong, Han-Seung
APPLICANT: Choi, Kyu-Whan
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
TITLE OF INVENTION: Expression Vector for Phytoacta
TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dady & Dady
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,858
FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/17986-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7770
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca americana
TISSUE TYPE: Leaf
US-08-373-858-1

Alignment Scores:
Pred. No.: 4,266-52 Length: 1195
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
Gaps: 0
DB: 2

US-09-978-274A-8 (1-110) x US-08-373-858-1 (1-1195)

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QY 22 ValSerG1uAlA1AaAgPheLySTyrl1eG1uBnG1nVal1ySThRanPheAsnArg 41
Db 618 GTATCAAGGCGACGACMAATTCAGTACATGAGATCAGGTGAAACTTAATTTTAACGA 677

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QY 82 G1YThLySTP1leVal1leuArgVal1AspG1u1leAsnArgAspVal1AlA1eU1eU1ys 101
Db 798 GGTCGCAAGTGAATGAGTGTGAGAGTGAATCAAGCTGATGTAGCACTCTTAAC 857

QY 102 TyTValAsnG1yThrCySG1nThrThr 110
Db 858 TACGTTGTGGAGACTGTGACAGCAACT 884

RESULT 2
US-08-342-786B-1
Sequence 1, Application US/08342786B
Patent No. 5648234
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
APPLICANT: Choi, Kyu-Whan
APPLICANT: Lee, Kwan-Ho
APPLICANT: Kim, Man-Keun
TITLE OF INVENTION: A No. 5648234el Expression Vector for Phytolacca
TITLE OF INVENTION: Antiviral Protein
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSER: Darby & Darby
STREET: 805 Third Ave.
CITY: New York
STATE: New York

COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,786B
FILING DATE: 21-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,024
FILING DATE: 01-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/08862-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
TELEFAX: (212)753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Phytolacca americana L.
IMMEDIATE SOURCE:
CLONE: PAP
US-08-342-786B-1

Alignment Scores:
Pred. No.: 4,266-52 Length: 1195
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
Gaps: 0
DB: 2

US-09-978-274A-8 (1-110) x US-08-342-786B-1 (1-1195)

QY 2 G1YVAlAspSerPheProVal1yThrG1uAlAphPheLeuLeuVal1Al1eG1mEc 21
Db 558 GGAGTGTATGTCATTCACCTGAGAAAACCGAAGCCGAATTCCTATTGCTAGCCATACAAATG 617

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Db 618 GTATCAAGGCGACGACMAATTCAGTACATGAGATCAGGTGAAACTTAATTTTAACGA 677

QY 42 AlAphETyRProAspProLySVal1leAsnLeuG1uG1uLySTPGLyLys1leSerG1u 61
Db 678 GCATTCAACCTATCCCAAGTACTTAATTGCAAGAGACATGGGGTAAAGATTCAACA 737

QY 62 AlAl1eH1sAsnAlA1ySaNG1yAlA1eUProLySProLeuG1uLeuVal1AspAlA1ys 81
Db 738 GCATTTCATGATGCGCAAGATGAGTTTACCCAAACCTCTCGAGCTAGTGATGCCAGT 797

QY 82 G1YThLySTP1leVal1leuArgVal1AspG1u1leAsnArgAspVal1AlA1eU1eU1ys 101
Db 798 GGTCGCAAGTGAATGAGTGTGAGAGTGAATCAAGCTGATGTAGCACTCTTAAC 857

QY 102 TyTValAsnG1yThrCySG1nThrThr 110
Db 858 TACGTTGTGGAGACTGTGACAGCAACT 884

RESULT 3
US-08-500-611-1

Sequence 1, Application US/08500611
Patent No. 5756322
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun E.
TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,611
FILING DATE: 11-JUL-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-611-1
Alignment Scores:
Pred. No.: 5,17e-52 Length: 1379
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
Gaps: 0
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QY 22 ValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPheAsnArg 41
DB 810 GATTCAGAGCGACGAGAGATTCAAGTACATGAGATCAGGTGAAACTTAATTTTAAACAGA 869
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DB 870 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGACAGACATGGGTTAAGATTTCACA 929
QY 62 AlalIleAsnAlaLysAsnGlyAlaLeuProLysProLeuGlnLeuValAspAlaLys 81

DB 930 GCAATTCATGATGCCAAGATGAGATTTCACCAACCTCTGACGACTAGTGAGCCAGT 989
QY 82 GlyThrIstPrlIleValLeuArgValAspGluIleAsnAgaPValAlaLeuLeuLys 101
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QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 1050 TACGTTGTGGAGCTGTCAACAACACT 1076
RESULT 4
US-08-500-694-1
Sequence 1, Application US/08500694
Patent No. 5880329
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun E.
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,694
FILING DATE: 11-JUL-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
US-08-500-694-1
Alignment Scores:
Pred. No.: 5,17e-52 Length: 1379
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
Gaps: 0
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DB: 3 Gaps: 0
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QY 22 ValSerGluAlaAlaArgPheIleTyrlleGluAengInValIleThrAspPheAsnArg 41
DB 810 GTATCAAGAGGACGACAAATTCAGATCAATAGATCAAGTACGAGAAATCTAATTTTAAACGA 869
QY 42 AlaPheTyProAspProLyseValIleAsnLeuGluGluTyrlleSerGlu 61
DB 870 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAAGTTTCAACA 929
QY 62 AlaIleHisAsnAlaIleArgPheIleTyrlleGluAengInValIleThrAspPheAsnArg 81
DB 930 GCAATTCATGATGCGCAAGATGAGATTACCCAAACCTCTCGAGCTAGGATGCCAGT 989
QY 82 GlyThrIleSTPrlleValleuArgValAspGluIleAsnArgAspValAlaIleuLeuLys 101
DB 990 GGTCCCAAGTGAATGATGTTGAGAGTGAATCAAGCTGATGACCTTAAC 1049
QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 1050 TACGTGTGGAGCTGTCAACAAC 1076
RESULT 7
US-09-005-273-1
Sequence 1, Application US/09005273
Patent No. 6137030
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun E.
TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
STREET: 600 South, Avenue West
CITY: Westfield
STATE: New Jersey
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005.273
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,611
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE: 11-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: OCIRS 3.3-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
NAME/KEY: sig peptide
LOCATION: 225..290
US-09-005-273-1
Alignment Scores:
Pred. No.: 5.17e-52 Length: 1379
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
Gaps: 0
US-09-978-274A-8 (1-110) x US-09-005-273-1 (1-1379)
QY 2 GlyValAspSerPheProValIleThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 750 GGAAGTATGATCTACTAGAGAAAACCGAAGCCGAATTCCTAATGGTGCCATCAAAATG 809
QY 22 ValSerGluAlaAlaArgPheIleTyrlleGluAengInValIleThrAspPheAsnArg 41
DB 810 GTATCAAGAGGACGACAAATTCAGATCAATAGATCAAGTACGAGAAATCTAATTTTAAACGA 869
QY 42 AlaPheTyProAspProLyseValIleAsnLeuGluGluTyrlleSerGlu 61
DB 870 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGAGACATGGGGTAAAGTTTCAACA 929
QY 62 AlaIleHisAsnAlaIleArgPheIleTyrlleGluAengInValIleThrAspPheAsnArg 81
DB 930 GCAATTCATGATGCGCAAGATGAGATTACCCAAACCTCTCGAGCTAGGATGCCAGT 989
QY 82 GlyThrIleSTPrlleValleuArgValAspGluIleAsnArgAspValAlaIleuLeuLys 101
DB 990 GGTCCCAAGTGAATGATGTTGAGAGTGAATCAAGCTGATGACCTTAAC 1049
QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 1050 TACGTGTGGAGCTGTCAACAAC 1076
RESULT 8
US-09-005-273-3
Sequence 3, Application US/09005273
Patent No. 6137030
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun E.
TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL
TITLE OF INVENTION: AND/OR ANTI-FUNGAL ACTIVITY IN PLANTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
STREET: 600 South, Avenue West
CITY: Westfield
STATE: New Jersey
COUNTRY: USA
ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005.273
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,611
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE: 11-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET INFORMATION:
TELEPHONE: 908-654-7866
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 225..290
US-09-005-273-3

Alignment Scores:
Pred. No.: 5,17e-52 Length: 1379
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
DB: 3 Gaps: 0

US-09-978-274A-8 (1-110) x US-09-005-273-3 (1-1379)

QY 2 G|YValAspSerPheProValIyThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 750 GGAAGTATGTCATTCACCTGAGAAAACCGAACCGAATTCCTATGTGTAAGCATTCAAATG 809
QY 22 ValSerGluAlaAlaArgPheIyValIleGluAngInValIyThrAsnPheAsnArg 41
DB 810 GATCAGAGCGCAGCAAGATTCAGTACATAGAGATCAGTGGAATACTAATTTTAAACAGA 869
QY 42 AlaPheTyProAspProIyValIleAsnLeuGluGluTyTPG|YlVylIleSerGlu 61
DB 870 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGAGATGGGGGTMAAATTTCACA 929
QY 62 AlaIleHisAsnAlaIyAsnG|YAlaLeuProIySProLeuGluLeuValAspAlaIyS 81
DB 930 GCAATTCATGATGTCAGAAATGAGATTACCCAACTTCGAGCTAGTGAATGCCAGT 989
QY 82 G|YThrIySTP|IleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIyS 101
DB 990 GGTGCCAAGTGAATGATGTTTGAAGTGAATGAATCAAGCCTGATGTAACCTTTAAAC 1049
QY 102 TyrValAsnG|YThrCySgInThrThr 110
DB 1050 TACGTTGGTGGAGCTGTCAAGCAACT 1076

RESULT 9
PCT-US96-11546-1
Sequence 1, Application PC/TUS9611546
GENERAL INFORMATION:
APPLICANT: Tumer, Nilgun E.
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein
TITLE OF INVENTION: Mutants
NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Menclik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11546
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,694
FILING DATE: 11-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039
TELEPHONE: 908-654-7866
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS
LOCATION: 225..1163
FEATURE:
NAME/KEY: mutation
LOCATION: replace(233, "a")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(349, "g")
FEATURE:
NAME/KEY: mutation
LOCATION: replace(435, "c")
PCT-US96-11546-1

Alignment Scores:
Pred. No.: 5,17e-52 Length: 1379
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
DB: 6 Gaps: 0

US-09-978-274A-8 (1-110) x PCT-US96-11546-1 (1-1379)

QY 2 G|YValAspSerPheProValIyThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 750 GGAAGTATGTCATTCACCTGAGAAAACCGAACCGAATTCCTATGTGTAAGCATTCAAATG 809
QY 22 ValSerGluAlaAlaArgPheIyValIleGluAngInValIyThrAsnPheAsnArg 41
DB 810 GATCAGAGCGCAGCAAGATTCAGTACATAGAGATCAGTGGAATACTAATTTTAAACAGA 869
QY 42 AlaPheTyProAspProIyValIleAsnLeuGluGluTyTPG|YlVylIleSerGlu 61
DB 870 GCATTCAACCTTAATCCCAAGTACTTAATTTGCAAGAGATGGGGGTMAAATTTCACA 929
QY 62 AlaIleHisAsnAlaIyAsnG|YAlaLeuProIySProLeuGluLeuValAspAlaIyS 81
DB 930 GCAATTCATGATGTCAGAAATGAGATTACCCAACTTCGAGCTAGTGAATGCCAGT 989
QY 82 G|YThrIySTP|IleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIyS 101

Db 990 GGTGCAAGTGAATGTTGAGAGTGAATCAACCTGATGACTCTTAAC 1049
Qy 102 TyrValaenglyThrCysGlnThrThr 110
Db 1050 TACGTTGTGGAGCTGTCAAGCAACT 1076

RESULT 10

US-08-501-253A-1
Sequence 1, Application US/08501253A
Patent No. 6146628

GENERAL INFORMATION:
APPLICANT: Uckun, Fatih
APPLICANT: Tumer, Nilgun
TITLE OF INVENTION: Biotherapeutic Agents Comprising
TITLE OF INVENTION: Recombinant PAP and PAP Mutants
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 6146628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: US
ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501.253A
FILING DATE: 11-JUL-1995
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Kettleberger, Denise M.

REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 600.323US01

TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-9081
TELEFAX: 612-332-5300

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1379 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 225..1163

US-08-501-253A-1

Alignment Scores:

Pred. No.: 1.32e-51

Score: 451.00

Percent Similarity: 87.2%

Best Local Similarity: 81.7%

Query Match: 79.3%

DB: 3

US-09-978-274A-8 (1-110) x US-08-501-253A-1 (1-1379)

Qy 2 G1ValaaspserPheProvallyeThrglunlaphPheleuauValaalegImet 21

Db 750 GAGGTATGTCATTCACCTGAGAAAACCAAGCCGAAATTCCTATTGTAGCCATACAAATG 809

Qy 22 ValserGluAlaalaargPheLyserTyrIlegluangInvallyeThraaspheasnarg 41

Db 810 GATACAGAGCAGAGAAATCAAGTACATAGAGATCAGGTGAAAACCTAATTTTAAACA 869

Qy 42 AlapherThrProappProlyseValaaleasnleugluululystyrglylylleserGlu 61

Db 870 GCATTCACCGTAATCCCAAGTACTTAATTTGCAAGAGACATGGGTAAAGATTCAACA 929

Qy 62 AlaIethsaenAlalyeAsnglyAlaleuProlyspProleugluLeuValaspAlalys 81
Db 930 GCATTCATGATGATGAGATGAGATTACCCAAACCTCTCAGCTAGTGAATCCAGT 989
Qy 82 G1ThrllystrPilevalleuargValaspGluileasnaAspValaAlaleuLeulys 101
Db 990 GGTGCAAGTGAATGTTGAGAGTGAATCAACCTGATGACTCTTAAC 1049
Qy 102 TyrValaenglyThrCysGlnThrThr 110
Db 1050 TACGTTGTGGAGCTGTCAAGCAACT 1076

RESULT 11

US-08-138-636-1
Sequence 1, Application US/08138636
Patent No. 5348865

GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seoh
APPLICANT: Choi, Kyu-Wan
APPLICANT: Lee, Kwan Ho

APPLICANT: Kim, Man Keun

TITLE OF INVENTION: No. 5348865e1 Genome Coding PhytoIacca Antiviral

TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSER: DARBY & DARBY

STREET: 805 THIRD AVE.

CITY: NEW YORK

STATE: NY

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/138.636

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, S. Peter

REGISTRATION NUMBER: 25,351

REFERENCE/DOCKET NUMBER: 0136/08818

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 527-7700

TELEFAX: (212) 753-6237

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 918 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: PhytoIacca insularis

IMMEDIATE SOURCE:

CLONE: antiviral protein (PIP)

US-08-138-636-1

Alignment Scores:

Pred. No.: 9.13e-45

Score: 399.00

Percent Similarity: 80.7%

Best Local Similarity: 72.5%

Query Match: 70.1%

DB: 2

US-09-978-274a-8 (1-110) x US-08-138-636-1 (1-918)

QY 2 G1YValAspSerPheProValYsThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 517 GGAGTACGCTATCTCTGAGAACCGAAGCTGAATCTCTACTGAGTACATCAATG 576

QY 22 ValSerGluAlaAlaArgPheYsYrIleGluAsnGlnValYsThraenPheAsnArg 41
DB 577 GTATCAGAGCAGCAGATTCAGTACATAGAGATCAAGTGAATAATTTTAAACA 636

QY 42 AlaphetYrProAspProYsValIleAsnLeuGluYsYrPglYsIleSerGlu 61
DB 637 CCATTCAACCTTATCCCAAGTACTTATTCAGAGACATGGCGTAAGATTCTTCA 696

QY 62 AlAlIleHisAsnAlaYsAsnGluAlaLeuProYsProLeuGluLeuValAspAlaYs 81
DB 697 GCAATTCATGCTCGAGAAATGAGGTTTACCAATCTCTACAGTACATGATCCCAAT 756

QY 82 G1YThrYsTrpIleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuYs 101
DB 757 GGTGCAAAATGGATAGTGTGAGAGTGGATGAATCAAGCTGATGTGTCACTTTAAC 816

QY 102 TyrValAsnGlyThrCysGlnThr 110
DB 817 TACGTATTGGAGCTGCCAGAGAACT 843

RESULT 12
US-08-319-622A-1
Sequence 1, Application US/08319622A
Patent No. 5656466
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Choi, Kyu-Whan
APPLICANT: Jeon, Hong-Seob
APPLICANT: Kim, Chul-Hwan
APPLICANT: Kim, Man-Keun
TITLE OF INVENTION: Process for Preparing Virus-Resistant
TITLE OF INVENTION: Transgenic Plant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,622A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0136/0A445
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SRO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: Phytolacca insularis Nakai
TISSUE TYPE: leaf
IMMEDIATE SOURCE:
CLONE: PIP
US-08-319-622A-1

Alignment Scores:
Pred. No.: 9.13e-45 Length: 918
Score: 399.00 Matches: 79
Percent Similarity: 80.7% Conservative: 21
Best Local Similarity: 72.5% Mismatches: 0
Query Match: 70.1% Indels: 0
Gaps: 0

US-09-978-274a-8 (1-110) x US-08-319-622A-1 (1-918)

QY 2 G1YValAspSerPheProValYsThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 517 GGAGTACGCTATCTCTGAGAACCGAAGCTGAATCTCTACTGAGTACATCAATG 576

QY 22 ValSerGluAlaAlaArgPheYsYrIleGluAsnGlnValYsThraenPheAsnArg 41
DB 577 GTATCAGAGCAGCAGATTCAGTACATAGAGATCAAGTGAATAATTTTAAACA 636

QY 42 AlaphetYrProAspProYsValIleAsnLeuGluYsYrPglYsIleSerGlu 61
DB 637 CCATTCAACCTTATCCCAAGTACTTATTCAGAGACATGGCGTAAGATTCTTCA 696

QY 62 AlAlIleHisAsnAlaYsAsnGluAlaLeuProYsProLeuGluLeuValAspAlaYs 81
DB 697 GCAATTCATGCTCGAGAAATGAGGTTTACCAATCTCTACAGTACATGATCCCAAT 756

QY 82 G1YThrYsTrpIleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuYs 101
DB 757 GGTGCAAAATGGATAGTGTGAGAGTGGATGAATCAAGCTGATGTGTCACTTTAAC 816

QY 102 TyrValAsnGlyThrCysGlnThr 110
DB 817 TACGTATTGGAGCTGCCAGAGAACT 843

RESULT 13
US-08-471-564-1
Sequence 1, Application US/08471564
Patent No. 5723326
GENERAL INFORMATION:
APPLICANT: Moon, Young-Ho
APPLICANT: Jeon, Hong-Seob
APPLICANT: Choi, Kyu-Whan
APPLICANT: Lee, Kwan Ho
APPLICANT: Kim, Man Keun
TITLE OF INVENTION: No. 5723326e1 Genome Coding Phytolacca Antiviral
TITLE OF INVENTION: Protein and a Recombinant Expression Vector Therefor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARBY & DARBY
STREET: 805 THIRD AVE.
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,564
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/210,396
FILING DATE:
APPLICATION NUMBER: US 08/138,636

```

? FILING DATE: 15-OCT-1993
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Ludwig, S. Peter
? REGISTRATION NUMBER: 25,351
? REFERENCE/DOCKET NUMBER: 0136/
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 527-7700
? TELEFAX: (212) 753-6237
? TELE: 236687
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 918 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? HYPOTHEetical: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Phytolacca insularis
? IMMEDIATE SOURCE:
? CLONE: antiviral protein (PIP)
US-08-471-364-1

```

Patent No. 5376546
GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27129/30910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-901-707-57
Alignment Scores:
Pred. No.: 1.38e-19 Length: 813
Score: 213.50 Matches: 47
Percent Similarity: 61.5% Conservative: 20
Best Local Similarity: 43.1% Mismatches: 41
Query Match: 37.5% Indels: 1
Gaps: 1
DB:
US-09-978-274A-8 (1-110) x US-07-901-707-57 (1-813)
QY 3 ValAspSerPheProValyThrcIuAAspPheLeuValAlaIleGluMetVal 22
Db 433 ATAGACATATTAAACCAACGAGTAGCTTCTATTGGTTGTTATTCAATGAGTG 492
QY 23 SerGluAlaAlaArgPheTyrlEgluAnGluValyThrAsnPhAsnArgAla 42
Db 493 TCTGACGACGCTCGATTCACTTATTGAGAACCAATTAATAAATTAATCTTCAACAGAGA 552
QY 43 PheTyrrProAspProLyValIleAsnLeuGluGluTyrrGlyLyIleSerGluAla 62
Db 553 ATTGCGCCGGGCAATATACATACAGCTTGAGATAAATGGGGTAAACTCTCGTTCAG 612
QY 63 IleHis---AsnAlaLyAsnGlyAlaLeuProLyProLeuGluLeuValAspAlaLy 81
Db 613 ATCCGACATCAGGTGCAATGGAATGTTTTCGAGGCAATTGAATGGAACGTGCAAT 672

QY 82 GlyThrLyrrPileValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLy 101
Db 673 GGCATAAAATACATATGTCACCGAGTTGATCAAGTAACCAAAATAGCATCTTGAG 732
QY 102 TyrValAsnGlyThrcysGlnThr 110
Db 733 TTGTCGATTAAGATCTCTAAACGAGC 759

Search completed: April 8, 2006, 14:01:58
Job time : 123.071 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 9, 2006, 01:45:16 ; Search time 393.829 Seconds
(without alignments)
2309.713 Million cell updates/sec

Title: US-09-978-274A-8

Perfect score: 569
Sequence: 1 MGVDSPFKTEAFPLVAIQ.....DEINRDVALKYNAGTCQT 110

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Delop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/abs/ABSSWEB.spool/US09978274/rnat.07042006.173040.28552/app.query.fasta.1
-DB=Published_Applications_NA_Main -QFMT=factcap -SUFFIX=p2n.rnpbm
-MIMATCH=0.1 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZE=500 -MITEM=0 -MAXLEN=200000000 -HOST=absweb03h
-USRR=US09978274 @CGN 1.1 239 @rnat.07042006.173040.28552 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DRV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	569	100.0	333	US-09-978-274A-7 Sequence 7, Appli
2	564	99.1	792	US-09-978-274A-3 Sequence 3, Appli
3	564	99.1	945	US-09-978-274A-1 Sequence 1, Appli
4	519	91.2	1092	US-09-978-274A-19 Sequence 19, Appli
5	454	79.8	1368	US-09-978-274A-31 Sequence 31, Appli
6	454	79.8	1376	US-10-467-009-1 Sequence 1, Appli
7	454	79.8	1379	US-09-978-274A-30 Sequence 30, Appli

8	454	79.8	1379	US-11-106-187-1 Sequence 1, Appli
9	213.5	37.5	813	US-09-765-527-246 Sequence 246, App
10	213.5	37.5	813	US-10-127-860-11 Sequence 11, Appli
11	213.5	37.5	813	US-10-717-243-11 Sequence 11, Appli
12	213.5	37.5	1176	US-10-074-596-2 Sequence 2, Appli
13	213.5	37.5	2407	US-11-084-080-25 Sequence 25, App
14	212.5	37.3	955	US-09-765-527-258 Sequence 258, App
15	212.5	37.3	1003	US-09-765-527-252 Sequence 252, App
16	212.5	37.3	1072	US-09-765-527-250 Sequence 250, App
17	212.5	37.3	1500	US-10-964-195-12 Sequence 12, Appli
18	212.5	37.3	1527	US-10-074-596-10 Sequence 10, Appli
19	209.5	36.8	1542	US-10-926-721A-11 Sequence 11, Appli
20	200	35.1	855	US-11-106-187-20 Sequence 20, Appli
21	200	35.1	934	US-09-978-274A-32 Sequence 32, Appli
22	200	35.1	934	US-11-106-187-3 Sequence 3, Appli
23	200	35.1	1517	US-10-964-195-10 Sequence 10, Appli
24	196.5	34.5	1855	US-10-394-511-35 Sequence 35, Appli
25	192	33.7	1698	US-09-785-921A-1 Sequence 1, Appli
26	192	33.7	1698	US-10-618-560-1 Sequence 1, Appli
27	192	33.7	1731	US-09-785-921A-2 Sequence 2, Appli
28	192	33.7	1731	US-09-785-921A-3 Sequence 3, Appli
29	192	33.7	1731	US-10-618-560-2 Sequence 2, Appli
30	192	33.7	1731	US-10-618-560-3 Sequence 3, Appli
31	192	33.7	1805	US-09-785-921A-10 Sequence 10, Appli
32	192	33.7	1805	US-10-618-560-10 Sequence 10, Appli
33	192	33.7	1855	US-10-394-511-3 Sequence 3, Appli
34	192	33.7	1855	US-10-394-511-5 Sequence 5, Appli
35	192	33.7	1855	US-10-394-511-7 Sequence 7, Appli
36	192	33.7	1855	US-10-394-511-9 Sequence 9, Appli
37	192	33.7	1855	US-10-394-511-13 Sequence 13, Appli
38	192	33.7	1855	US-10-394-511-15 Sequence 15, Appli
39	192	33.7	1855	US-10-394-511-17 Sequence 17, Appli
40	192	33.7	1855	US-10-394-511-19 Sequence 19, Appli
41	192	33.7	1855	US-10-394-511-21 Sequence 21, Appli
42	192	33.7	1855	US-10-394-511-23 Sequence 23, Appli
43	192	33.7	1855	US-10-394-511-25 Sequence 25, Appli
44	192	33.7	1855	US-10-394-511-27 Sequence 27, Appli
45	192	33.7	1855	US-10-394-511-29 Sequence 29, Appli

ALIGNMENTS

RESULT 1
US-09-978-274A-7
Sequence 7, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Atkinson, Howard
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 333
TYPE: DNA
ORGANISM: Phytolacca americana
US-09-978-274A-7

Alignment Scores:

Pred. No.: 2.31e-73
Score: 569.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 3
Length: 333
Matches: 110
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-978-274A-8 (1-110) x US-09-978-274A-7 (1-333)

QY 1 MetGlyValAspSerPheProValIleThrGluAlaPhePheLeuLeuValAlaIleGln 20
DB 1 ATGGGAGTTGATTCATTCCTCGTAAAAAAGAGGCTTTTCTTACGTGGAGCCATCCAA 60

QY 21 MetValSerGluAlaAlaArgPheLeuYrIleGluAsnGlnValIleYThrAsnPheAsn 40
DB 61 ATGGTTTCAGAGGCGAGGCGCATTCAGTACATAGAGAACCAAGTCAGCAAGATTTTAAT 120

QY 41 ArgAlaPheYrProAspProLeuValIleAsnLeuGluGluYrTPGIlyYrIleSer 60
DB 121 AGAGCATTCCTACCTGATCCCAAGTAATTAATTTGAGAGGAAGTGGGCAAAATCTCT 180

QY 61 GluAlaIleIleHisAsnAlaIleAsnGlyValAlaLeuProIleYrPheGluLeuValAspAla 80
DB 181 GAGGCAATTCACATGCAAGAAATGGGGCTTTACCCCAACCACTGAGCTAGTGATGCC 240

QY 81 LysGlyThrIleYrPleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeu 100
DB 241 AAGGTRCCAGTGGATGATGTTCTTAGAGTGATGAATCATCTGATGTGGCACTCTT 300

QY 101 LysYrValAsnGlyThrCysGlnThrThr 110
DB 301 AAGTACGTTAATGGAACCTGTGACAGCAACT 330

RESULT 2
US-09-978-274A-3
; Sequence 3, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Neelam, Anil
; APPLICANT: Atkinson, Howard
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Phycolacca americana
; US-09-978-274A-3

Alignment Scores:
Pred. No.: 4.47e-72 Length: 792
Score: 564.00 Matches: 109
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.1% Indels: 0
Gaps: 0

US-09-978-274A-8 (1-110) x US-09-978-274A-3 (1-792)

QY 2 GlyValAspSerPheProValIleThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
DB 463 GAGGTTGATTCATTCCTCGTAAAAAAGAGGCTTTTCTTACGTGGAGCCATCCAAATG 522

QY 22 ValSerGluAlaAlaArgPheLeuYrIleGluAsnGlnValIleYThrAsnPheAsnArg 41
DB 523 GTTTCAGAGGCGAGGCGCATTCAGTACATAGAGAACCAAGTCAGCAAGATTTTAATGA 582

QY 42 AlaPheYrProAspProLeuValIleAsnLeuGluGluYrTPGIlyYrIleSerGlu 61
DB 583 GCATTCCTACCTGATCCCAAGTAATTAATTTGAGAGGAAGTGGGCAAAATCTCTGAG 642

QY 62 AlaIleHisAsnAlaIleAsnGlyValAlaLeuProIleYrPheGluLeuValAspAlaIle 81

DB 643 GCATTCACAAATGCCAAGATGGGCTTTACCCAAACCACTTGAGCTAGTGCCAA 702

QY 82 GlyThrIleYrPleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIle 101
DB 703 GGTACCAAGTGGATGATGTTCTTAGAGTGATGAATCATCTGATGTGGCACTCTTAAG 762

QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 763 TACGTTAATGGAACCTGTGACAGCAACT 789

RESULT 3
US-09-978-274A-1
; Sequence 1, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Neelam, Anil
; APPLICANT: Atkinson, Howard
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Phycolacca americana
; US-09-978-274A-1

Alignment Scores:
Pred. No.: 5.79e-72 Length: 945
Score: 564.00 Matches: 109
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.1% Indels: 0
Gaps: 0

US-09-978-274A-8 (1-110) x US-09-978-274A-1 (1-945)

QY 2 GlyValAspSerPheProValIleThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
DB 532 GAGGTTGATTCATTCCTCGTAAAAAAGAGGCTTTTCTTACGTGGAGCCATCCAAATG 591

QY 22 ValSerGluAlaAlaArgPheLeuYrIleGluAsnGlnValIleYThrAsnPheAsnArg 41
DB 592 GTTTCAGAGGCGAGGCGCATTCAGTACATAGAGAACCAAGTCAGCAAGATTTTAATGA 651

QY 42 AlaPheYrProAspProLeuValIleAsnLeuGluGluYrTPGIlyYrIleSerGlu 61
DB 652 GCATTCCTACCTGATCCCAAGTAATTAATTTGAGAGGAAGTGGGCAAAATCTCTGAG 711

QY 62 AlaIleHisAsnAlaIleAsnGlyValAlaLeuProIleYrPheGluLeuValAspAlaIle 81
DB 712 GCATTCACATGCCAAGATGGGCTTTACCCAAACCACTTGAGCTAGTGCCAA 771

QY 82 GlyThrIleYrPleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIle 101
DB 772 GGTACCAAGTGGATGATGTTCTTAGAGTGATGAATCATCTGATGTGGCACTCTTAAG 831

QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 832 TACGTTAATGGAACCTGTGACAGCAACT 858

RESULT 4
US-09-978-274A-19
; Sequence 19, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher


```

; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PAP-S/Cytostatin fusion
US-09-978-274a-19

Alignment Scores:
Pred. No.: 2,866-65      Length: 1092
Score: 519.00           Matches: 101
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 91.2%      Indels: 0
DB: 3                   Gaps: 0

US-09-978-274A-8 (1-110) x US-09-978-274A-19 (1-1092)
QY 2 GlyValAspSerPheProValIyThrGluAlaPhePheLeuValAlaIleGlnMet 21
Db 463 GGAGTGTGATTCATTCCTCGTAAACCTGAGGCTTTTCTACTGAGCCATCCAAATG 522
QY 22 ValSerGluAlaIaArgPheIyTrIleGluSngInValIyThrAsnPhaAsnArg 41
Db 523 GTTTCAGAGGAGGCGCATTAAGACATGACAGAACCAAGTCACAACTAATTTTAATGA 582
QY 42 AlaPheTyRProAspProIySValIleAsnLeuGluGluIySTpGlyIySileSerGlu 61
Db 583 GCATTTACCTGATCCCAAGTAATTAATTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 642
QY 62 AlaIleHisAsnAlaIyAsnGlyAlaLeuProIySProIySLeuValAspAlaIyS 81
Db 643 GCATTTCAACATGCGCAAGATGAGGCTTTACCAACCACTGAGCTAGTGAGATGCCAA 702
QY 82 GlyThrIySTpIleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIyS 101
Db 703 GGTACCAAGTGAATGTTCTTAGAGTGATGAATCAATCGTAGTGCACTCCTTAAG 762
QY 102 Tyr 102
Db 763 TAC 765

RESULT 5
US-09-978-274A-31
; Sequence 31, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 1368
; TYPE: DNA
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; ORGANISM: Phytolacca americana
US-09-978-274A-31

Alignment Scores:
Pred. No.: 1,376-55      Length: 1368
Score: 454.00           Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8%      Indels: 0
DB: 3                   Gaps: 0

US-09-978-274A-8 (1-110) x US-09-978-274A-31 (1-1368)
QY 2 GlyValAspSerPheProValIyThrGluAlaPhePheLeuValAlaIleGlnMet 21
Db 750 GGAGTGTGATTCATTCCTCGTAAACCTGAGGCTTTTCTACTGAGCCATCCAAATG 809
QY 22 ValSerGluAlaIaArgPheIyTrIleGluSngInValIyThrAsnPhaAsnArg 41
Db 810 GTATCAGAGGAGCAAGATTCAGTACATAGAGATCAGTGAAACTAATTTTAACAGA 869
QY 42 AlaPheTyRProAspProIySValIleAsnLeuGluGluIySTpGlyIySileSerGlu 61
Db 870 GCATTTCAACCTTAATCCCAAGTACTTAATTTGCAAGACATGGGTAAAGATTCAACA 929
QY 62 AlaIleHisAsnAlaIyAsnGlyAlaLeuProIySProIySLeuValAspAlaIyS 81
Db 930 GCAATTCAGATGCGCAAGATGAGTTTTACCAACCTCTGAGCTAGTGAGATGCCAGT 989
QY 82 GlyThrIySTpIleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuIyS 101
Db 990 GGTGCCAAGTGAATGTTCTTAGAGTGATGAATCAACCTGATGTAGCACTCTTAAC 1049
QY 102 TyrValAsnGlyThrCySerIleThr 110
Db 1050 TACGTGTGTGGAGCTGTCAAGACAAC 1076

RESULT 6
US-10-467-009-1
; Sequence 1, Application US/10467009
; Publication No. US20040241673A1
; GENERAL INFORMATION:
; APPLICANT: RUTGERS, THE STATE UNIVERSITY
; TITLE OF INVENTION: NON-CYTOTOXIC PAP MUTANTS
; FILE REFERENCE: OCIRS 3.4-076
; CURRENT APPLICATION NUMBER: US/10/467,009
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: 60/266,396
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: Phytolacca americana
; NAME/KEY: CDS
; LOCATION: (225)..(1160)
US-10-467-009-1

Alignment Scores:
Pred. No.: 1,386-55      Length: 1376
Score: 454.00           Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8%      Indels: 0
DB: 8                   Gaps: 0

US-09-978-274A-8 (1-110) x US-10-467-009-1 (1-1376)
QY 2 GlyValAspSerPheProValIyThrGluAlaPhePheLeuValAlaIleGlnMet 21
Db 747 GGAGTGTGATTCATTCCTGAGAAACCGAAGCGGAATTCCTATTTGTAGCAATCAATG 806
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QY 22 ValSerGluAlaAlaArgPheLysTrpIleGluAsnGlnValLysThrAsnPheAsnArg 41
DB 807 GTATCAGAGGACCAAGATTCAAGTACATGAGAAATCAGGTGAATACTAATTTTAAACAGA 866
QY 42 AlaPheTyrProAspProLysValIleAsnLeuGluLysTrpGlyLysIleSerGlu 61
DB 867 GCATTCAACCTTAATCCCAAGTACTTAATTTCAGAGACATGGGGTAAAGATTTCACA 926
QY 62 AlaIleHisAsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLys 81
DB 927 GCATTCAATGATGCCAAGATGAGGTTTACCCAAACCTCTCGAGCTAGTGAGTCCAGT 986
QY 82 GlyThrLysTrpIleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 101
DB 987 GGTGCCAAGTGAATGATGTGAGAGTGATGAATCAAGCCTGATGACACTCTTAAAC 1046
QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 1047 TACGTTGGTGGAGCTGTCAAGACACT 1073

RESULT 7
US-09-978-274a-30
; Sequence 30, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Ackinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; PRIORITY FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIORITY FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Phytolacca americana
US-09-978-274a-30

Alignment Scores:
Pred. No.: 1,39e-55 Length: 1379
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
Gaps: 0
DB: 3

US-09-978-274a-8 (1-110) x US-09-978-274a-30 (1-1379)
QY 2 GlyValAspSerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
DB 750 GAGAGTATGTCATCTACTGAGAAACCGAAGCCGAATTCCTATTGTGAGCCATCAATG 809
QY 22 ValSerGluAlaAlaArgPheLysTrpIleGluAsnGlnValLysThrAsnPheAsnArg 41
DB 810 GTATCAGAGGACCAAGATTCAAGTACATGAGAAATCAGGTGAATACTAATTTTAAACAGA 869
QY 42 AlaPheTyrProAspProLysValIleAsnLeuGluLysTrpGlyLysIleSerGlu 61
DB 870 GCATTCAACCTTAATCCCAAGTACTTAATTTCAGAGACATGGGGTAAAGATTTCACA 929
QY 62 AlaIleHisAsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLys 81
DB 930 GCATTCAATGATGCCAAGATGAGGTTTACCCAAACCTCTCGAGCTAGTGAGTCCAGT 989
QY 82 GlyThrLysTrpIleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 101
DB 990 GGTGCCAAGTGAATGATGTGAGAGTGATGAATCAAGCCTGATGACACTCTTAAAC 1049
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QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 1050 TACGTTGGTGGAGCTGTCAAGACACT 1076

RESULT 8
US-11-106-187-1
; Sequence 1, Application US/11106187
; Publication No. US20050183162A1
; GENERAL INFORMATION:
; APPLICANT: TUNER, NITGUN E.
; APPLICANT: WANG, PINGER
; TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
; FILE REFERENCE: OCIRS 3.9-060 CONT
; CURRENT APPLICATION NUMBER: US/11/106,187
; PRIORITY FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US/09/721,047
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: PCT/US99/11301
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/086,374
; PRIORITY FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Phytolacca americana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (225)..(1163)
US-11-106-187-1

Alignment Scores:
Pred. No.: 1,39e-55 Length: 1379
Score: 454.00 Matches: 90
Percent Similarity: 87.2% Conservative: 5
Best Local Similarity: 82.6% Mismatches: 14
Query Match: 79.8% Indels: 0
Gaps: 0
DB: 10

US-09-978-274a-8 (1-110) x US-11-106-187-1 (1-1379)
QY 2 GlyValAspSerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
DB 750 GAGAGTATGTCATCTACTGAGAAACCGAAGCCGAATTCCTATTGTGAGCCATCAATG 809
QY 22 ValSerGluAlaAlaArgPheLysTrpIleGluAsnGlnValLysThrAsnPheAsnArg 41
DB 810 GTATCAGAGGACCAAGATTCAAGTACATGAGAAATCAGGTGAATACTAATTTTAAACAGA 869
QY 42 AlaPheTyrProAspProLysValIleAsnLeuGluLysTrpGlyLysIleSerGlu 61
DB 870 GCATTCAACCTTAATCCCAAGTACTTAATTTCAGAGACATGGGGTAAAGATTTCACA 929
QY 62 AlaIleHisAsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLys 81
DB 930 GCATTCAATGATGCCAAGATGAGGTTTACCCAAACCTCTCGAGCTAGTGAGTCCAGT 989
QY 82 GlyThrLysTrpIleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 101
DB 990 GGTGCCAAGTGAATGATGTGAGAGTGATGAATCAAGCCTGATGACACTCTTAAAC 1049
QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 1050 TACGTTGGTGGAGCTGTCAAGACACT 1076

RESULT 9
US-09-765-527-246
; Sequence 246, Application US/09765527
; Patent No. US2002006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
```

TITLE OF INVENTION: Methods for Recombinant Microbial Production of
Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 246:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: "gelonin"
SEQUENCE DESCRIPTION: SEQ ID NO: 246:
US-09-978-274a-8 (1-110) x US-09-765-527-246 (1-813)
Alignment Scores:
Pred. No.: 1,24e-20 Length: 813
Score: 213.50 Matches: 47
Percent Similarity: 61.5% Conservative: 20
Best Local Similarity: 43.1% Mismatches: 41
Query Match: 37.5% Indels: 1
DB: 3 Gaps: 1
US-09-978-274A-8 (1-110) x US-09-765-527-246 (1-813)
3 ValAspSerPheProValIysThrGluAlaPhePheLeuValAlaIleGlnMetVal 22
433 ATGACCAATTAATAACCAACGAGATAGCTTCTCTATTGCTGTGTTATTCATTAATGCTG 492
23 SerGluAlaIaIaArgPheIysTyrIleGluAsnGlnValIysThrAsnPheAsnArgAla 42
493 TCTGACGACCTGCATTCACCTTATTGAGAACCAAAATTAAATAACTTTCACCAACGAGA 552
43 PheTyrProAspProIysValIleAsnLeuGlnIubIysTyrGlyTyrIleSerGluAla 62
553 ATTCGCCCGCGAATAATATACATCAGCTTGAGAAATTAATGGGTAAACTCTGCTTCAG 612
63 IleHis---AsnAlaIysAsnGlyAlaLeuProIysPheLeuGlnIubLeuValAspAlaIys 81
613 ATCCGACATCAAGGTGCAATGAGATGTTTCGAGAGCGAGTTGAAATTGGAACGTGCAAT 672
82 GlyThrTyrPheIleValIleuArgValAspGluIleAsnArgAspValAlaIleuLeuIys 101
673 GCGCAAAATAATACATGATGTCACCGCAGTTCATCAATAAACCAAAATGCACTCTTGAG 732
102 TyrValAsnGlyThrCysGlnThrThr 110

Db 733 TTCGTCGATAAAGATCCCTAAACGAGC 759
RESULT 10
US-10-127-890-11
Sequence 11, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSER: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-127-890-11
Alignment Scores:
Pred. No.: 1,24e-20 Length: 813
Score: 213.50 Matches: 47
Percent Similarity: 61.5% Conservative: 20
Best Local Similarity: 43.1% Mismatches: 41
Query Match: 37.5% Indels: 1
DB: 6 Gaps: 1
US-09-978-274A-8 (1-110) x US-10-127-890-11 (1-813)
3 ValAspSerPheProValIysThrGluAlaPhePheLeuValAlaIleGlnMetVal 22

```

Db      433 ATAGACATTATAACCAACGAGATGCTTCTCTATTGTTGTTATTCAATGGTG 492
Qy      23 SerGluAlaAlaArgPheIysTrIleGluAenGlnValIysThrAenPheAnaGAla 42
        |||
        |||
        |||
Db      493 TCTGAAGACAGCTCGATTCACTTATTGAGAACCAATTAAGAAATACCTTCAACGAGA 552
Qy      43 PheTy-ProAspProIysValIleAenIeugIuIystrIpGlyIysIleSerGluAla 62
        |||
        |||
        |||
Db      553 ATTCGCCCGCGGAATATATACATACGCTTGAGAAATTAAGGGGTAACTCTGTTCCAG 612
Qy      63 IleHle---AsnAlaIysAenGlyAlaLeuProIysPheIeugIuLeuValAspAlaIys 81
        |||
        |||
        |||
Db      613 ATCCGACATCAGGTGGAATGGAATGTTTCGAGCGCATGGAATGGAACGCAAT 672
Qy      82 GlyThrIysTrIleValIleAenIeugIuIystrIpGluIleAenIysAspValAlaLeuLeuIys 101
        |||
        |||
        |||
Db      673 GGCAGAAAATATCATGTGTACCGCGAGTTGATCAAGTAACCAAAATATGACCTTTGAG 732
Qy      102 TyrValAsnGlyThrCysGlnThr 110
        |||
        |||
        |||
Db      733 TTGCTGATTAAGATCTTAACGAGC 759

RESULT 11
US-10-717-243-11
; Sequence 11, Application US/10717243
; Publication No. US2005054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
;               Carroll, Stephen F.
;               Stunlike, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;               Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-Nov-2003
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8869
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-717-243-11

Alignment Scores:
Pred. No.: 1,248-20 Length: 813
Score: 213.50 Matches: 47
Percent Similarity: 61.5% Conservative: 20
Best Local Similarity: 43.1% Mismatches: 41
Query Match: 37.5% Indels: 1
DB: 9 Gaps: 1

US-09-978-274a-8 (1-110) x US-10-717-243-11 (1-813)
Qy      3 ValAspSerPheProValIysThrGluAlaPhePheLeuLeuValAlaIleGlnMetVal 22
        |||
        |||
        |||
Db      433 ATAGACATTATAACCAACGAGATGCTTCTCTATTGTTGTTATTCAATGGTG 492
Qy      23 SerGluAlaAlaArgPheIysTrIleGluAenGlnValIysThrAenPheAnaGAla 42
        |||
        |||
        |||
Db      493 TCTGAAGACAGCTCGATTCACTTATTGAGAACCAATTAAGAAATACCTTCAACGAGA 552
Qy      43 PheTy-ProAspProIysValIleAenIeugIuIystrIpGlyIysIleSerGluAla 62
        |||
        |||
        |||
Db      553 ATTCGCCCGCGGAATATATACATACGCTTGAGAAATTAAGGGGTAACTCTGTTCCAG 612
Qy      63 IleHle---AsnAlaIysAenGlyAlaLeuProIysPheIeugIuLeuValAspAlaIys 81
        |||
        |||
        |||
Db      613 ATCCGACATCAGGTGGAATGGAATGTTTCGAGCGCATGGAATGGAACGCAAT 672
Qy      82 GlyThrIysTrIleValIleAenIeugIuIystrIpGluIleAenIysAspValAlaLeuLeuIys 101
        |||
        |||
        |||
Db      673 GGCAGAAAATATCATGTGTACCGCGAGTTGATCAAGTAACCAAAATATGACCTTTGAG 732
Qy      102 TyrValAsnGlyThrCysGlnThr 110
        |||
        |||
        |||
Db      733 TTGCTGATTAAGATCTTAACGAGC 759

RESULT 12
US-10-074-596-2
; Sequence 2, Application US/10074596
; Publication No. US2003017633A1
; GENERAL INFORMATION:
; APPLICANT: ROSENBLUM, MICHAEL G.
; APPLICANT: CHEUNG, LAWRENCE
; TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
; TITLE OF INVENTION: MAKING THEROF
; FILE REFERENCE: CLFR.007US
; CURRENT APPLICATION NUMBER: US/10/074,596
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/268,402
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Gelonium multiflorum
US-10-074-596-2

Alignment Scores:
Pred. No.: 2,136-20 Length: 1176
Score: 213.50 Matches: 47
Percent Similarity: 61.5% Conservative: 20
Best Local Similarity: 43.1% Mismatches: 41
Query Match: 37.5% Indels: 1
DB: 6 Gaps: 1

US-09-978-274a-8 (1-110) x US-10-074-596-2 (1-1176)

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QY 3 ValAspSerPheProValIleThrGluAlaPhePheLeuValAlaIleGlnMetVal 22
DB 594 ATAGCAATTAATAACCAACGAGATAGTCTCTATTGGTTGTTATTCAATGGTG 653
QY 23 SerGluAlaIleArgPheIleTyrIleGluGlnValIleThrAsnPheAsnArgAla 42
DB 654 TCTGAGCAGCTCGATTCACCTTATTAAGAACCAATTAAGAAATTAATCTTCACAGGA 713
QY 43 PheTyrProAspProIleValIleAsnLeuGluGluTyrPglIleValIleSerGluAla 62
DB 714 ATTCGCCCGGAGATTAATCAATCACTGAGATTAATGGGTAACTCTCGTCCAG 773
QY 63 IleHis--AsnAlaIleAsnGlyAlaLeuProIleProLeuGluLeuValAspAlaIle 81
DB 774 ATCCGACATCAGGTGCAATGAGATGTTTCGAGGACGATTAATGGAACGTCAAT 833
QY 82 GlyThrIleTyrPleValIleValIleAspGluIleAsnArgAspValAlaLeuLeuIle 101
DB 834 GGCAGAAATATCTATGTCACCGCAGTGTATCAAGTAAACCAAAATAGCACTTGAAG 893
QY 102 TyrValAsnGlyThrCysGlnThrThr 110
DB 894 TTCGTCATTAAGATCCTAAACGAGC 920
RESULT 13
US-11-084-080-25
Sequence 25, Application US/11084080
Publication No. US20050238642A1
GENERAL INFORMATION:
APPLICANT: BAKER, Matthew
APPLICANT: CARR, Francis J.
APPLICANT: HELLENDORF, Koen
APPLICANT: CIZEAU, Jeanick
APPLICANT: MACDONALD, Glen Christopher
APPLICANT: ENTWISTLE, Joycelyn
APPLICANT: BOSCH, Denis Georges
APPLICANT: GLOVER, Nicholas Ronald
TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
FILE REFERENCE: 10241-44
CURRENT APPLICATION NUMBER: US/11/084,080
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US 60/554,580
PRIOR FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: US 60/630,571
PRIOR FILING DATE: 2004-11-26
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn version 3.3
SEQ ID NO 25
LENGTH: 2407
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VB6-845-geloniin
US-11-084-080-25
Alignment Scores:
Pred. No.: 6,08e-20 Length: 2407
Score: 213.50 Matches: 46
Percent Similarity: 62.1% Conservative: 18
Best Local Similarity: 44.7% Mismatches: 38
Query Match: 37.5% Indels: 1
DB: 10 Gaps: 1
US-09-978-274a-8 (1-110) x US-11-084-080-25 (1-2407)
QY 3 ValAspSerPheProValIleThrGluAlaPhePheLeuValAlaIleGlnMetVal 22
DB 1257 ATAGCAATTAATAACCAACGAGATAGTCTCTATTGGTTGTTATTCAATGGTG 1316
QY 23 SerGluAlaIleArgPheIleTyrIleGluGlnValIleThrAsnPheAsnArgAla 42
DB 1317 TCTGAGCAGCTCGATTCACCTTATTAAGAACCAATTAAGAAATTAATCTTCACAGGA 1376

QY 43 PheTyrProAspProIleValIleAsnLeuGluGluTyrPglIleValIleSerGluAla 62
DB 1377 ATCCGCCCGGAGATTAATCAATCACTGAGATTAATGGGTAACTCTCGTCCAG 1436
QY 63 IleHis--AsnAlaIleAsnGlyAlaLeuProIleProLeuGluLeuValAspAlaIle 81
DB 1437 ATCCGACATCAGGTGCAATGAGATGTTTCGAGGACGATTAATGGAACGTGCAAT 1496
QY 82 GlyThrIleTyrPleValIleValIleAspGluIleAsnArgAspValAlaLeuLeuIle 101
DB 1497 GGCAGAAATATCTATGTCACCGCAGTGTATCAAGTAAACCAAAATAGCACTTGAAG 1556
QY 102 TyrValAsn 104
DB 1557 TTCGTCAT 1565
RESULT 14
US-09-765-527-258
Sequence 258, Application US/09765527
Patent No. US20020006638A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 258:
SEQUENCE CHARACTERISTICS:
LENGTH: 955 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: protein
FEATURE:
NAME/KEY: CDS
LOCATION: 66..944
FEATURE:
NAME/KEY: misc_feature
LOCATION: residues 1-65
OTHER INFORMATION: /label= BcORI
/note="residues 1-65 comprise EcoRI site to beginning of pel B."
FEATURE:
NAME/KEY: misc_feature
LOCATION: AA 1-32
OTHER INFORMATION: /label= pel B
/note="pel B is the leader sequence from the pectate lyase

gene of Erwinia carotovora."

FEATURE:
NAME/KEY: misc_feature
LOCATION: AA 23-273
OTHER INFORMATION: /label="gelonin"
/note="gelonin (see U.S. Patent No. 5,416,202)."

FEATURE:
NAME/KEY: misc_feature
LOCATION: AA 274-275
OTHER INFORMATION: /label= EagI
/note="EagI cloning site."

FEATURE:
NAME/KEY: misc_feature
LOCATION: AA 276-279
OTHER INFORMATION: /label= cleavage linker
/note="Ala-Leu-Asp-Pro linking sequence with Asp-Pro cleavage site."

FEATURE:
NAME/KEY: misc_feature
LOCATION: AA 280-293
OTHER INFORMATION: /label= peptide sequence
/note="BPI-derived peptide."

FEATURE:
NAME/KEY: misc_feature
LOCATION: residues 945-954
OTHER INFORMATION: /label= XhoI
/note="residues 945-955 comprise stop codon and XhoI site."

SEQUENCE DESCRIPTION: SEQ ID NO: 258

US-09-765-527-258

Alignment Scores:
Pred. No.: 2.2e-20 Length: 955
Score: 212.50 Matches: 46
Percent Similarity: 62.1% Conservatives: 18
Best Local Similarity: 44.7% Mismatches: 38
Query Match: 37.3% Indels: 1
Gaps: 1

US-09-978-274A-8 (1-110) x US-09-765-527-258 (1-955)

Qy 3 ValAspSerPheProValIyThrGluAlaPhePheLeuValAlaIleGlnMetVal 22
:::|||||
Db 564 ATAGACATTAATAACCAAGAGATAGCTCTCTATTGTTGTTATTCATATGGTG 623
Qy 23 SerGluAlaAlaArgPheIySTyTlEGluGlnGlnValIySThrAsnPheAsnArgAla 42
|||||
Db 624 TCTGAAACAGCTCGATTCACTTATTGAGAACCAATTGAAATTACTTTCACACAGAGA 683
Qy 43 PheTyPProAspProIySValIleAsnLeuGluGluIySTPGIYLySleSerGluAla 62
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Db 684 ATTCGCGCGGCGAATTAATACATCACTTGAGAAATTAAGGTTAACTCTCGTCCAG 743
Qy 63 IleHis--AsnAlaIySAsnGlyAlaLeuPProIySProLeuGluLeuValAspAlaIyS 81
|||||
Db 744 ATCCGACATCAGGTGCAATGGAATGTTTCGAGGCGCATGTAATGGAACGTCGAAT 803
Qy 82 GlyThrySTPleValleuArgValAspGluIleAsnArgPheValAlaLeuLeuIyS 101
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Db 804 GGCAGAAAAATCACTATGTCACCGCAGTGTGATCAAGTAAACCCAAATGCACTCTTAAG 863
Qy 102 TyrValAsn 104
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Db 864 TTCGTGAT 872

RESULT 15
US-09-765-527-252
Sequence 252: Application US/09765527
Patent No. US20020006638A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerslein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 1003 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

FEATURE:
NAME/KEY: CDS
LOCATION: 66..992

FEATURE:
NAME/KEY: misc_feature
LOCATION: residues 1-65
OTHER INFORMATION: /label= EcoRI
/note="residues 1-65 comprise EcoRI site to beginning of pel B."

FEATURE:
NAME/KEY: misc_feature
LOCATION: AA 1-22
OTHER INFORMATION: /label= pel B
/note="pel B is the leader sequence from the pectate lyase gene of Erwinia carotovora."

FEATURE:
NAME/KEY: misc_feature
LOCATION: AA 23-273
OTHER INFORMATION: /label= "gelonin"
/note="gelonin (see U.S. Patent No. 5,416,202)."

FEATURE:
NAME/KEY: misc_feature
LOCATION: AA 274-275
OTHER INFORMATION: /label= EagI
/note="EagI cloning site."

FEATURE:
NAME/KEY: misc_feature
LOCATION: AA 276-279
OTHER INFORMATION: /label= cleavage linker
/note="Ala-Leu-Asp-Pro linking sequence with Asp-Pro cleavage site."

FEATURE:
NAME/KEY: misc_feature
LOCATION: AA 280-309
OTHER INFORMATION: /label= peptide sequence
/note="BPI-derived peptide."

FEATURE:
NAME/KEY: misc_feature
LOCATION: residues 993-1011
OTHER INFORMATION: /label= XhoI

:/note="residues 993-1003 comprise stop codon and xhoi site."
: SEQUENCE DESCRIPTION: SEQ ID NO: 252:
US-09-765-527-252

Alignment Scores:

Pred. No.:	2,366-20	Length:	1003
Score:	212.50	Matches:	46
Percent Similarity:	62.1%	Conservative:	18
Best Local Similarity:	44.7%	Mismatches:	38
Query Match:	37.3%	Indels:	1
DB:	3	Gaps:	1

US-09-978-274a-8 (1-110) x US-09-765-527-252 (1-1003)

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QY      3 ValAspSerPheProValIysThrGluAlaPhePheLeuValAlaIleGlnMetVal 22
      ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      564 ATAGCAATTATTAACCAACGAGATAGCTAGTCTCTATTGGTTGTTATTCAAATGSGTG 623

QY      23 SerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPhenArgAla 42
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      624 TCTGAGCAGCTCGATTCACTTATGTGAGAACCAATTAGAAATTAACCTTCAACAGAGA 683

QY      43 PheTyrProAspProLysValIleAsnLeuGluLysTyrGlyLysIleSerGluAla 62
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      684 ATTGCCCCGGCGAATPAATACATCAGCCTTGAGATAATGGGTAAACTCTCGTTCAG 743

QY      63 IleHis--AsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLys 81
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      744 ATCCGACATCAGGTGCAATGCAATGTTTCGAGGCAAGTGAATGGAAAGTGCATAT 803

QY      82 GlyThrLysTyrPileValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 101
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      804 GGCATAAAATACTATGTCACCGCAGTTGATCAAGTAAACCAAAATATGCACTTGAAAG 863

QY      102 TyrValAsn 104
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      864 TTGCTCGATT 872
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Search completed: April 9, 2006, 03:12:39
Job time : 396.829 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 9, 2006, 01:48:26 ; Search time 288.537 Seconds
(without alignments)
1525.144 Million cell updates/sec

Title: US-09-978-274A-8

Percent score: 569
Sequence: 1 MGVDSPVKTAEAPFLVAIQ.....DEINRDVALKYVNGTCQTT 110

Scoring table:

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Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Zgapop 6.0 , Zgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 9267905 segs, 2000278028 residues

Total number of hits satisfying chosen parameters: 18535810

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Published.Applications.NA.New -QFMT=fastest -SUFFIX=p2n.rnpbn -MINMATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODR=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abes03p
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-NO MMAP -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG -DEV TIMEOUT=120
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA.New:*
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2: /SID55/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /SID55/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /SID55/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /SID55/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /SID55/ptodata/1/pubpna/US09_NEW_PUB.seq1:*
7: /SID55/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
8: /SID55/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
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11: /SID55/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
12: /SID55/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
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14: /SID55/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
15: /SID55/ptodata/1/pubpna/US60_NEW_PUB.seq4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454	79.8	1360	14	US-11-010-795-19
2	200	35.1	934	14	US-11-010-795-21

3	196.5	34.5	1855	8	US-10-893-584-35	Sequence 35, Appl
4	195.5	34.4	1813	8	US-10-893-584-245	Sequence 245, App
5	194	34.1	1810	8	US-10-893-584-168	Sequence 168, App
6	193.5	34.0	1807	8	US-10-893-584-196	Sequence 196, App
7	192	33.7	807	14	US-11-010-795-23	Sequence 23, Appl
8	192	33.7	1623	8	US-10-893-584-273	Sequence 273, App
9	192	33.7	1819	8	US-10-893-584-238	Sequence 238, App
10	192	33.7	1822	8	US-10-893-584-175	Sequence 175, App
11	192	33.7	1822	8	US-10-893-584-182	Sequence 182, App
12	192	33.7	1822	8	US-10-893-584-231	Sequence 231, App
13	192	33.7	1828 <th>8</th> <th>US-10-893-584-210</th> <th>Sequence 210, App</th>	8	US-10-893-584-210	Sequence 210, App
14	192	33.7	1831 <th>8</th> <th>US-10-893-584-161</th> <th>Sequence 161, App</th>	8	US-10-893-584-161	Sequence 161, App
15	192	33.7	1834 <th>8</th> <th>US-10-893-584-203</th> <th>Sequence 203, App</th>	8	US-10-893-584-203	Sequence 203, App
16	192	33.7	1834 <th>8</th> <th>US-10-893-584-154</th> <th>Sequence 154, App</th>	8	US-10-893-584-154	Sequence 154, App
17	192	33.7	1837 <th>8</th> <th>US-10-893-584-266</th> <th>Sequence 266, App</th>	8	US-10-893-584-266	Sequence 266, App
18	192	33.7	1843 <th>8</th> <th>US-10-893-584-259</th> <th>Sequence 259, App</th>	8	US-10-893-584-259	Sequence 259, App
19	192	33.7	1849 <th>8</th> <th>US-10-893-584-252</th> <th>Sequence 252, App</th>	8	US-10-893-584-252	Sequence 252, App
20	192	33.7	1855 <th>8</th> <th>US-10-893-584-3</th> <th>Sequence 3, Appl1</th>	8	US-10-893-584-3	Sequence 3, Appl1
21	192	33.7	1855 <th>8</th> <th>US-10-893-584-5</th> <th>Sequence 5, Appl1</th>	8	US-10-893-584-5	Sequence 5, Appl1
22	192	33.7	1855 <th>8</th> <th>US-10-893-584-7</th> <th>Sequence 7, Appl1</th>	8	US-10-893-584-7	Sequence 7, Appl1
23	192	33.7	1855 <th>8</th> <th>US-10-893-584-9</th> <th>Sequence 9, Appl1</th>	8	US-10-893-584-9	Sequence 9, Appl1
24	192	33.7	1855 <th>8</th> <th>US-10-893-584-13</th> <th>Sequence 13, Appl1</th>	8	US-10-893-584-13	Sequence 13, Appl1
25	192	33.7	1855 <th>8</th> <th>US-10-893-584-15</th> <th>Sequence 15, Appl1</th>	8	US-10-893-584-15	Sequence 15, Appl1
26	192	33.7	1855 <th>8</th> <th>US-10-893-584-17</th> <th>Sequence 17, Appl1</th>	8	US-10-893-584-17	Sequence 17, Appl1
27	192	33.7	1855 <th>8</th> <th>US-10-893-584-19</th> <th>Sequence 19, Appl1</th>	8	US-10-893-584-19	Sequence 19, Appl1
28	192	33.7	1855 <th>8</th> <th>US-10-893-584-21</th> <th>Sequence 21, Appl1</th>	8	US-10-893-584-21	Sequence 21, Appl1
29	192	33.7	1855 <th>8</th> <th>US-10-893-584-23</th> <th>Sequence 23, Appl1</th>	8	US-10-893-584-23	Sequence 23, Appl1
30	192	33.7	1855 <th>8</th> <th>US-10-893-584-25</th> <th>Sequence 25, Appl1</th>	8	US-10-893-584-25	Sequence 25, Appl1
31	192	33.7	1855 <th>8</th> <th>US-10-893-584-27</th> <th>Sequence 27, Appl1</th>	8	US-10-893-584-27	Sequence 27, Appl1
32	192	33.7	1855 <th>8</th> <th>US-10-893-584-29</th> <th>Sequence 29, Appl1</th>	8	US-10-893-584-29	Sequence 29, Appl1
33	192	33.7	1855 <th>8</th> <th>US-10-893-584-31</th> <th>Sequence 31, Appl1</th>	8	US-10-893-584-31	Sequence 31, Appl1
34	192	33.7	1855 <th>8</th> <th>US-10-893-584-33</th> <th>Sequence 33, Appl1</th>	8	US-10-893-584-33	Sequence 33, Appl1
35	192	33.7	1855 <th>8</th> <th>US-10-893-584-37</th> <th>Sequence 37, Appl1</th>	8	US-10-893-584-37	Sequence 37, Appl1
36	192	33.7	1855 <th>8</th> <th>US-10-893-584-39</th> <th>Sequence 39, Appl1</th>	8	US-10-893-584-39	Sequence 39, Appl1
37	192	33.7	1855 <th>8</th> <th>US-10-893-584-48</th> <th>Sequence 48, Appl1</th>	8	US-10-893-584-48	Sequence 48, Appl1
38	192	33.7	1855 <th>8</th> <th>US-10-893-584-50</th> <th>Sequence 50, Appl1</th>	8	US-10-893-584-50	Sequence 50, Appl1
39	192	33.7	1855 <th>8</th> <th>US-10-893-584-52</th> <th>Sequence 52, Appl1</th>	8	US-10-893-584-52	Sequence 52, Appl1
40	192	33.7	1855 <th>8</th> <th>US-10-893-584-54</th> <th>Sequence 54, Appl1</th>	8	US-10-893-584-54	Sequence 54, Appl1
41	192	33.7	1855 <th>8</th> <th>US-10-893-584-74</th> <th>Sequence 74, Appl1</th>	8	US-10-893-584-74	Sequence 74, Appl1
42	192	33.7	1855 <th>8</th> <th>US-10-893-584-77</th> <th>Sequence 77, Appl1</th>	8	US-10-893-584-77	Sequence 77, Appl1
43	192	33.7	1855 <th>8</th> <th>US-10-893-584-80</th> <th>Sequence 80, Appl1</th>	8	US-10-893-584-80	Sequence 80, Appl1
44	192	33.7	1855 <th>8</th> <th>US-10-893-584-83</th> <th>Sequence 83, Appl1</th>	8	US-10-893-584-83	Sequence 83, Appl1
45	192	33.7	1855 <th>8</th> <th>US-10-893-584-86</th> <th>Sequence 86, Appl1</th>	8	US-10-893-584-86	Sequence 86, Appl1

ALIGNMENTS

RESULT 1
US-11-010-795-19
: Sequence 19, Application US/11010795
: Publication No. US20060005271A1
: GENERAL INFORMATION:
: APPLICANT: TUMER, NILGUN E.
: APPLICANT: DI, RONG
: TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
: TITLE OF INVENTION: RESISTANT TO TRICHOHECENE FUNGAL TOXINS
: FILE REFERENCE: OCIRS 3.0-065
: CURRENT APPLICATION NUMBER: US/11/010,795
: PRIOR APPLICATION NUMBER: 2004-12-13
: PRIOR FILING DATE: 2003-12-12
: NUMBER OF SEQ ID NOS: 44
: SOFTWARE: PatentIn Ver. 3.3
: SEQ ID NO 19
: LENGTH: 1360
: TYPE: DNA
: ORGANISM: Phytolacca americana
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (207)..(1145)
: US-11-010-795-19
Alignment Scores:

Pred. No.: 1,58e-52 Length: 1360
 Score: 454.00 Matches: 90
 Percent Similarity: 87.2% Conservative: 5
 Best Local Similarity: 82.6% Mismatches: 14
 Query Match: 79.8% Indels: 0
 DB: 14 Gaps: 0

US-09-978-274A-8 (1-110) x US-11-010-795-19 (1-1360)

QY 2 GlyValAspSerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
 Db 732 GGAGTAGTGCATTCCTACTGAGAAACCGAAGCCCAATTCCTATTGGTAGCCATACAAATG 791
 QY 22 ValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsnPheAsnArg 41
 Db 792 GTATCAGAGCAGCAGATTCACATACATAGAGATACGCTGAAATCTTTTAAACA 851
 QY 42 AlaPheTyrProAspProLysValIleAsnLeuGluLysTyrGlyLysIleSerGlu 61
 Db 852 GCATTCAACCTAATCCCAAGTACTTAATTGCAAGAGACATGGGTTAAGATTCAACA 911
 QY 62 AlaIleHisAsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAspAlaLys 81
 Db 912 GCAATTCATGATGCCAAGATGAGTTTACCCAAACCTTCGAGTAAAGATGCCAGT 971
 QY 82 GlyThrLysTrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLys 101
 Db 972 GGTGCCAAGCGATAGCTTGAGAGTGATGAATCAACCTGATGTAGCACTTTAAAC 1031
 QY 102 TyrValAsnGlyThrCysGlnThrThr 110
 Db 1032 TACGTGTGGAGCTGCAGACACT 1058

RESULT 2

US-11-010-795-21
 ; Sequence 21, Application US/11010795
 ; Publication No. US20060005271A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TUMER, NITGUN E.
 ; APPLICANT: DI, RONG
 ; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
 ; TITLE OF INVENTION: RESISTANT TO TRICHOECENE FUNGAL TOXINS
 ; FILE REFERENCE: OCIRS 3.0-085
 ; CURRENT APPLICATION NUMBER: US/11/010,795
 ; CURRENT FILING DATE: 2004-12-13
 ; PRIOR APPLICATION NUMBER: 60/529,348
 ; PRIOR FILING DATE: 2003-12-12
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn Ver. 3.3
 ; SEQ ID NO 21
 ; LENGTH: 934
 ; TYPE: DNA
 ; ORGANISM: Phytolacca americana
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(930)
 US-11-010-795-21

Alignment Scores:

Pred. No.: 1.94e-17 Length: 934
 Score: 200.00 Matches: 47
 Percent Similarity: 62.0% Conservative: 20
 Best Local Similarity: 43.5% Mismatches: 29
 Query Match: 35.1% Indels: 12
 DB: 14 Gaps: 5

US-09-978-274A-8 (1-110) x US-11-010-795-21 (1-934)

QY 9 LysThrGluAlaPhePheLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 28
 Db 544 AAAAATAGAGCTGAATTTCTTCTTATAGCCCTTCAATAGGTACTAGAGGCAATCAAGGTTT 603
 QY 29 LysTyrIleGluAsnGlnValLysThrAsnPheAsnArgAla-----PheTyrProAsp 46

Db 604 AAATACCTTGAGAAACAGGAGGCTAAATTTGATGATGCCAATGGGTATCAGCCAGAT 663
 QY 47 ProLysValIleAsnLeuGluLysTyrGlyLysIleSerGluAlaIleHisAsnAla 66
 Db 664 CTTAAAGCTATTTTCTTACGAGAAATTTGGACAGTGTTCCTAAGGTCAAT-----GCA 717
 QY 67 LysAsnGly-----AlaLeuProLysProLeuGluLeuValAspAlaLys 81
 Db 718 AAAGTTGGACACCTCCGGTATATGATCTTACTTACCTTGAGACCTTAAAGATAGGAAT 777
 QY 82 GlyThrLysTrpIleValLeuArgValAspGluIleAsnArgAspVal--AlaLeuLeu 100
 Db 778 AATTAACCTTGACCTACGAGCCACCATGAAACGACTTAAGACGACTTATGACATCTCTA 837
 QY 101 LysTyrValAsnGlyThrCysGln 108
 Db 838 ACCCAGCTT-----ACTTGCAG 855

RESULT 3

US-10-893-584-35
 ; Sequence 35, Application US/10893584
 ; Publication No. US20050272048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Borgford, Thor
 ; APPLICANT: Braum, Curtis
 ; APPLICANT: Purac, Adam
 ; APPLICANT: Stoll, Dominik
 ; TITLE OF INVENTION: Ricin-like Toxin Variants for Treatment of Cancer,
 ; TITLE OF INVENTION: Viral or Parasitic Infections
 ; FILE REFERENCE: 10447-025
 ; CURRENT APPLICATION NUMBER: US/10/893,584
 ; CURRENT FILING DATE: 2004-07-19
 ; PRIOR APPLICATION NUMBER: US 09/551,151
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: US 09/403,752
 ; PRIOR FILING DATE: 1999-10-29
 ; PRIOR APPLICATION NUMBER: US 10/089,058
 ; PRIOR FILING DATE: 2000-10-04
 ; NUMBER OF SEQ ID NOS: 274
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 35
 ; LENGTH: 1855
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PAP-246 insert
 US-10-893-584-35

Alignment Scores:

Pred. No.: 1.43e-16 Length: 1855
 Score: 196.50 Matches: 44
 Percent Similarity: 53.3% Conservative: 21
 Best Local Similarity: 36.1% Mismatches: 40
 Query Match: 34.5% Indels: 17
 DB: 8 Gaps: 3

US-09-978-274A-8 (1-110) x US-10-893-584-35 (1-1855)

QY 2 GlyValAspSerPheProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMet 21
 Db 580 GGAGCAGCTGAGCTTCCAACTGCTGCTGCTCTT-----ATTAATTCATCCAAATG 633
 QY 22 ValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThr-----AsnPhe 39
 Db 634 ATTTCAAGCAGCAGCAATTCATATATTGAGGAGAAATGCGCAGAGAAATTAGGTAC 693
 QY 40 AsnArgAlaPheTyrProAspProLysValIleAsnLeuGluLysTyrGlyLysIle 59
 Db 694 AACCGAGATCTGCACCAAGATCTCAGGTAATTACATTTGAGATATAGTTGGGAGAGCTT 753
 QY 60 SerGluAlaIleHisAsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAsp 79

Db 754 TCCACTGCATTCAGAGCTTAACCAAGACCTTGTAGTCCATTCACCTGCAGAGA 813
Qy 80 AAlaySGlyThrylYstrpIleValleuArgValaspGluileAsnArgAspValAlaleu 99
Db 814 CGTATAGTTCAGAAATTCAGTGTGTAACGATGATATATTAATCCCTATCAAGCTCTC 873
Qy 100 LeuYstrYr-----ValAsnglyThr 106
Db 874 ATGGGTATAGATGCGACCTCCACCATGTCAGATTTTCTGGGGTGTAAATGATCG 933
Qy 107 Cysgin 108
Db 934 TGTACA 939

RESULT 4
US-10-893-584-245
; Sequence 245, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 245
; LENGTH: 1813
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-245

Alignment Scores:
Pred. No.: 1,91e-16 Length: 1813
Score: 195.50 Matches: 44
Percent Similarity: 54.8% Conservative: 19
Best Local Similarity: 38.3% Mismatches: 41
Query Match: 34.4% Indels: 11
DB: 8 Gaps: 3

US-09-978-274A-8 (1-110) x US-10-893-584-245 (1-1813)
Qy 2 G1yValaspSerPheProValylThrcIuAlaPhePheLeuValAlaileGlnMet 21
Db 580 GGTGGCACTGAGCTTCCAACTCTGCTGCTCTTT-----ATTAATTGCATCCAAATG 633
Qy 22 ValSerGluAlaAlaArgPheLysTyrilleGluAsnGlnValylStr-----AsnPh 39
Db 634 ATTTCAGAGCAGCAGATTCATATATATTAAGGAGAAATGCCACAGAAATTAAGTAC 693
Qy 40 AsnArgAlaPheTyrProAspProLysValileAsnLeuGlnGluLysTyrGlyLysile 59
Db 694 AACCGAGATCTGCACGATCCTAGGTAATTAACCTTGAGTAAGTATGAGTGGGAGACTT 753
Qy 60 SerGluAlaileHisAsnAlaLysAsnglyAlaLeuProLysProLeuGluLeuValasp 79
Db 754 TCCACTGCATTCAGAGCTTAACCAAGACCTTGTAGTCCATTCACCTGCAGAGA 813
Qy 80 AAlaySGlyThrylYstrpIleValleuArgValaspGluileAsnArgAspValAlaleu 99
Db 814 CGTATAGTTCAGAAATTCAGTGTGTAACGATGATATATTAATCCCTATCAAGCTCTC 873
Qy 100 LeuYstrYr-----ValAsnglyThrCys 107

Db 874 ATGGGTATAGATGCGACACGACGAGAGTATGTCGGGGGCTGT 918
RESULT 5
US-10-893-584-168
; Sequence 168, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 168
; LENGTH: 1810
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-168

Alignment Scores:
Pred. No.: 3.08e-16 Length: 1810
Score: 194.00 Matches: 43
Percent Similarity: 55.3% Conservative: 20
Best Local Similarity: 37.7% Mismatches: 41
Query Match: 34.1% Indels: 10
DB: 8 Gaps: 3

US-09-978-274A-8 (1-110) x US-10-893-584-168 (1-1810)
Qy 2 G1yValaspSerPheProValylThrcIuAlaPhePheLeuValAlaileGlnMet 21
Db 580 GGTGGCACTGAGCTTCCAACTCTGCTGCTCTTT-----ATTAATTGCATCCAAATG 633
Qy 22 ValSerGluAlaAlaArgPheLysTyrilleGluAsnGlnValylStr-----AsnPh 39
Db 634 ATTTCAGAGCAGCAGATTCATATATATTAAGGAGAAATGCCACGAGAAATTAAGTAC 693
Qy 40 AsnArgAlaPheTyrProAspProLysValileAsnLeuGlnGluLysTyrGlyLysile 59
Db 694 AACCGAGATCTGCACGATCCTAGGTAATTAACCTTGAGTAAGTATGAGTGGGAGACTT 753
Qy 60 SerGluAlaileHisAsnAlaLysAsnglyAlaLeuProLysProLeuGluLeuValasp 79
Db 754 TCCACTGCATTCAGAGCTTAACCAAGACCTTGTAGTCCATTCACCTGCAGAGA 813
Qy 80 AAlaySGlyThrylYstrpIleValleuArgValaspGluileAsnArgAspValAlaleu 99
Db 814 CGTATAGTTCAGAAATTCAGTGTGTAACGATGATATATTAATCCCTATCAAGCTCTC 873
Qy 100 LeuYstrYr-----ValAsnglyThrCys 107
Db 874 ATGGGTATAGATGCTCTCCGCAAGAAATTAAGGAGGAGT 915

RESULT 6
US-10-893-584-196
; Sequence 196, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir

```

; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 196
; LENGTH: 1807
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-196

Alignment Scores:
Pred. No.: 3.61e-16 Length: 1807
Score: 193.50 Matches: 44
Percent Similarity: 55.8% Conservative: 19
Best Local Similarity: 38.9% Mismatches: 41
Query Match: 34.0% Indels: 9
DB: Gaps: 3

US-09-978-274a-8 (1-110) x US-10-893-584-196 (1-1807)
QY 2 GtYvalAspSerPheProVallyThrGluAlaPheLeuValAlaIleGluMet 21
Db 580 GGTGGCACTCAGCTTCCAACTCTGCTGCTCTT-----ATTAATTGCATCCAAATG 633
QY 22 ValSerGluAlaAlaArgPheLyThrIleGluAsnGluVallyThr-----AsnPh 39
Db 634 ATTTCAGAGACGACAAATTCATATATTGAGGAGAAATCCGACAGAAATTAAGGTAC 693
QY 40 AsnArgAlaPheTyrrProAspProLyValIleAsnLeuGluGluLyThrGlyLysIle 59
Db 694 AACCGAGATCTGCACGACGATCTAGCGTAATTAACATTGAGAAATAGTTGGGGAGACTT 753
QY 60 SerGluAlaIleHisAsnAlaLysAsnGluValaleuProLyProLeuGluLeuValAsp 79
Db 754 TCCACTCGCAATTCAGAGCTTAACCAAGAGCCTTGTCTAGTCCAAATTCACCTGCAAGA 813
QY 80 AlaLysGlyThrLystrPileValleuArgValAspGluIleAsnArgAspValAlaLeu 99
Db 814 CGTAATGTTCCAAATTCAGTGTGACATGTGATATTAATCCCTATCATAGCTCTC 873
QY 100 LeuLystrYr-----ValAsnGlyThrCys 107
Db 874 ATGGGTATAGATGCCGACGACGAGTACTGCGCGGCTGT 912

RESULT 7
US-11-010-795-23
; Sequence 23, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NIGUN E.
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS AND
; FILE REFERENCE: OCIRS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 23
; LENGTH: 807
; TYPE: DNA
```

```

; ORGANISM: Ricinus communis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(804)
US-11-010-795-23

Alignment Scores:
Pred. No.: 2.08e-16 Length: 807
Score: 192.00 Matches: 41
Percent Similarity: 58.3% Conservative: 19
Best Local Similarity: 39.8% Mismatches: 39
Query Match: 33.7% Indels: 4
DB: Gaps: 2

US-09-978-274a-8 (1-110) x US-11-010-795-23 (1-807)
QY 2 GtYvalAspSerPheProVallyThrGluAlaPheLeuValAlaIleGluMet 21
Db 472 GGTGGCACTCAGCTTCCAACTCTGCTGCTCTT-----ATTAATTGCATCCAAATG 525
QY 22 ValSerGluAlaAlaArgPheLyThrIleGluAsnGluVallyThr-----AsnPh 39
Db 526 ATTTCAGAGACGACAAATTCATATATTGAGGAGAAATCCGACAGAAATTAAGGTAC 585
QY 40 AsnArgAlaPheTyrrProAspProLyValIleAsnLeuGluGluLyThrGlyLysIle 59
Db 586 AACCGAGATCTGCACGACGATCTAGCGTAATTAACATTGAGAAATAGTTGGGGAGACTT 645
QY 60 SerGluAlaIleHisAsnAlaLysAsnGluValaleuProLyProLeuGluLeuValAsp 79
Db 646 TCCACTCGCAATTCAGAGCTTAACCAAGAGCCTTGTCTAGTCCAAATTCACCTGCAAGA 705
QY 80 AlaLysGlyThrLystrPileValleuArgValAspGluIleAsnArgAspValAlaLeu 99
Db 706 CGTAATGTTCCAAATTCAGTGTGACATGTGATATTAATCCCTATCATAGCTCTC 765
QY 100 LeuLystrYr 102
Db 766 ATGGGTAT 774

RESULT 8
US-10-893-584-273
; Sequence 273, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admlr
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 273
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ricin-like toxin (TST10054)
US-10-893-584-273

Alignment Scores:
Pred. No.: 5.08e-16 Length: 1623
Score: 192.00 Matches: 41
```

Percent Similarity: 58.3%
Best Local Similarity: 39.8%
Query Match: 33.7%
DB: 8
Conservative: 19
Mismatches: 39
Indels: 4
Gaps: 2

US-09-978-274a-8 (1-110) x US-10-893-584-273 (1-1623)

QY 2 G1YValaAspSerPheProVallyThrgluAlaPheLeuValAlaIleGlnMet 21
DB 469 GGTCGACCTGACCTTCCAACTGCTGCTCTTT-----ATAATTGATCCAAATG 522
QY 22 ValSerGluAlaAlaArgPheLeuYrTlIleGluAsnGlnVallyThr-----AsnDhe 39
DB 523 ATTTCAGAGACGACCAAGATTCCTAATATATGAGGAGAAATCGCAGCAAGATTAAGTAC 582
QY 40 AsnArgAlaPheYrProAspProLyValIleAsnLeuGluGluYrTgLylyle 59
DB 583 AACCGAGATCTGCACCGATCTTACCGTAAATTACATTGAGAAATAGTGGGGAGACTT 642
QY 60 SerGluAlaIleHisAsnAlaLyAsnGlyAlaLeuProLyProLeuGluLeuValAsp 79
DB 643 TCCACTGCAATTCAGAGCTTACCAAGAGCTTTGCTAGTCAATTCACCTGACAGAGA 702
QY 80 AlAlayeglyThrlyStrPileValleuArgValAspGluIleAsnArgAspValAlaLeu 99
DB 703 CGTATGCTTCCAAATTCAGTGTGACGATGATATATTAAATCCATATACATGCTCTC 762
QY 100 LeuLystrYr 102
DB 763 ATGGTGAT 771

RESULT 9

US-10-893-584-238
; Sequence 238, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 238
; LENGTH: 1819
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-238

Alignment Scores:

Pred. No.: 5.89e-16 Length: 1819
Score: 192.00 Matches: 41
Percent Similarity: 58.3% Conservative: 19
Best Local Similarity: 39.8% Mismatches: 39
Query Match: 33.7% Indels: 4
Gaps: 2

US-09-978-274a-8 (1-110) x US-10-893-584-238 (1-1819)

QY 2 G1YValaAspSerPheProVallyThrgluAlaPheLeuValAlaIleGlnMet 21
DB 580 GGTCGACCTGACCTTCCAACTGCTGCTCTTT-----ATAATTGATCCAAATG 633

QY 22 ValSerGluAlaAlaArgPheLeuYrTlIleGluAsnGlnVallyThr-----AsnDhe 39
DB 634 ATTTCAGAGACGACCAAGATTCCTAATATATGAGGAGAAATCGCAGCAAGATTAAGTAC 693
QY 40 AsnArgAlaPheYrProAspProLyValIleAsnLeuGluGluYrTgLylyle 59
DB 694 AACCGAGATCTGCACCGATCTTACCGTAAATTACATTGAGAAATAGTGGGGAGACTT 753
QY 60 SerGluAlaIleHisAsnAlaLyAsnGlyAlaLeuProLyProLeuGluLeuValAsp 79
DB 754 TCCACTGCAATTCAGAGCTTACCAAGAGCTTTGCTAGTCAATTCACCTGACAGAGA 813
QY 80 AlAlayeglyThrlyStrPileValleuArgValAspGluIleAsnArgAspValAlaLeu 99
DB 814 CGTATGCTTCCAAATTCAGTGTGACGATGATATATTAAATCCATATACATGCTCTC 873
QY 100 LeuLystrYr 102
DB 874 ATGGTGAT 882

RESULT 10

US-10-893-584-175
; Sequence 175, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 1822
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-175

Alignment Scores:

Pred. No.: 5.89e-16 Length: 1822
Score: 192.00 Matches: 41
Percent Similarity: 58.3% Conservative: 19
Best Local Similarity: 39.8% Mismatches: 39
Query Match: 33.7% Indels: 4
Gaps: 2

US-09-978-274a-8 (1-110) x US-10-893-584-175 (1-1822)

QY 2 G1YValaAspSerPheProVallyThrgluAlaPheLeuValAlaIleGlnMet 21
DB 580 GGTCGACCTGACCTTCCAACTGCTGCTCTTT-----ATAATTGATCCAAATG 633
QY 22 ValSerGluAlaAlaArgPheLeuYrTlIleGluAsnGlnVallyThr-----AsnDhe 39
DB 634 ATTTCAGAGACGACCAAGATTCCTAATATATGAGGAGAAATCGCAGCAAGATTAAGTAC 693
QY 40 AsnArgAlaPheYrProAspProLyValIleAsnLeuGluGluYrTgLylyle 59
DB 694 AACCGAGATCTGCACCGATCTTACCGTAAATTACATTGAGAAATAGTGGGGAGACTT 753
QY 60 SerGluAlaIleHisAsnAlaLyAsnGlyAlaLeuProLyProLeuGluLeuValAsp 79
DB 754 TCCACTGCAATTCAGAGCTTACCAAGAGCTTTGCTAGTCAATTCACCTGACAGAGA 813

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QY 80 AlAlaYsGlyThrlySTrPileValLeuArgValAspGluIleAsnArgAspValAlaIleu 99
DB 814 CGTAATGTTCCAAATTCAGTGTACGATGTATATATATCCCTATAGCTCTC 873
QY 100 LeuLySTyr 102
DB 874 ATGGTGTAT 882

RESULT 11
US-10-893-584-182
; Sequence 182, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 182
; LENGTH: 1822
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-182

Alignment Scores:
Pred. No.: 5,99e-16 Length: 1822
Score: 192.00 Matches: 41
Percent Similarity: 58.3% Conservative: 19
Best Local Similarity: 39.8% Mismatches: 39
Query Match: 33.7% Indels: 4
DB: Gaps: 2

US-09-978-274A-8 (1-110) x US-10-893-584-182 (1-1822)
QY 2 G1VAlAspSerPheProVallySThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 580 GGTGGCACTCAGCTTCCAACTCTGGCTCGTCTTT-----ATAATTGCATCCAAATG 633
QY 22 ValSerGluAlaAlaArgPheLySTyrIleGluAsnGlnVallySThr-----AsnPhe 39
DB 634 ATTTCAAGACAGCAAGATTCATATATTGAGGAGAAATGCCACGAGAAATTAGGTAC 693
QY 40 AsnArgAlaPheTyrProAspProLyValIleAsnLeuGluGluLySTrPGlyLyAsIle 59
DB 694 AACCGAGATCTGCACCAATCTTACGCTTAATTCACCTTGAGAAATAGTTGGGGAGACTT 753
QY 60 SerGluAlaIleHisAsnAlaLyAsnGlyAlaLeuProLySProlLeuValAsp 79
DB 754 TCCACTGCATTCAGAGCTTAACCAAGAGCCTTTGCTAGTCCAAATTCAGCAAGA 813
QY 80 AlAlaYsGlyThrlySTrPileValLeuArgValAspGluIleAsnArgAspValAlaIleu 99
DB 814 CGTAATGTTCCAAATTCAGTGTACGATGTATATATATCCCTATAGCTCTC 873
QY 100 LeuLySTyr 102
DB 874 ATGGTGTAT 882

RESULT 12
US-10-893-584-231
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; Sequence 231, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 231
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-231

Alignment Scores:
Pred. No.: 5,9e-16 Length: 1825
Score: 192.00 Matches: 41
Percent Similarity: 58.3% Conservative: 19
Best Local Similarity: 39.8% Mismatches: 39
Query Match: 33.7% Indels: 4
DB: Gaps: 2

US-09-978-274A-8 (1-110) x US-10-893-584-231 (1-1825)
QY 2 G1VAlAspSerPheProVallySThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 580 GGTGGCACTCAGCTTCCAACTCTGGCTCGTCTTT-----ATAATTGCATCCAAATG 633
QY 22 ValSerGluAlaAlaArgPheLySTyrIleGluAsnGlnVallySThr-----AsnPhe 39
DB 634 ATTTCAAGACAGCAAGATTCATATATTGAGGAGAAATGCCACGAGAAATTAGGTAC 693
QY 40 AsnArgAlaPheTyrProAspProLyValIleAsnLeuGluGluLySTrPGlyLyAsIle 59
DB 694 AACCGAGATCTGCACCAATCTTACGCTTAATTCACCTTGAGAAATAGTTGGGGAGACTT 753
QY 60 SerGluAlaIleHisAsnAlaLyAsnGlyAlaLeuProLySProlLeuValAsp 79
DB 754 TCCACTGCATTCAGAGCTTAACCAAGAGCCTTTGCTAGTCCAAATTCAGCAAGA 813
QY 80 AlAlaYsGlyThrlySTrPileValLeuArgValAspGluIleAsnArgAspValAlaIleu 99
DB 814 CGTAATGTTCCAAATTCAGTGTACGATGTATATATATCCCTATAGCTCTC 873
QY 100 LeuLySTyr 102
DB 874 ATGGTGTAT 882

RESULT 13
US-10-893-584-210
; Sequence 210, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admit
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
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;; CURRENT FILING DATE: 2004-07-19
;; PRIOR APPLICATION NUMBER: US 09/551,151
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: US 09/403,752
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: US 10/089,058
;; NUMBER OF SEQ ID NOS: 274
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 210
;; LENGTH: 1828
;; TYPE: DNA
;; ORGANISM: E. coli
US-10-893-584-210

Alignment Scores:
Pred. No.: 5,91e-16 Length: 1828
Score: 192.00 Matches: 41
Percent Similarity: 58.3% Conservative: 19
Best Local Similarity: 39.8% Mismatches: 39
Query Match: 33.7% Indels: 4
Gaps: 2

US-09-978-274a-8 (1-110) x US-10-893-584-210 (1-1828)

QY 2 GlyValAspSerPheProValIleThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 580 GGTGGCACTGACCTTCCAACTCTGCTGCTCTT-----ATTAATTGCAATCCAAATG 633

QY 22 ValSerGluAlaAlaArgPheLeuTyrIleGluAsnGlnValIleThr-----AsnDhe 39
DB 634 ATTTCAAGAGCAGCAGATTTCCAAATATTTTGGAGGAGAAATGCCGACGAAATTAAGTAC 693

QY 40 AsnArgAlaPheTyrProAspProIleValIleAsnLeuGlnIleValIleTyrGlyValIle 59
DB 694 AACCGAGATCTGCACCAAGCTCTAGCTTAATTAACATTAAGTAATGTTGGGGAGACTT 753

QY 60 SerGluAlaIleHisAsnAlaIleAsnGlyAlaLeuProIleValIleValIleValIle 79
DB 754 TCCACTGCAATTCAGAGCTTAACCAAGAGCTTTGTAATCCCAATTCGACGAAAGA 813

QY 80 AlaIleGlyThrIleTyrPileValIleValIleValIleValIleValIleValIleValIle 99
DB 814 CGTATGTTCCAAATTCAGTGTACGATGTGATATTAATCCCATATAGCTCTC 873

QY 100 LeuIleTyr 102
DB 874 ATGGTGTAT 882

RESULT 14
US-10-893-584-161
;; Sequence 161, Application US/10893584
;; Publication No. US20050272048A1
;; GENERAL INFORMATION:
;; APPLICANT: Borgford, Thor
;; APPLICANT: Braun, Curtis
;; APPLICANT: Putac, Dmitri
;; APPLICANT: Stoll, Dominik
;; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
;; TITLE OF INVENTION: Viral or Parasitic Infections
;; FILE REFERENCE: 10447-025
;; CURRENT APPLICATION NUMBER: US/10/893,584
;; CURRENT FILING DATE: 2004-07-19
;; PRIOR APPLICATION NUMBER: US 09/551,151
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: US 09/403,752
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: US 10/089,058
;; NUMBER OF SEQ ID NOS: 274
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 161
;; LENGTH: 1831
;; TYPE: DNA
;; ORGANISM: E. coli
US-10-893-584-203

;; TYPE: DNA
;; ORGANISM: E. coli
US-10-893-584-161

Alignment Scores:
Pred. No.: 5,93e-16 Length: 1831
Score: 192.00 Matches: 41
Percent Similarity: 58.3% Conservative: 19
Best Local Similarity: 39.8% Mismatches: 39
Query Match: 33.7% Indels: 4
Gaps: 2

US-09-978-274a-8 (1-110) x US-10-893-584-161 (1-1831)

QY 2 GlyValAspSerPheProValIleThrGluAlaPhePheLeuValAlaIleGlnMet 21
DB 580 GGTGGCACTGACCTTCCAACTCTGCTGCTCTT-----ATTAATTGCAATCCAAATG 633

QY 22 ValSerGluAlaAlaArgPheLeuTyrIleGluAsnGlnValIleThr-----AsnDhe 39
DB 634 ATTTCAAGAGCAGCAGATTTCCAAATATTTTGGAGGAGAAATGCCGACGAAATTAAGTAC 693

QY 40 AsnArgAlaPheTyrProAspProIleValIleAsnLeuGlnIleValIleTyrGlyValIle 59
DB 694 AACCGAGATCTGCACCAAGCTCTAGCTTAATTAACATTAAGTAATGTTGGGGAGACTT 753

QY 60 SerGluAlaIleHisAsnAlaIleAsnGlyAlaLeuProIleValIleValIleValIleValIle 79
DB 754 TCCACTGCAATTCAGAGCTTAACCAAGAGCTTTGTAATCCCAATTCGACGAAAGA 813

QY 80 AlaIleGlyThrIleTyrPileValIleValIleValIleValIleValIleValIleValIle 99
DB 814 CGTATGTTCCAAATTCAGTGTACGATGTGATATTAATCCCATATAGCTCTC 873

QY 100 LeuIleTyr 102
DB 874 ATGGTGTAT 882

RESULT 15
US-10-893-584-203
;; Sequence 203, Application US/10893584
;; Publication No. US20050272048A1
;; GENERAL INFORMATION:
;; APPLICANT: Borgford, Thor
;; APPLICANT: Braun, Curtis
;; APPLICANT: Putac, Dmitri
;; APPLICANT: Stoll, Dominik
;; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
;; TITLE OF INVENTION: Viral or Parasitic Infections
;; FILE REFERENCE: 10447-025
;; CURRENT APPLICATION NUMBER: US/10/893,584
;; CURRENT FILING DATE: 2004-07-19
;; PRIOR APPLICATION NUMBER: US 09/551,151
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: US 09/403,752
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: US 10/089,058
;; NUMBER OF SEQ ID NOS: 274
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 203
;; LENGTH: 1831
;; TYPE: DNA
;; ORGANISM: E. coli
US-10-893-584-203

Alignment Scores:
Pred. No.: 5,93e-16 Length: 1831
Score: 192.00 Matches: 41
Percent Similarity: 58.3% Conservative: 19
Best Local Similarity: 39.8% Mismatches: 39
Query Match: 33.7% Indels: 4
Gaps: 2

US-09-978-274a-8 (1-110) x US-10-893-584-203 (1-1831)

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Qy      2 GlyValAspSerPheProValLysrthGluAlaPhePheLeuValAlaIleGlnMet 21
Db      580 GGTGGCACTCAGCTTCCAAGCTGCTCGTCTCTT-----ATTAATTGCAATCCAATG 633
Qy      22 ValSerGluAlaAlaArgPheLysrTyrIleGluAsnGlnValLysThr-----AsnPhe 39
Db      634 ATTTGAGAGACAGCAAGATTCCAATATATTGAGGAGAGAAAGCGCACGAGATTAGGTAC 693
Qy      40 AsnArgAlaPheTyrProAspProLysValIleAsnLeuGluLysrTyrPylLysIle 59
Db      694 AACCGAGATCTGCACCAAGATCTCAGGTAATTACACTTGGAATAGTTGGGGAGACTT 753
Qy      60 SerGluAlaIleHisAsnAlaLysAsnGlyAlaLeuProLysProLeuGluLeuValAsp 79
Db      754 TCCACTGCAATTCAAGAGCTTAACCAAGAGCCTTTGCTAGTCCCAATTCAACTGCATAAGA 813
Qy      80 AlaLysGlyThrLysrTyrPylLeuValLeuArgValAspGluIleAsnArgAspValAlaLeu 99
Db      814 CGTAATGGTTCCAATTCAGTGTGTACGATGTGAGTATATTATCCCTATCATAGCTCTC 873
Qy      100 LeuLysrTyr 102
Db      874 ATGCTGTAT 882

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Search completed: April 9, 2006, 05:01:27
 Job time : 291.537 secs

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 00:31:27 ; Search time 915.096 Seconds
(without alignments)
7157.007 Million cell updates/sec

Title: US-09-978-274A-3

Perfect score: 792
1 atgataatcagcaccctt.....gaacctgcagacactta 792

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA_Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	792	100.0	792	3	US-09-978-274A-3
2	786.4	99.3	945	3	US-09-978-274A-1
3	766	96.7	1092	3	US-09-978-274A-19
4	532.6	67.2	1379	3	US-09-978-274A-30
5	532.6	67.2	1379	10	US-11-106-187-1
6	529.4	66.8	1368	3	US-09-978-274A-31
7	518.2	65.4	1376	8	US-10-467-009-1
8	462	58.3	465	3	US-09-978-274A-5
9	328.4	41.5	333	3	US-09-978-274A-7
10	101	12.8	855	10	US-11-106-187-20
11	101	12.8	934	3	US-09-978-274A-32
12	101	12.8	934	10	US-11-106-187-3
13	86.4	10.9	765	3	US-09-978-274A-66
14	86.4	10.9	765	6	US-10-375-209A-66
15	86.4	10.9	984	3	US-09-978-274A-60
16	86.4	10.9	984	6	US-10-375-209A-60
17	86.4	10.9	993	3	US-09-978-274A-63
18	86.4	10.9	993	6	US-10-375-209A-63
19	86.4	10.9	999	3	US-09-978-274A-54
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22	86.4	10.9	999	6	US-10-375-209A-57
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25	83.8	10.6	2404	10	US-11-084-080-19	Sequence 19, Appl
26	83.8	10.6	2404	10	US-11-084-080-21	Sequence 21, Appl
27	83.8	10.6	2404	10	US-11-084-080-23	Sequence 23, Appl
28	83.8	10.6	2431	10	US-11-084-080-27	Sequence 27, Appl
29	82	10.4	1233	3	US-09-861-257-24	Sequence 24, Appl
30	82	10.4	1233	6	US-10-189-360-80	Sequence 80, Appl
31	81	10.2	804	3	US-09-861-257-37	Sequence 37, Appl
32	81	10.2	804	3	US-09-861-257-38	Sequence 38, Appl
33	81	10.2	804	6	US-10-189-360-22	Sequence 22, Appl
34	81	10.2	804	6	US-10-189-360-23	Sequence 23, Appl
35	75	9.5	1230	6	US-10-189-360-53	Sequence 53, Appl
36	75	9.5	1251	3	US-09-861-257-77	Sequence 77, Appl
37	75	9.5	1251	6	US-10-189-360-74	Sequence 74, Appl
38	75	9.5	1260	3	US-09-861-257-75	Sequence 75, Appl
39	75	9.5	1260	6	US-10-189-360-72	Sequence 72, Appl
40	75	9.5	1266	3	US-09-861-257-78	Sequence 78, Appl
41	75	9.5	1266	6	US-10-189-360-75	Sequence 75, Appl
42	75	9.5	1269	3	US-09-861-257-81	Sequence 81, Appl
43	75	9.5	1269	6	US-10-189-360-78	Sequence 78, Appl
44	75	9.5	1275	3	US-09-861-257-76	Sequence 76, Appl
45	75	9.5	1275	6	US-10-189-360-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1									
US-09-978-274A-3									
Sequence 3, Application US/09978274A									
Patent No. US20020116737A1									
GENERAL INFORMATION:									
APPLICANT: Thomas, Christopher									
APPLICANT: McPherson, Michael									
APPLICANT: Atkinson, Howard									
APPLICANT: Neelam, Anil									
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM									
FILE REFERENCE: 9341-028									
CURRENT APPLICATION NUMBER: US/09/978,274A									
CURRENT FILING DATE: 2001-10-15									
PRIOR APPLICATION NUMBER: 0025225.4									
PRIOR FILING DATE: 2000-10-14									
NUMBER OF SEQ ID NOS: 32									
SOFTWARE: PatentIn version 3.1									
SEQ ID NO 3									
LENGTH: 792									
TYPE: DNA									
ORGANISM: Phytolacca americana									
US-09-978-274A-3									
Query Match									
Best Local Similarity 100.0%; Score 792; DB 3; Length 792;									
Best Local Similarity 100.0%; Pred. No. 1.9e-220; Indels 0; Gaps 0;									
Matches 792; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	1	ATGATAATACGATC	ACCTTGGATGCGGAATGCCACATTAACAAATATGCACTT	60					
QY	61	ATGGAATCTCTTGG	ATATCAAGGAAAGATCCAAATTAATATGTCATACCATG	120					
DB	61	ATGGAATCTCTTGG	ATATCAAGGAAAGATCCAAATTAATATGTCATACCATG	120					
QY	121	CTACCTGATCTAAT	TGACCCCTTAAGTACTTATGTTAAGCTCCAAAGTGCACCTTA	180					
DB	121	CTACCTGATCTAAT	TGACCCCTTAAGTACTTATGTTAAGCTCCAAAGTGCACCTTA	180					
QY	181	AAAACATACATCA	TAAAGTGAAGCAAAATTAAGTGAAGGCTTATTCGATCCC	240					
DB	181	AAAACATACATCA	TAAAGTGAAGCAAAATTAAGTGAAGGCTTATTCGATCCC	240					
QY	241	TTCAATGCAATAG	TAGTGTCTTACCATATATTAATGATATTAACAAGCAGACGACT	300					
DB	241	TTCAATGCAATAG	TAGTGTCTTACCATATATTAATGATATTAACAAGCAGACGACT	300					

QY 301 GATGTGAGAAATCTTTTGTCTCAAGTTCTAGTTCGTGTGCAATGTCATTACTAC 360
DB 301 GATGTGAGAAATCTTTTGTCTCAAGTTCTAGTTCGTGTGCAATGTCATTACTAC 360
QY 361 AATAGCTTAATCCGACATGAGAAAGAGAGAAATCTCAAGAAATCAAGTCCAA 420
DB 361 AATAGCTTAATCCGACATGAGAAAGAGAGAAATCTCAAGAAATCAAGTCCAA 420
QY 421 TTGGGAATTCAAATCTCAGCAGTGAATGAAATAATCTGTGAGTTGATTCATTCCT 480
DB 421 TTGGGAATTCAAATCTCAGCAGTGAATGAAATAATCTGTGAGTTGATTCATTCCT 480
QY 481 GTTAAATCTAGAGCTTTTCTTCTGAGTCCAAATGATTTTCAGAGGACGCGA 540
DB 481 GTTAAATCTAGAGCTTTTCTTCTGAGTCCAAATGATTTTCAGAGGACGCGA 540
QY 541 TTCAAGTACATAGAGAACAGTCAATCTTAATTAAGATCTCAATCCCTGATCC 600
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DB 601 AATGTAATTAATCTGAGAGAAAGTGGGCAAAATCTGAGGCAATTCATGCGAAG 660
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DB 661 AATGGGCTTTTACCACCACTTGAAGCTGAGTCCAAAGGTTCAAGTGGATGTT 720
QY 721 CTGAGTGTGATGAATCAATCGTATGAGCACTCCTTAAGTCTTAATGAACTGT 780
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QY 781 CAGACCACTTAA 792
DB 781 CAGACCACTTAA 792

RESULT 2

US-09-978-274A-1
; Sequence 1, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 945
; TYPE: DNA
; ORGANISM: *Phytolacca americana*
US-09-978-274A-1

Query Match 99.3%; Score 786.4; DB 3; Length 945;
Best Local Similarity 99.9%; Pred. No. 9.1e-219;
Matches 787; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 73 AATAATACGATCACTTTGATGCTGAGAAATGCAACATTAACAAATATGCACTTTTANG 132
QY 64 GAATCTCTTCTGTAATCAAGGAAAGATCCAAATCTAATGCTATGCAATGCTTA 123
DB 133 GAATCTCTTCTGTAATCAAGGAAAGATCCAAATCTAATGCTATGCAATGCTTA 192

QY 124 CTGATTAATTAATGACCCCTTAAGTACTTAATGTTAAGTCCAGGTGCAAACTTAAA 183
DB 193 CTGATTAATTAATGACCCCTTAAGTACTTAATGTTAAGTCCAGGTGCAAACTTAAA 252
QY 184 ACCATTAATTAATGCTGAGAGCAATTAATTAATGAGTGGCTAATTTGATCCCTTC 243
DB 253 ACCATTAATTAATGCTGAGAGCAATTAATTAATGAGTGGCTAATTTGATCCCTTC 312
QY 244 AATGGCAATTAATGCTGAGTCAATTAATTAATTAATTAATTAATTAATTAATTAAT 303
DB 313 AATGGCAATTAATGCTGAGTCAATTAATTAATTAATTAATTAATTAATTAATTAAT 372
QY 304 GTGAGAAATCTCTTGTCTCAAGTTCTAGTTCGTGTGCAATGTCATTAACTCAAT 363
DB 373 GTGAGAAATCTCTTGTCTCAAGTTCTAGTTCGTGTGCAATGTCATTAACTCAAT 432
QY 364 AGCTTAATTAATGCAATGAGAAAGAGAGCAATGCAATGCAATGCAATGCAATG 423
DB 433 AGCTTAATTAATGCAATGAGAAAGAGAGCAATGCAATGCAATGCAATGCAATG 492
QY 424 GGAATTCAAATTAATCTCAGCAGTGAATTTGAAATAATCTGAGAGTTGATTCATTCCTGTA 483
DB 493 GGAATTCAAATTAATCTCAGCAGTGAATTTGAAATAATCTGAGAGTTGATTCATTCCTGTA 552
QY 484 AATAGTGAAGCTTTTCTTCTGAGTCCAAATGATTTTCAGAGGACGCGATTC 543
DB 553 AATAGTGAAGCTTTTCTTCTGAGTCCAAATGATTTTCAGAGGACGCGATTC 612
QY 544 AATGTAATTAATGAGAAAGTGGGCAAAATCTGAGGCAATTCATGCGAAGTTC 603
DB 613 AATGTAATTAATGAGAAAGTGGGCAAAATCTGAGGCAATTCATGCGAAGTTC 672
QY 604 GTAAATTAATCTGAGAGAAAGTGGGCAAAATCTGAGGCAATTCATGCGAAGTTC 653
DB 673 GTAAATTAATCTGAGAGAAAGTGGGCAAAATCTGAGGCAATTCATGCGAAGTTC 732
QY 724 AGAGTGTGATGAATCAATCGTATGAGCACTCCTTAAGTCTTAATGAACTGTGAG 783
DB 793 AGAGTGTGATGAATCAATCGTATGAGCACTCCTTAAGTCTTAATGAACTGTGAG 852
QY 784 ACAACTTA 791
DB 853 ACAACTTA 860

RESULT 3

US-09-978-274A-19
; Sequence 19, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: PAP-S/Cybetatin fusion
US-09-978-274A-19

Query Match 96.7%; Score 766; DB 3; Length 1092;
Best Local Similarity 100.0%; Pred. No. 9e-213;
Matches 766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 661 AATGGGCTTTTACCAACCACTTGAGCTAGTGAATGCAAGGTAACCAATGATAGTT 720
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QY 721 CTTAGAGTGAATCAATCGTATGTCACCTCTTAAGTACG 766
DB 721 CTTAGAGTGAATCAATCGTATGTCACCTCTTAAGTACG 766
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RESULT 4
US-09-978-274A-30
; Sequence 30, Application US/0978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Howard
; APPLICANT: Atkinson, Michael
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14

NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: *Phytolacca americana*
US-09-978-274A-30

Query Match 67.2%; Score 532.6; DB 3; Length 1379;
Best Local Similarity 79.8%; Pred. No. 1.7e-144;
Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

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DB 292 TGAATCAATCATCTACAAATGTTGAAATGACCAATTAAGCAATGACCACTTTCTGA 351
QY 65 AATCTTTCGTAAATCAAGCGAAGATCCAAAACCTAAAATGCTATGCAATCAATGCTAC 124
DB 352 ATGATCTTCGTAAATCAAGCGAAGATCCAAAATGCTATGCAATCAATGCTAC 411
QY 125 CTGATCTAATTCGACCCCTTAAGCTTAATGTTAAGCTCAAGTGCAGAACTTA 184
DB 412 CCAATTAACAAATCAAAATCAAGTGTGTTGAGCTCAAGGTTCAAAATTA 471
QY 185 CCATTACATTAATGCTGAGACGAATAATCTTAATGATGAGGCTATTCGATCCCTCA 244
DB 472 CCATTACATTAATGCTGAGACGAATAATCTTAATGATGAGGCTATTCGATCCCTCA 531
QY 245 ATGGCAATTAATGCTGATCAATTAATTAATTAATTAATTAATTAATTAATTAAT 304
DB 532 AAACCAATTAATGCTGATCAATTAATTAATTAATTAATTAATTAATTAATTAAT 591
QY 305 TGGGAATTAATCTTTGCTCAAGTCTAGTTCTGCTGTTGCAATGTCATTAAC 364
DB 592 TAGAGCTACTCTTTGCTCAAGTCTAGTTCTGCTGTTGCAATGTCATTAAC 651
QY 365 GCTTAATTCGACCAATGAAAGAAAGCAAGATTAATCAAGAAATCAAGTCAAT 424
DB 652 GTGATTAATTCGACCAATGAAAGAAAGCAAGATTAATCAAGAAATCAAGTCAAT 711
QY 425 GAATTAATTAATTCGACGAGTGAATTTGAAAAATCTCTGAGTTGATTCATTCCTG 484
DB 712 GAATTAATTAATTCGACGAGTGAATTTGAAAAATCTCTGAGTTGATTCATTCCTG 771
QY 485 AAACTGAGGCTTTTCTCTGCTGATGACATTCGAAATGTTTTCAGAGGACGCGA 544
DB 772 AAACCGAAGCGAATTCCTATGCTGATGACATTAATGATGAGGCAAGATTC 831
QY 545 AGTACATAGAGAACCAAGTCAAGCTAATTTAATAGAGCAATTCCTGATCCCAAG 604
DB 832 AGTACATAGAGAACCAAGTCAAGCTAATTTAATAGAGCAATTCCTGATCCCAAG 891
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DB 952 GAGTTTACCAACCACTTGAGCTAGTGAATGCAAGGTAACCAATGATAGTTCTTA 1011
QY 725 GAGTGAATGAATCAATCGTATGTCACCTCTTAAGTACGTTAATGAACCTGTGAGA 784
DB 1012 GAGTGAATGAATCAATCGTATGTCACCTCTTAAGTACGTTAATGAACCTGTGAGA 1071
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RESULT 5
US-11-106-187-1
; Sequence 1, Application US/11106187
; Publication No. US20050183162A1

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/ GENERAL INFORMATION:
/ APPLICANT: TUMER, NILGUN E.
/ APPLICANT: WANG, PINGER
/ TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
/ FILE REFERENCE: COTRS 3.9-060 CONT
/ CURRENT APPLICATION NUMBER: US/11/106,187
/ PRIOR FILING DATE: 2005-04-14
/ PRIOR APPLICATION NUMBER: US/09/721,047
/ PRIOR FILING DATE: 2000-11-22
/ PRIOR APPLICATION NUMBER: PCT/US99/11301
/ PRIOR FILING DATE: 1999-05-21
/ PRIOR APPLICATION NUMBER: 60/086,374
/ PRIOR FILING DATE: 1998-05-22
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 1
/ LENGTH: 1379
/ TYPE: DNA
/ ORGANISM: PhytoIacca americana
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (225)..(1163)
US-11-106-187-1
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Query Match      67.2%; Score 532.6; DB 10; Length 1379;
Best Local Similarity 79.8%; Pred. No. 1.7e-144;
Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;
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QY 5 TAAATACGATCACCTTGTGATGCTGGAATGCCACCATTAACAAATATGCACTTTATG 64
DB 292 TGAATACATCATCTCAATGTTGGAAGTACCAACATTAACAAATATGCACTTTCTGA 351
QY 65 AATCTCTGTATCAAGCAAGAAAGATCCAAATCAAAATGCTATGCGATCAATGCTAC 124
DB 352 ATGATCTTGTATGAGCAAGCAAGATCAAGTTAAATGCTATGCAATGCTGCTGC 411
QY 125 CTGATACATTAATGACCCCTAAGTACTTATGTTAGTCAAGGTCGAAGCTCAAACTTAAAA 184
DB 412 CCAATCAAAATCAAAATCCAAAGTACGTTGGTGAAGTCCAAAGGTTCAAAATAAAAA 471
QY 185 CCATTACATTAATGCTGAGCGAAATTAATTAATGCTGATGAGGCTATTCGATCCCTTCA 244
DB 472 CCATCAACATTAATGCTGAGCGAAATTAATTAATGCTGATGAGGCTATTCGATCCCTTGG 531
QY 245 ATGCAATTAAGTGTGCTTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 304
DB 532 AAACCATTAATTAATGCTTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 591
QY 305 TGAAGATTAATCTTGTGCTCAAGTTCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 364
DB 592 TAGAGCTACTCTTTGGCCAAATGCGCAATTCGATGTTAGTAAAAAATTAATTAATTAATTA 651
QY 365 GCTTAATTCGACATGAGAAAGAAAGCAAGTAACTCAAGAAATCAAGTCAATTTGG 424
DB 652 GTGATTAATTCGACATGAGAAAGCAAGTAACTCAAGAAATCAAGTCAATTTGG 711
QY 425 GAATTAATTAATCTCAGCAAGTGAATGAAATTAATTAATTAATTAATTAATTAATTAATTA 484
DB 712 GAATTAATTAATCTCAGCAAGTGAATGAAATTAATTAATTAATTAATTAATTAATTAATTA 771
QY 485 AAACGAGGCTTTTCTTCTAATGATGCTCAATGATGCTTCAAGGCAAGCGGATTTCA 544
DB 772 AAACGAGGCGAATTCCTATTTGTTGATCAATTAATGATGATCAAGGCAAGGATTTCA 831
QY 545 AGTACATTAAGCAAGTCAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 604
DB 832 AGTACATTAAGCAAGTCAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 891
QY 605 TAAATTAATTAATCTCAGCAAGTGAATGAAATTAATTAATTAATTAATTAATTAATTAATTA 664
DB 892 TAACTTAATTAATCTCAGCAAGTGAATGAAATTAATTAATTAATTAATTAATTAATTAATTA 951
QY 665 GAGGCTTTTACCAAAACCTTGAAGTGAATGCAAGGTAACCAAGTGAATGATTTCTTA 724
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DB 952 GAGTTTACCAAAACCTCTCAGCTAGTGAATGCCAGTGTGCCAAGTGAATGATGTTGA 1011
QY 725 GAGTGAATGAATCAATCTGATGATGCACTCTTAAATGATTAATGAACCTGTGAGA 784
DB 1012 GAGTGAATGAATCAATCAAGCTGATGATGCACTTTAAATCAATGATGATGATGATGATGATG 1071
QY 785 CAACCTTA 791
DB 1072 CAACCTTA 1078
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RESULT 6
US-09-978-274A-31
/ Sequence 31, Application US/09978274A
/ Patent No. US20020116737A1
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/ GENERAL INFORMATION:
/ APPLICANT: Thomas, Christopher
/ APPLICANT: McPherson, Michael
/ APPLICANT: Atkinson, Howard
/ APPLICANT: Neelam, Anil
/ TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
/ FILE REFERENCE: 9341-028
/ CURRENT APPLICATION NUMBER: US/09/978,274A
/ PRIOR FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: 0025225.4
/ PRIOR FILING DATE: 2000-10-14
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 31
/ LENGTH: 1368
/ TYPE: DNA
/ ORGANISM: PhytoIacca americana
US-09-978-274A-31
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Query Match      66.8%; Score 529.4; DB 3; Length 1368;
Best Local Similarity 79.5%; Pred. No. 1.4e-143;
Matches 626; Conservative 0; Mismatches 161; Indels 0; Gaps 0;
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QY 65 AATCTCTGTATCAAGCAAGAAAGATCCAAATCAAAATGCTATGCGATCAATGCTAC 124
DB 352 ATGATCTTGTATGAGCAAGCAAGATCAAGTTAAATGCTATGCAATGCTGCTGC 411
QY 125 CTGATACATTAATGACCCCTAAGTACTTATGTTAGTCAAGGTCGAAGCTCAAACTTAAAA 184
DB 412 CCAATCAAAATCAAAATCCAAAGTACGTTGGTGAAGTCCAAAGGTTCAAAATAAAAA 471
QY 185 CCATTACATTAATGCTGAGCGAAATTAATTAATGCTGATGAGGCTATTCGATCCCTTCA 244
DB 472 CCATCAACATTAATGCTGAGCGAAATTAATTAATGCTGATGAGGCTATTCGATCCCTTGG 531
QY 245 ATGCAATTAAGTGTGCTTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 304
DB 532 AAACCATTAATTAATGCTTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 591
QY 305 TGAAGATTAATCTTGTGCTCAAGTTCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 364
DB 592 TAGAGCTACTCTTTGGCCAAATGCGCAATTCGATGTTAGTAAAAAATTAATTAATTAATTA 651
QY 365 GCTTAATTCGACATGAGAAAGAAAGCAAGTAACTCAAGAAATCAAGTCAATTTGG 424
DB 652 GTGATTAATTCGACATGAGAAAGCAAGTAACTCAAGAAATCAAGTCAATTTGG 711
QY 425 GAATTAATTAATCTCAGCAAGTGAATGAAATTAATTAATTAATTAATTAATTAATTAATTA 484
DB 712 GAATTAATTAATCTCAGCAAGTGAATGAAATTAATTAATTAATTAATTAATTAATTAATTA 771
QY 485 AAACGAGGCTTTTCTTCTAATGATGCTCAATGATGCTTCAAGGCAAGCGGATTTCA 544
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Db 772 AACCGAAGCCGAATTCCTATTGGTAGCCATACAAATGATACAGAGGACAGCAAGATTC 831
Qy 545 AGTACATAGAGAACCAAGTCAAGCTAATTTTAAATAGCAATTCACCTTGATCCCAAG 604
Db 832 AGTACATAGAGAACCAAGTCAAGCTAATTTTAAATAGCAATTCACCTTGATCCCAAG 891
Qy 605 TAAATTAATCTGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACCAATGCAAGATG 664
Db 892 TACTTAATTTGCAAGAGACATGGGTAAGATTTCAACGCAATTCATGATGCCAAGATG 951
Qy 665 GGGCTTACCCAAACCACTGAGTATGATGATGCCAAAGGTAACCAAGTGAATGTTCTTA 724
Db 952 GAGTTTACCCAAACCTCTCGAGCTAGTGATGCCAAGTGCCAAAGTGAATGTTGA 1011
Qy 725 GAGTGAATGAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 784
Db 1012 GAGTGAATGAATCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1071
Qy 785 CAACTTA 791
Db 1072 CAACTTA 1078

RESULT 7
US-10-467-009-1

; Sequence 1, Application US/10467009
; Publication No. US20040241673A1
; GENERAL INFORMATION:
; APPLICANT: RUTGERS, THE STATE UNIVERSITY
; TITLE OF INVENTION: NON-CYTOXIC PAP MUTANTS
; FILE REFERENCE: OCIRS 3.4-076
; CURRENT APPLICATION NUMBER: US/10/467,009
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: 60/266,396
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: *Physolacca americana*
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (225)..(1160)
US-10-467-009-1

Query Match 65.4%; Score 518.2; DB 8; Length 1376;
Best Local Similarity 79.5%; Pred. No. 2.7e-140;
Matches 626; Conservative 0; Mismatches 158; Indels 3; Gaps 1;

Qy 5 TAAATAGATCACTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 64
Db 292 TGAATACATCATCTACAAATGTGAAATGATCACCATTTAGCAATACGCCCTTTTGA 351
Qy 65 AATCTCTTGTGATCAAGCAAGATCCAAATCTAAATGCTATGATGATGATGATGATG 124
Db 352 ATGATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 411
Qy 125 CTGATCTAATTCGACCCCTTAAGTATGATGATGATGATGATGATGATGATGATG 184
Db 412 CCAATACAAATACAAATCCAAAGTATGATGATGATGATGATGATGATGATGATG 471
Qy 185 CCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 244
Db 472 CCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 531
Qy 245 ATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 304
Db 532 AAACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591
Qy 305 TGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 364
Db 592 TAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 648

Qy 365 GCTTAATCCGACCATGGAAGAAAGAAAGCAAGATTAATCTCAAGAAATCAATCCAAATTG 424
Db 649 GTGATATCCAAATGGAATCAAAAGCGGAGTAATCAAGATCAAGATGATCCAACTGG 708
Qy 425 GAATTCAAATCTGAGAGTACATGTAAGAAATCTCTGAGTGAATTCATTCCCTGTA 484
Db 709 GAATTCAAATCTGAGAGTACATGTAAGAAATCTCTGAGTGAATTCATTCCCTGTA 768
Qy 485 AAATGAGGCTTTTCTACTGTGATGATGATGATGATGATGATGATGATGATGATG 544
Db 769 AAACCGAAGCCGAATTCCTATTGGTAGCCATACAAATGATACAGAGGCAAGATTC 828
Qy 545 AGTACATAGAGAACCAAGTCAAGCTAATTTTAAATAGACATTCATCCGATCCCAAG 604
Db 829 AGTACATAGAGAACCAAGTCAAGCTAATTTTAAATAGACATTCATCCGATCCCAAG 888
Qy 605 TAAATTAATCTGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACATGCAAGATG 664
Db 889 TACTTAATTTGCAAGAGACATGGGTAAGATTTCAACGCAATTCATGATCCCAAGATG 948
Qy 665 GGGCTTACCCAAACCACTGAGTATGATGATGATGATGATGATGATGATGATGATG 724
Db 949 GAGTTTACCCAAACCTCTCGAGCTAGTGATGCCAAGTGCCAAAGTGAATGTTGA 1008
Qy 725 GAGTGAATGAATCAATGATGATGATGATGATGATGATGATGATGATGATGATG 784
Db 1009 GAGTGAATGAATCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1068
Qy 785 CAACTTA 791
Db 1069 CAACTTA 1075

RESULT 8
US-09-978-274A-5

; Sequence 5, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 465
; TYPE: DNA
; ORGANISM: *Physolacca americana*
US-09-978-274A-5

Query Match 58.3%; Score 462; DB 3; Length 465;
Best Local Similarity 100.0%; Pred. No. 4e-124;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
Db 1 ATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
Qy 61 ATGGAATCTCTGATATCAAGCAAGATCCAAATCTAATAATGCTATGCAATGCAATG 120
Db 61 ATGGAATCTCTGATATCAAGCAAGATCCAAATCTAATAATGCTATGCAATGCAATG 120
Qy 121 CTACTGATATCAATTCGACCCCTTAAGTATGATGATGATGATGATGATGATGATG 180
Db 121 CTACTGATATCAATTCGACCCCTTAAGTATGATGATGATGATGATGATGATGATG 180

QY 181 AAAACCTTACCTAATGCTGAGACGAATACTTAATCGATGGCTATTCTGATCCC 240
DB 181 AAAACCTTACCTAATGCTGAGACGAATACTTAATCGATGGCTATTCTGATCCC 240
QY 241 TTGAATGCAATAGTCTGCTTACCATATTTTAATGATATTAACGACCGAAGCACT 300
DB 241 TTGAATGCAATAGTCTGCTTACCATATTTTAATGATATTAACGACCGAAGCACT 300
QY 301 GATGTGAGAACTCTTTGCTCAAGTTCTGATCTGCTGTTGCAATGTCATTAATAC 360
DB 301 GATGTGAGAACTCTTTGCTCAAGTTCTGATCTGCTGTTGCAATGTCATTAATAC 360
QY 361 AATGCTTATATCCGACCATGAGAAAGACAGAGTAATCTAAGAAATCAAGTCCAA 420
DB 361 AATGCTTATATCCGACCATGAGAAAGACAGAGTAATCTAAGAAATCAAGTCCAA 420
QY 421 TTGGGAATTCGAATACCTCAGAGTGAATGGAATAATCTCT 462
DB 421 TTGGGAATTCGAATACCTCAGAGTGAATGGAATAATCTCT 462

RESULT 9
US-09-978-274A-7
Sequence 7, Application US/09978274A
Patent No. US20020116737A1
GENERAL INFORMATION:
APPLICANT: Thomas, Christopher
APPLICANT: McPherson, Michael
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978, 274A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 333
TYPE: DNA
ORGANISM: *Phytolacca americana*
US-09-978-274A-7

Query Match 41.5%; Score 328.4; DB 3; Length 333;
Best Local Similarity 99.7%; Pred. No. 3.7e-85;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 463 GGAATTGATTCATTCCTCTGTAATAAAGTGAAGCTTTTCTACTGTCGATCCAAATG 522
DB 4 GGAATTGATTCATTCCTCTGTAATAAAGTGAAGCTTTTCTACTGTCGATCCAAATG 522
QY 523 GTTTCAGAGCAGCGGATTCAGATGATAGAGCAAGCAAGCACTAATTTTAATAGA 562
DB 64 GTTTCAGAGCAGCGGATTCAGATGATAGAGCAAGCAAGCACTAATTTTAATAGA 562
QY 583 GCATTCACCTGATCCCAAGTAATTAATCTTGAGAGAGAGTGGGCAAAATCTCGAG 642
DB 124 GCATTCACCTGATCCCAAGTAATTAATCTTGAGAGAGAGTGGGCAAAATCTCGAG 642
QY 643 GCATTCACCAATGCAAGATGAGGCTTTTACCAAACTGTAAGTGAATGCCAA 702
DB 184 GCATTCACCAATGCAAGATGAGGCTTTTACCAAACTGTAAGTGAATGCCAA 702
QY 703 GGTACCAAGTGAATGATCTTGAAGTGAATGAATCAATGATGAGGATCCCTTAAG 762
DB 244 GGTACCAAGTGAATGATCTTGAAGTGAATGAATCAATGATGAGGATCCCTTAAG 762
QY 763 TACGTTAATGAACTGTGACAGAACTTAA 792
DB 304 TACGTTAATGAACTGTGACAGAACTTAA 792

RESULT 10
US-11-106-187-20
Sequence 20, Application US/11106187
Publication No. US20050183162A1
GENERAL INFORMATION:
APPLICANT: TURNER, NILDUN E.
APPLICANT: WANG, PINGER
TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
FILE REFERENCE: ODIRS 3.9-060 CONT
CURRENT APPLICATION NUMBER: US/11/106,187
CURRENT FILING DATE: 2005-04-14
PRIOR APPLICATION NUMBER: US/09/721,047
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: PCT/US99/11301
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/086,374
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 20
LENGTH: 855
TYPE: DNA
ORGANISM: *Phytolacca americana*
FEATURE:
NAME/KEY: CDS
LOCATION: (1) .. (855)
US-11-106-187-20

Query Match 12.8%; Score 101; DB 10; Length 855;
Best Local Similarity 53.3%; Pred. No. 1.8e-18;
Matches 349; Conservative 0; Mismatches 270; Indels 36; Gaps 5;

QY 19 TTTGATGCTGGAATGCAACCATTAACAATATGCCATTAATGAAATCTCTGTAAT 78
DB 10 TTTGATGCTGGAATGCAACCATTAACAATATGCCATTAATGAAATCTCTGTAAT 78
QY 79 CAAGCAAGATCAAAATCAAAATCTATGCAATCAATGCTATCTATTAATTCG 138
DB 70 GCTGTGAAGAACAAGAAATGACATGCAATGATATATGCGCAACCCCATGAA 129
QY 139 ACCCTTAATGATTTATGTTAGTTCAGAGTGCAGAACTTAACCATTAATCAATG 198
DB 130 CAAGCAAGATCAAAATCAAAATCTATGCAATCAATGCTATCTGAAATTC--ACATTAAGCA 186
QY 199 CTGAGAGAAATTAATCTTATACGATGAGGCTATTCGATCCCTCAATGCAATTAAGT 258
DB 187 ATGAGAGGAGAACTTAATTTTGAGAGGCTATTCGATTCATTAATG--AAATGT 243
QY 259 CGTTACCATTAATTAATGATTAATTAACAGCAAGCAAGCACTGATGAGAAATCTCT 318
DB 244 CGTTACCATTAATTAATGATTAATTAACAGCAAGCAAGCACTGATGAGAAATCTCT 318
QY 319 TGTCAAGTTCTAGTCTGCTGTCAGATGTCATTAATCAATAGCTTAATCCGACC 378
DB 292 TGTCCCGGAGCAAAAGCAAGCTGCTCAAGAAATTAATCCCTATGAAAGATTC 351
QY 379 ATGAGAAAGAAAGCAGAGTAATCAAGAAATCAAGCAATGGAATTCGAATTAATC 438
DB 352 AAAGGATGAAATCAAGAGTGGGCTTAATTAATGAGTTAGGTTAGAAAGATTAACATC 411
QY 439 AGCAGTGAATGGAATAATCTCTGAGTTGAATCA-----TTCCCTGTAA 486
DB 412 AAGAGTGAATGGAATAATCTCTGAGTTGAATCAAGAGATCAAGAGATTAACAA 471
QY 487 ACTGAGGCTTTTCTTACTGATGATCAATGTTTCAAGAGCAGCGGATTCAG 546
DB 472 AATGAGGCTGAATTTCTTCTTAATGCGTTCAAAATGTTTCAAGGATCAAGGTTCA 531
QY 547 TACATGAGAAACAGTCAAGCTAATTTTAAT-----AGAGCAATTAACCTGATCC 600
DB 532 TACATGAGAAACAGTCAAGGCTTAATTTGATGATCCAAATGAGGATTAATGAGTCC 591
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Db      361 TACAGTCCATCGAAGAACGCCAGATCACCCAGGGCGATCAATCCCGAAGAACTG 420
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Qy      658 AAGATGGGGCTTTACCCAA 677
Db      658 GCGAAGAACGTTGTTTCA 677
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RESULT 15
US-09-792-793A-60
; Sequence 60, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Cogging, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792,793A
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Construct encoding chemokine-
; NAME/KEY: CDS
; LOCATION: (1)..(984)
US-09-792-793A-60
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Query Match 10.9%; Score 86.4; DB 3; Length 984;
Best Local Similarity 47.5%; Pred. No. 3.5e-14;
Matches 323; Conservative 0; Mismatches 351; Indels 6; Gaps 2;

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Qy      1 ATGATAAATACGATCACCTTGTGATCTGGAATGCCACCATTAACAATATGCCACTTT 60
Db      220 ATGGTACTAGTATTAACCTGACCTGTCAATCCGACCGCGCAATATAGCAGCTTC 279
Qy      61 ATGGAATCTCTTCTGATCAAGGAAAGATCCAAACTTAAATGCTATGACATCAATG 120
Db      280 GTGATTAAGATTCGTAACAAGTAAGATCCGAATCGAAATACGGGTGATCTGATATT 339
Qy      121 CTACCTGATTAATGACCCCTAAGTACTTATTTGTTAGTCCAAAGTGCAAACTTA 180
Db      340 GCGGTATCGGTCCGCGAAGAAAGAAAGTTCTCGGCAATTAATTTCAAGCTCCCT 399
Qy      181 AAAACCTTAACATAAGCTGAGACGAATAATTAATTAAGTATGATGGCTATTTGATCC 240
Db      400 GGCAGCTGTTCTCTGGGCTGAAAGCGGATTAACCTGATGTTGTGCTATCTGGCATG 459
Qy      241 TTCAATGGCAATAGTGTGT--TACCATATTTAATGATATTAAGACACGAAAGC 297
Db      460 GATTAATCGAAGCGAAACGGGCTACTTCTTGAGCGAGATTACGAGCGGAAATCC 519
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Qy      298 ACTGATGAGGAATACTCTTTTGCTCAAGTTTATGTTCTGCTGTGCAATGTCATTAA 357
Db      520 ACTGCTCTGTTCCCGAGGGGACACATGCAAAACCAAAAGCATGGAATATACGGAAT 579
Qy      358 TACAAATGCTTAATATCCGACCATGAAAGAAAGCAAGATTAATCTCAAGAAATCAA 417
Db      580 TACCAATGCTAATCGAAGAAAGCGCAGATCAACCAAGGCGATCAATCCCGAAGAA 639
Qy      418 CAATTGGGAATTCAAATATCTCAGACGATGACATTTGAAAAATCTCTGAGATTTGAT 477
Db      640 GGTCTGGGATATGATCTGCTGAGACGAGATGAAACGGTCAACAA--AAAGCTCGC 696
Qy      478 CCTGTAAAACTGAGGCTTTTCTCTAGTGGTACCATCAAAATGTTTCAAGAGCGACG 537
Db      697 GTGTTAAAGACGAAAGCCCGCTTCTCTGATGCCATTTAGATGACGAGAAAGCCGC 756
Qy      538 CGATTCAAGTACATAGAAACCAAGTCAAGCTAATTTTAATAGACATTTACCTGAT 597
Db      757 CGTTCCGCTACATTCAGAACTGTGATCAAAAATTTCCGAAACAAGTTCAATTCGAG 816
Qy      598 CCCAAGTAATTAATCTTGAGAGAGAAAGTGGGCAAAATCTTGAGGCAATTCACATGCC 657
Db      817 AATTAAGTCATTCAGTTGAGGTTAATTTGAAAAAATTTCCACCGCATTTATGTGAC 876
Qy      658 AAGATGGGGCTTTACCCAA 677
Db      877 GCGAAGAACGTTGTTTCA 896
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SUMMARIES

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2	101	12.8	934	US-11-010-795-21	Sequence 21, Appl
3	63	8.0	1623	US-10-893-584-273	Sequence 273, Appl
4	61.4	7.8	807	US-11-010-795-23	Sequence 23, Appl
5	61.4	7.8	1807	US-10-893-584-196	Sequence 196, Appl
6	61.4	7.8	1810	US-10-893-584-168	Sequence 168, Appl
7	61.4	7.8	1813	US-10-893-584-245	Sequence 245, Appl
8	61.4	7.8	1819	US-10-893-584-238	Sequence 238, Appl
9	61.4	7.8	1822	US-10-893-584-175	Sequence 175, Appl
10	61.4	7.8	1822	US-10-893-584-182	Sequence 182, Appl
11	61.4	7.8	1825	US-10-893-584-231	Sequence 231, Appl
12	61.4	7.8	1828	US-10-893-584-210	Sequence 210, Appl
13	61.4	7.8	1831	US-10-893-584-161	Sequence 161, Appl
14	61.4	7.8	1831	US-10-893-584-203	Sequence 203, Appl
15	61.4	7.8	1834	US-10-893-584-154	Sequence 154, Appl
16	61.4	7.8	1837	US-10-893-584-266	Sequence 266, Appl
17	61.4	7.8	1843	US-10-893-584-259	Sequence 259, Appl
18	61.4	7.8	1849	US-10-893-584-252	Sequence 252, Appl

19	61.4	7.8	1855	8	US-10-893-584-3	Sequence 3, Appl
20	61.4	7.8	1855	8	US-10-893-584-5	Sequence 5, Appl
21	61.4	7.8	1855	8	US-10-893-584-7	Sequence 7, Appl
22	61.4	7.8	1855	8	US-10-893-584-9	Sequence 9, Appl
23	61.4	7.8	1855	8	US-10-893-584-13	Sequence 13, Appl
24	61.4	7.8	1855	8	US-10-893-584-15	Sequence 15, Appl
25	61.4	7.8	1855	8	US-10-893-584-17	Sequence 17, Appl
26	61.4	7.8	1855	8	US-10-893-584-19	Sequence 19, Appl
27	61.4	7.8	1855	8	US-10-893-584-21	Sequence 21, Appl
28	61.4	7.8	1855	8	US-10-893-584-23	Sequence 23, Appl
29	61.4	7.8	1855	8	US-10-893-584-25	Sequence 25, Appl
30	61.4	7.8	1855	8	US-10-893-584-27	Sequence 27, Appl
31	61.4	7.8	1855	8	US-10-893-584-29	Sequence 29, Appl
32	61.4	7.8	1855	8	US-10-893-584-31	Sequence 31, Appl
33	61.4	7.8	1855	8	US-10-893-584-33	Sequence 33, Appl
34	61.4	7.8	1855	8	US-10-893-584-35	Sequence 35, Appl
35	61.4	7.8	1855	8	US-10-893-584-37	Sequence 37, Appl
36	61.4	7.8	1855	8	US-10-893-584-39	Sequence 39, Appl
37	61.4	7.8	1855	8	US-10-893-584-48	Sequence 48, Appl
38	61.4	7.8	1855	8	US-10-893-584-50	Sequence 50, Appl
39	61.4	7.8	1855	8	US-10-893-584-52	Sequence 52, Appl
40	61.4	7.8	1855	8	US-10-893-584-54	Sequence 54, Appl
41	61.4	7.8	1855	8	US-10-893-584-74	Sequence 74, Appl
42	61.4	7.8	1855	8	US-10-893-584-77	Sequence 77, Appl
43	61.4	7.8	1855	8	US-10-893-584-80	Sequence 80, Appl
44	61.4	7.8	1855	8	US-10-893-584-83	Sequence 83, Appl
45	61.4	7.8	1855	8	US-10-893-584-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1
US-11-010-795-19
Sequence 19, Application US/11010795
Publication No. US20060005271A1
GENERAL INFORMATION:
APPLICANT: TUMER, NIIIGUN E.
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
TITLE OF INVENTION: RESISTANT TO TRICHOHECENE FUNGAL TOXINS
FILE REFERENCE: OCIRS 3.0-085
CURRENT APPLICATION NUMBER: US/11/010,795
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: 60/529,348
PRIOR FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 19
LENGTH: 1360
TYPE: DNA
ORGANISM: Phytolacca americana
FEATURE:
NAME/KEY: CDS
LOCATION: (207)..(1145)
US-11-010-795-19

Query Match 67.2%; Score 532.6; DB 14; Length 1360;
Best Local Similarity 79.8%; Pred. No. 4.5e-129;
Matches 628; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

Qy	5	TAATATGATCACCCTTGATGCTGGGAATGCCACCATTAACAATATGCCACCTTATNG	64
Db	274	TGAATACACATCATTAACATGTTGAAATGACCAATTAACAATATGACCACTTTTGA	333
Qy	65	AATCTCTGTAATCAAGCAAGATCCAAACTTAATGCTATGACATCAATGCTAC	124
Db	334	ATGATCTTGTAATGAAGCAAGATCAAGTTTAATGCTATGATGATGCTGC	393
Qy	125	CTGATTAATTAATGACCCCTTAAGTCTTATGTTAAGTCCAAAGTCCAAACTTAAAA	184
Db	394	CCATTAACAATTAACAATCAAGTCAAGTCTGTTGAGTCCAAAGTTCAAATTAATAAAAA	453

```
Qy 185 CCATTACATTAATGCTGAGACGAATACTTATACGTGATGGGCTATTCTGATCCCTTCA 244
    |||||
Db 454 CCATCACATTAATGCTGAGACGAACAATTTGATGTGATGGGTTATTTGATCCCTTGG 513
Qy 245 ATGGCAATAGTGTCTTACCATTAATTTATGATATTTACAGACCGAAACGACTGATG 304
    |||||
Db 514 AAACCAATTAATGTCGTACCATTAATTTATGATATTTCTAGGTACGAAACGCAATG 573
Qy 305 TGGAGATATCTTTGCTCAAGTTCTGATTCGTGTTGCAATGTCATTACATCAATA 364
    |||||
Db 574 TAGAGACTACTTTTGGCCAAATGCCAATTCCTGCTGTTAGTAAACATTAATCTTGATA 633
Qy 365 GCTTATATCCGACCATGAAAGAAAGACAGATTAATCTCAAGAAATCAAGTCATTTG 424
    |||||
Db 634 GTGATATCCCATGATGAAATCAAAAGCGGAGTAAATCAAGAAATCAAGTCAAGTGG 693
Qy 425 GAATTCATAATCTCAGAGATGACATTTGAAAAATCTCTGAGATGATTCATTCCTGTAA 484
    |||||
Db 694 GAATTCATAATCTCAGAGATGATTAATTTGAAAAATTTCTGAGATGATTCATTCAGAGA 753
Qy 485 AAACGTGAGCTTTTCTTCTACTGTAGCCATCCAAATGTTTCAAGGACGCGATTTCA 544
    |||||
Db 754 AAACGGAAGCCGAATTCCTTATTTGTTAGCCATACAAATGTATCAGAGGACGAAGTTCA 813
Qy 545 AGTACATAGAAACCAAGTCAAGCTAATTTTATAGACATTTCTACCTGATCCCAAG 604
    |||||
Db 814 AGTACATAGAAATCAGGTGAAATCTAATTTTAAACAGACATTCACCTTAATCCCAAG 873
Qy 605 TAATTAATCTTGGAGAAAGTGGGGCAAAATCTCTGAGCAATTCACAAATGCCAAGATG 664
    |||||
Db 874 TACTTAATTTGCAAGAGACATGGGGTAAAGATTTCAACAGCAATTCAGATGCCAAGATG 933
Qy 665 GGGCTTTACCCAAACCACTGAGCTAGTGTGATGCCAAAGGTACCAAGTGTGATGTTCTTA 724
    |||||
Db 934 GAGTTTACCCAAACCTCTGAGAGTAGTGTGATGCCAGTGTGCCAAGTGTGATGTTGA 993
Qy 725 GAGTGTGATGAATCAATCGTGTGTGGCACTCTCTTAAGTACGTTAATGAAACCTGTGAGA 784
    |||||
Db 994 GAGTGTGATGAATCAAGCTGTGTGTAGCACTCTTAACCTAAGTTGTGTGGAGCTGTGAGA 1053
Qy 785 CAACCTTA 791
    |||||
Db 1054 CAACCTTA 1060
```

RESULT 2
US-11-010-795-21

```
/ Sequence 21, Application US/11010795
/ Publication No. US2006005271A1
/ GENERAL INFORMATION:
/ APPLICANT: TUMER, NITGUN E.
/ APPLICANT: DI, RONG
/ TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING I3 DELTA PROTEINS ARE
/ TITLE OF INVENTION: RESISTANT TO TRICHOHECENE FUNGAL TOXINS
/ FILE REFERENCE: OCINS 3.0-085
/ CURRENT APPLICATION NUMBER: US/11/010.795
/ PRIOR FILING DATE: 2004-12-13
/ PRIOR APPLICATION NUMBER: 60/529.348
/ PRIOR FILING DATE: 2003-12-12
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 21
/ LENGTH: 934
/ TYPE: DNA
/ ORGANISM: Phytolacca americana
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(930)
US-11-010-795-21
```

Query Match 12.8%; Score 101; DB 14; Length 934;
Best Local Similarity 53.3%; Pred. No. 2.8e-16;
Matches 349; Conservative 0; Mismatches 270; Indels 36; Gaps 5;

```
Qy 19 TTTGATGCTGGAATATGACACCATTAACAATATGCCACTTATGGAATCTCTGTAAT 78
    |||||
Db 85 TTTGACGTTGAGAAATGACACACGAACCACTACTCTTAATTTTGTGACTAGTTGGCAGAA 144
Qy 79 CAAGCAAAAGATCCAAACTAAATGCTATGAGTACCAATGCTACCTGATTAATTTG 138
    |||||
Db 145 GCTGTGAAGAACAAGAAATTTGACATGCATGGAATGATATATGCGCAACACCTCACTGAA 204
Qy 139 ACCCTTAAGTACTTATTTGTTAAGCTCCAAAGTGCAACCTTAACCAATTAACATTAATG 198
    |||||
Db 205 CAACCAAGATGATGTTGTTGACCTCAATTCGATCTGGAACATTC--ACATTAAGCA 261
Qy 199 CTGAGACGAATTAATTAATACGTATGAGGCTATTTGATCCCTTCAATGGAATTAAGTGT 258
    |||||
Db 262 ATCAGAAAGGGGAACTTAATTTTGGAGGCTATTTGACATTTTCAATG--AAATGT 318
Qy 259 GCTTACCATTAATTTAATGATTAATTAACAAGACCGAAACGACGTGATGGAATTAATCTTT 318
    |||||
Db 319 CGTTATCGATCTTCAAGATTCAGAAATCC-----GATGCCCAAGACCGTT 366
Qy 319 TGCTCAAGTTCTAGTTCTGCTGTGTTGCAATGTCATTAATCAATAGCTTAATCCGACC 378
    |||||
Db 367 TGCCCCGGGGAACAAAGCAAGCCTGGCACTCAGAAATTAATTCCTATGAAAAAGATTAC 426
Qy 379 ATGAAAAAGAAAGCAGAAAGTAACTCAAGAAATCAAGTCCAAATTTGGAAATTCAAATATCTC 438
    |||||
Db 427 AAAGGATGGAATCAAAAGGTTGGGGCTTAGAATTAATTTAGGTTAGGAAGAAATACATCTC 486
Qy 439 AGCAGTGAATTTGAAAAATCTCTGAGATTGATCA-----TTCCCTGTAAAA 486
    |||||
Db 487 AAGAGTCGAATGGTTAAAAATCTACGGCAAGATGCAACGATCAGAAAGATTAACAAAA 546
Qy 487 ACTGAGGCTTTTCTTACTGTGATCCAAATGTTTCAAGGACAGCGCATTCAG 546
    |||||
Db 547 AATGAGGCTGAATTTTCTTATAGCGTTCAAAATGTTACTGAGGATCAAGGTTCAAA 606
Qy 547 TACATGAGAACCAAGTCAAGACTAATTTTAAT-----AGAGCATTTCAACCTGATCC 600
    |||||
Db 607 TACATGAGAACCAAGTCAAGGCTAATTTGATGATGCCAATGGTATCAGCCAGATCTCT 666
Qy 601 AAAGTAATTAATCTTGGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACAAATG 655
    |||||
Db 667 AAAGTAATTTCCCTAGAGAAAAATTTGGACAAGTGTCTTAAGGTCAATTCACAAAG 721
```

RESULT 3
US-10-893-584-273

```
/ Sequence 273, Application US/10893584
/ Publication No. US20050272048A1
/ GENERAL INFORMATION:
/ APPLICANT: Borgford, Thor
/ APPLICANT: Braun, Curtis
/ APPLICANT: Purac, Adamir
/ APPLICANT: Stoll, Dominik
/ TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
/ TITLE OF INVENTION: Viral or Parasitic Infections
/ FILE REFERENCE: 10447-025
/ CURRENT APPLICATION NUMBER: US/10/893.584
/ PRIOR FILING DATE: 2004-07-19
/ PRIOR APPLICATION NUMBER: US 09/551.151
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: US 09/403.752
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 10/089.058
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 274
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 273
/ LENGTH: 1623
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
```

OTHER INFORMATION: Ricin-like toxin (YSL10054)
US-10-893-584-273

Query Match 8.0%; Score 63; DB 8; Length 1623;
Best Local Similarity 54.0%; Pred. No. 3e-06;
Matches 154; Conservative 0; Mismatches 125; Indels 6; Gaps 1;

Qy 486 AACTGAGGCTTTTCTACTAGTGGTCCATCCAAATGGTTTCAGAGGAGCGGCAATTCAA 545
Db 486 AACTGAGGCTTTTCTACTAGTGGTCCATCCAAATGGTTTCAGAGGAGCGGCAATTCAA 545
Qy 546 GTACATAGAGAACCAAGTCAAGACTAATTTT-----AATAGAGCAATTCACCTGATCC 599
Db 546 ATATATTGAGGAGAAATGCGCAGAGAAATTAGTACACCGAGATCTGCACCGATGCC 605
Qy 600 CAAGTAATTAATCTTGAGAGAGAAATGGGGCAAAATCTCTGAGGCAATTCACATGCCAA 659
Db 606 TAGCGTAATTAACACTTGAAATAGTGGGGGAGACTTCCACTGCAATTCAGAGCTCTAA 665
Qy 660 GAATGGGCTTTTACCACCAACCACTGAGCTAGTGGATGCCAAAGGTACAGTGGATAGT 719
Db 666 CCAAGGAGCCTTTGCTACTGATCCATTCACATGCAAGAGATAGTGTTCCAATTCAGTGT 725
Qy 720 TCTTAGAGTGATGAATCAATCGTATGAGTGGCACTCCTTAAGTA 764
Db 726 GTACGATGTAGATATTAATCCCTATCATAGCTCATGCTGTA 770

RESULT 4

US-11-010-795-23
Sequence 23, Application US/11010795
Publication No. US20060005271a1
GENERAL INFORMATION:
APPLICANT: TUMER, NILGUN B.
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
TITLE OF INVENTION: RESISTANT TO TRICHOHEMENE FUNGAL TOXINS
FILE REFERENCE: OCIRS 3.0-085
CURRENT APPLICATION NUMBER: US/11/010,795
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: 60/529,348
PRIOR FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 23
LENGTH: 807
TYPE: DNA
ORGANISM: Ricinus communis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(804)
US-11-010-795-23

Query Match 7.8%; Score 61.4; DB 14; Length 807;
Best Local Similarity 53.7%; Pred. No. 6e-06;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

Qy 486 AACTGAGGCTTTTCTACTAGTGGTCCATCCAAATGGTTTCAGAGGAGCGGCAATTCAA 545
Db 489 AACTGAGGCTTTTCTACTAGTGGTCCATCCAAATGGTTTCAGAGGAGCGGCAATTCAA 548
Qy 546 GTACATAGAGAACCAAGTCAAGACTAATTTT-----AATAGAGCAATTCACCTGATCC 599
Db 549 ATATATTGAGGAGAAATGCGCAGAGAAATTAGTACACCGAGATCTGCACCGATGCC 608
Qy 600 CAAGTAATTAATCTTGAGAGAGAAATGGGGCAAAATCTCTGAGGCAATTCACATGCCAA 659
Db 609 TAGCGTAATTAACACTTGAAATAGTGGGGGAGACTTCCACTGCAATTCAGAGCTCTAA 668
Qy 660 GAATGGGCTTTTACCACCAACCACTGAGCTAGTGGATGCCAAAGGTACAGTGGATAGT 719
Db 669 CCAAGGAGCCTTTGCTACTGATCCATTCACATGCAAGAGATAGTGTTCCAATTCAGTGT 728

Qy 720 TCTTAGAGTGATGAATCAATCGTATGAGTGGCACTCCTTAAGTA 764
Db 729 GTACGATGTAGATATTAATCCCTATCATAGCTCATGCTGTA 773

RESULT 5

US-10-893-584-196
Sequence 196, Application US/10893584
Publication No. US20050272048A1
GENERAL INFORMATION:
APPLICANT: Borgford, Thor
APPLICANT: Braun, Curtis
APPLICANT: Purac, Admit
APPLICANT: Stoll, Dominik
TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
TITLE OF INVENTION: Viral or Parasitic Infections
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 196
LENGTH: 1807
TYPE: DNA
ORGANISM: B. coli
US-10-893-584-196

Query Match 7.8%; Score 61.4; DB 8; Length 1807;
Best Local Similarity 53.7%; Pred. No. 8.3e-06;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

Qy 486 AACTGAGGCTTTTCTACTAGTGGTCCATCCAAATGGTTTCAGAGGAGCGGCAATTCAA 545
Db 597 AACTGAGGCTTTTCTACTAGTGGTCCATCCAAATGGTTTCAGAGGAGCGGCAATTCAA 656
Qy 546 GTACATAGAGAACCAAGTCAAGACTAATTTT-----AATAGAGCAATTCACCTGATCC 599
Db 657 ATATATTGAGGAGAAATGCGCAGAGAAATTAGTACACCGAGATCTGCACCGATGCC 716
Qy 600 CAAGTAATTAATCTTGAGAGAGAAATGGGGCAAAATCTCTGAGGCAATTCACATGCCAA 659
Db 717 TAGCGTAATTAACACTTGAAATAGTGGGGGAGACTTCCACTGCAATTCAGAGCTCTAA 776
Qy 660 GAATGGGCTTTTACCACCAACCACTGAGCTAGTGGATGCCAAAGGTACAGTGGATAGT 719
Db 777 CCAAGGAGCCTTTGCTACTGATCCATTCACATGCAAGAGATAGTGTTCCAATTCAGTGT 836
Qy 720 TCTTAGAGTGATGAATCAATCGTATGAGTGGCACTCCTTAAGTA 764
Db 837 GTACGATGTAGATATTAATCCCTATCATAGCTCATGCTGTA 881

RESULT 6

US-10-893-584-168
Sequence 168, Application US/10893584
Publication No. US20050272048A1
GENERAL INFORMATION:
APPLICANT: Borgford, Thor
APPLICANT: Braun, Curtis
APPLICANT: Purac, Admit
APPLICANT: Stoll, Dominik
TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
TITLE OF INVENTION: Viral or Parasitic Infections
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151

;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: US 09/403,752
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: US 10/089,058
;; PRIOR FILING DATE: 2000-10-04
;; NUMBER OF SEQ ID NOS: 274
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 168
;; LENGTH: 1810
;; TYPE: DNA
;; ORGANISM: E. coli
US-10-893-584-168

Query Match 7.8%; Score 61.4; DB 8; Length 1810;
Best Local Similarity 53.7%; Pred. No. 8.3e-06;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 486 AACGAGGCTTTTCTTCTAGCGTACGACCAATGTTTCCAGAGCAGCGGATTCAA 545
DB 597 AACTCTGGCTCGTCTTCTTAATTTGTCATCCAAATGATTTTCAGAAACGACGAGATTCCA 656
QY 546 GTACATAGAGAACCAAGTCAAGCTAATTTT-----AATAGACATTTTACCTGTATCC 599
DB 657 ATATATTAGAGGAGAAATGCGACGAGAAATTAGTACACCGAGATCTGCACCATCC 716
QY 600 CAAAGTAATTAATCTGGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACATGCGCAA 659
DB 717 TAGCGTAATTAACATTTGAGAAATAGTTGGGGAGACTTCCATGCAATTCAGAGTCTAA 776
QY 660 GAATGGGCTTTTACCCAAACCTGAGCTAGTGAATGCCAAAGTACCAAGTGAATGT 719
DB 777 CCAAGAGCCTTTGCTAGTCAATTCACATTCGCAAAAGCGTAATGTTCCAAATTCAGTGT 836
QY 720 TCTTAAGTGAATGAATCAATCGATGTCGACTCTCTTAAGTA 764
DB 837 GTACAGTGTGATATTAATCCCTATCATAGCTCTCATGTGTA 881

RESULT 7

US-10-893-584-245
;; Sequence 245, Application US/10893584
;; Publication No. US20050272048A1
;; GENERAL INFORMATION:
;; APPLICANT: Borgford, Thor
;; APPLICANT: Braun, Curtis
;; APPLICANT: Purac, Admit
;; APPLICANT: Scoll, Dominik
;; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
;; TITLE OF INVENTION: Viral or Parasitic Infections
;; FILE REFERENCE: 10447-025
;; CURRENT APPLICATION NUMBER: US/10/893,584
;; CURRENT FILING DATE: 2004-07-19
;; PRIOR APPLICATION NUMBER: US 09/551,151
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: US 09/403,752
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: US 10/089,058
;; PRIOR FILING DATE: 2000-10-04
;; NUMBER OF SEQ ID NOS: 274
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 245
;; LENGTH: 1813
;; TYPE: DNA
;; ORGANISM: E. coli
US-10-893-584-245

Query Match 7.8%; Score 61.4; DB 8; Length 1813;
Best Local Similarity 53.7%; Pred. No. 8.3e-06;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;
QY 486 AACGAGGCTTTTCTTCTAGCGTACGACCAATGTTTCCAGAGCAGCGGATTCAA 545
DB 597 AACTCTGGCTCGTCTTCTTAATTTGTCATCCAAATGATTTTCAGAAACGACGAGATTCCA 656

QY 546 GTACATAGAGAACCAAGTCAAGCTAATTTT-----AATAGACATTTTACCTGTATCC 599
DB 657 ATATATTAGAGGAGAAATGCGACGAGAAATTAGTACAAACGAGATCTGCACCAATCC 716
QY 600 CAAAGTAATTAATCTGGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACATGCGCAA 659
DB 717 TAGCGTAATTAACATTTGAGAAATAGTTGGGGAGACTTCCATGCAATTCAGAGTCTAA 776
QY 660 GAATGGGCTTTTACCCAAACCTGAGCTAGTGAATGCCAAAGTACCAAGTGAATGT 719
DB 777 CCAAGAGCCTTTGCTAGTCAATTCATCTGCAAAAGCGTAATGTTCCAAATTCAGTGT 836
QY 720 TCTTAAGTGAATGAATCAATCGATGTCGACTCTCTTAAGTA 764
DB 837 GTACAGTGTGATATTAATCCCTATCATAGCTCTCATGTGTA 881

RESULT 8

US-10-893-584-238
;; Sequence 238, Application US/10893584
;; Publication No. US20050272048A1
;; GENERAL INFORMATION:
;; APPLICANT: Borgford, Thor
;; APPLICANT: Braun, Curtis
;; APPLICANT: Purac, Admit
;; APPLICANT: Scoll, Dominik
;; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
;; TITLE OF INVENTION: Viral or Parasitic Infections
;; FILE REFERENCE: 10447-025
;; CURRENT APPLICATION NUMBER: US/10/893,584
;; CURRENT FILING DATE: 2004-07-19
;; PRIOR APPLICATION NUMBER: US 09/551,151
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: US 09/403,752
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: US 10/089,058
;; PRIOR FILING DATE: 2000-10-04
;; NUMBER OF SEQ ID NOS: 274
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 238
;; LENGTH: 1819
;; TYPE: DNA
;; ORGANISM: E. coli
US-10-893-584-238

Query Match 7.8%; Score 61.4; DB 8; Length 1819;
Best Local Similarity 53.7%; Pred. No. 8.3e-06;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 486 AACGAGGCTTTTCTTCTAGCGTACGACCAATGTTTCCAGAGCAGCGGATTCAA 545
DB 597 AACTCTGGCTCGTCTTCTTAATTTGTCATCCAAATGATTTTCAGAAACGACGAGATTCCA 656
QY 546 GTACATAGAGAACCAAGTCAAGCTAATTTT-----AATAGACATTTTACCTGTATCC 599
DB 657 ATATATTAGAGGAGAAATGCGACGAGAAATTAGTACAAACGAGATCTGCACCAATCC 716
QY 600 CAAAGTAATTAATCTGGAGAGAAAGTGGGCAAAATCTCTGAGGCAATTCACATGCGCAA 659
DB 717 TAGCGTAATTAACATTTGAGAAATAGTTGGGGAGACTTCCATGCAATTCAGAGTCTAA 776
QY 660 GAATGGGCTTTTACCCAAACCTGAGCTAGTGAATGCCAAAGTACCAAGTGAATGT 719
DB 777 CCAAGAGCCTTTGCTAGTCAATTCATCTGCAAAAGCGTAATGTTCCAAATTCAGTGT 836
QY 720 TCTTAAGTGAATGAATCAATCGATGTCGACTCTCTTAAGTA 764
DB 837 GTACAGTGTGATATTAATCCCTATCATAGCTCTCATGTGTA 881

RESULT 9
US-10-893-584-175

```
; Sequence 175, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Putac, Admitr
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 1822
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-175
```

```
Query Match 7.8%; Score 61.4; DB 8; Length 1822;
Best Local Similarity 53.7%; Pred. No. 8.3e-06;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;
```

```
QY 486 AACTGAGGCTTTTCTTCTAGTGGCCCAATGCTTTCAGAGGAGCGGCAATTCAA 545
DB 597 AACTGCGCTGCTTCTTATTAATTTGATCCAAATGATTTTCAAGAGAGCAAGATTC 656
QY 546 GTACATAGAGACCAAGTCAAGACTAATTTT-----AATAGACATTCTACCTGATCC 599
DB 657 ATATATTGAGGAGAAATGCGCAGAGATTAGGTACAAACCGAGATCTGCAACGATCC 716
QY 600 CAAATGTAATTAATCTTGAGAGAGAAAGTGGGCAAAATCTGAGCAATTCAATGCCAA 659
DB 717 TAGGTAAATTAACCTTGAGAAATGATGGGGAGACTTTCACCTGAAATTCAGAGTCTAA 776
QY 660 GAATGGGCTTTTACCAACCACTTGAGCTAGTGATGCCAAAGGTACCAAGTGGATAGT 719
DB 777 CCAAGGAGCCTTGTCTAGTCCAAATTCAGACTGCAAGAGCTAATGTTCCAAATTCAGGT 836
QY 720 TCTTAGAGTGATGAATCAATCGTATGTGGCACTCTTAAGTA 764
DB 837 GTACGATGTGAGTATTAATTCCTATCATAGTCTCATGTGTGA 881
```

RESULT 10

```
US-10-893-584-182
; Sequence 182, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Putac, Admitr
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 182
; LENGTH: 1822
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-182
```

```
Query Match 7.8%; Score 61.4; DB 8; Length 1822;
Best Local Similarity 53.7%; Pred. No. 8.3e-06;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;
```

```
QY 486 AACTGAGGCTTTTCTTCTAGTGGCCCAATGCTTTCAGAGGAGCGGCAATTCAA 545
DB 597 AACTGCGCTGCTTCTTATTAATTTGATCCAAATGATTTTCAAGAGAGCAAGATTC 656
QY 546 GTACATAGAGACCAAGTCAAGACTAATTTT-----AATAGACATTCTACCTGATCC 599
DB 657 ATATATTGAGGAGAAATGCGCAGAGATTAGGTACAAACCGAGATCTGCAACGATCC 716
QY 600 CAAATGTAATTAATCTTGAGAGAGAAAGTGGGCAAAATCTGAGCAATTCAATGCCAA 659
DB 717 TAGGTAAATTAACCTTGAGAAATGATGGGGAGACTTTCACCTGAAATTCAGAGTCTAA 776
QY 660 GAATGGGCTTTTACCAACCACTTGAGCTAGTGATGCCAAAGGTACCAAGTGGATAGT 719
DB 777 CCAAGGAGCCTTGTCTAGTCCAAATTCAGACTGCAAGAGCTAATGTTCCAAATTCAGGT 836
QY 720 TCTTAGAGTGATGAATCAATCGTATGTGGCACTCTTAAGTA 764
DB 837 GTACGATGTGAGTATTAATTCCTATCATAGTCTCATGTGTGA 881
```

RESULT 11

```
US-10-893-584-231
; Sequence 231, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Putac, Admitr
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 231
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-231
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Query Match 7.8%; Score 61.4; DB 8; Length 1825;
Best Local Similarity 53.7%; Pred. No. 8.3e-06;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;
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QY 486 AACTGAGGCTTTTCTTCTAGTGGCCCAATGCTTTCAGAGGAGCGGCAATTCAA 545
DB 597 AACTGCGCTGCTTCTTATTAATTTGATCCAAATGATTTTCAAGAGAGCAAGATTC 656
QY 546 GTACATAGAGACCAAGTCAAGACTAATTTT-----AATAGACATTCTACCTGATCC 599
DB 657 ATATATTGAGGAGAAATGCGCAGAGATTAGGTACAAACCGAGATCTGCAACGATCC 716
QY 600 CAAATGTAATTAATCTTGAGAGAGAAAGTGGGCAAAATCTGAGCAATTCAATGCCAA 659
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Db 717 TAGCGTAATTAACCTTGAGAAATAGTTGGGGGAGACTTTCACCTGCAATTCAGAGTCTAA 776
Qy 660 GAATGGGGCTTTTACCCAAACCACTTGAGTAGTGATGCCAAAGTCAAGTGGATAGT 719
Db 777 CCAGAGAGCCTTTGCTAGTGTCAATTCACCTGCAAGACGTAATGTTCCAAATTCAGTGT 836
Qy 720 TCTTAAGTGAATGAATCAATCGTGAATGGGCACTCCTTAAGTA 764
Db 837 GTACGATGTGATATTAATTCCTATCATAGCTCTCATGTGTGA 881

RESULT 12

US-10-893-584-210
; Sequence 210, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Adamir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 210
; LENGTH: 1828
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-210

Query Match 7.8%; Score 61.4; DB 8; Length 1828;
Best Local Similarity 53.7%; Pred. No. 8.3e-06;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

Qy 486 AACTGAGGCTTTTCTTCTACTGTAGCCATCCAAATGTTTCAGAGCGAGCGATTCAA 545
Db 597 AACTCTGGCTCGTTCCTTTATTAATTCATCCAAATGATTCAGAGCAGCAAGATTCCA 656
Qy 546 GTACATAGAGAACCAAGTCAAGCTAATTTT-----AATAGAGCTTCTACCTGATCC 599
Db 657 AATATATTGAGGAGAAATGCGACGAAATTAAGTACACCGAGANTCTGCACCAAGATCC 716
Qy 600 CAAAGTAATTAATCTTGAGAGAGAGAGTGGGCAAAATCTTGAGGCAATTCACAAATGCCAA 659
Db 717 TAGCGTAATTAACCTTGAGAAATAGTTGGGGAGACTTTCACCTGCAATTCAGAGTCTAA 776
Qy 660 GAATGGGGCTTTTACCCAAACCACTTGAGTAGTGATGCCAAAGTACCAAGTGGATAGT 719
Db 777 CCAGAGAGCCTTTGCTAGTGTCAATTCACCTGCAAGACGTAATGTTCCAAATTCAGTGT 836
Qy 720 TCTTAAGTGAATGAATCAATCGTGAATGGGCACTCCTTAAGTA 764
Db 837 GTACGATGTGATATTAATTCCTATCATAGCTCTCATGTGTGA 881

RESULT 13

US-10-893-584-161
; Sequence 161, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Adamir
; APPLICANT: Stoll, Dominik

; TITLE OF INVENTION: Ricin-like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 161
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-161

Query Match 7.8%; Score 61.4; DB 8; Length 1831;
Best Local Similarity 53.7%; Pred. No. 8.3e-06;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

Qy 486 AACTGAGGCTTTTCTTCTACTGTAGCCATCCAAATGTTTCAGAGCGAGCGATTCAA 545
Db 597 AACTCTGGCTCGTTCCTTTATTAATTCATCCAAATGATTCAGAGCAGCAAGATTCCA 656
Qy 546 GTACATAGAGAACCAAGTCAAGCTAATTTT-----AATAGAGCTTCTACCTGATCC 599
Db 657 AATATATTGAGGAGAAATGCGACGAAATTAAGTACACCGAGANTCTGCACCAAGATCC 716
Qy 600 CAAAGTAATTAATCTTGAGAGAGAGTGGGCAAAATCTTGAGGCAATTCACAAATGCCAA 659
Db 717 TAGCGTAATTAACCTTGAGAAATAGTTGGGGAGACTTTCACCTGCAATTCAGAGTCTAA 776
Qy 660 GAATGGGGCTTTTACCCAAACCACTTGAGTAGTGATGCCAAAGTACCAAGTGGATAGT 719
Db 777 CCAGAGAGCCTTTGCTAGTGTCAATTCACCTGCAAGACGTAATGTTCCAAATTCAGTGT 836
Qy 720 TCTTAAGTGAATGAATCAATCGTGAATGGGCACTCCTTAAGTA 764
Db 837 GTACGATGTGATATTAATTCCTATCATAGCTCTCATGTGTGA 881

RESULT 14

US-10-893-584-203
; Sequence 203, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Adamir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 203
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-203

Query Match 7.8%; Score 61.4; DB 8; Length 1831;

Best Local Similarity 53.7%; Pred. No. 8.3e-06;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 486 AACTGAGGCTTTTCTTCTACTGCTAGCCATCCAAATGGTTTACAGGCGACGCCGATTCAA 545
DB 597 AACTGAGGCTTTTCTTCTACTGCTAGCCATCCAAATGGTTTACAGGCGACGCCGATTCAA 545
QY 546 GTACATAGAGAACCAAGTCAAGACTAATTTT-----AATAGAGCAATTCACCGATGCC 599
DB 657 ATATATTAGAGGAGAAATGCCGACAGAAATTAGTACAAACCGAGATCTGCACCAATCC 716
QY 600 CAAGTAATTAATCTTGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACATGCCA 659
DB 717 TAGGCTAATTAACCTTGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACATGCCA 659
QY 660 GAATGGGCTTTACCCAAACCACTGAGTATGATGACCAAGTACCAAGTATGAT 719
DB 777 CCAGAGACCTTTGCTAGTCCAAATTCACATGCAAGAGTAAATGCTTCCAAATTCAGTGT 836
QY 720 TCTTAGAGTGAATCAATCGTATGTCCTTAAGTA 764
DB 837 GTACAGTGTAGTATTAATCCCTATCATAGCTCTCATGTGTA 881

RESULT 15

US-10-893-584-154
; Sequence 154; Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 154
; LENGTH: 1834
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-154

Query Match 7.8%; Score 61.4; DB 8; Length 1834;
Best Local Similarity 53.7%; Pred. No. 8.3e-06;
Matches 153; Conservative 0; Mismatches 126; Indels 6; Gaps 1;

QY 486 AACTGAGGCTTTTCTTCTACTGCTAGCCATCCAAATGGTTTACAGGCGACGCCGATTCAA 545
DB 597 AACTGAGGCTTTTCTTCTACTGCTAGCCATCCAAATGGTTTACAGGCGACGCCGATTCAA 545
QY 546 GTACATAGAGAACCAAGTCAAGACTAATTTT-----AATAGAGCAATTCACCGATGCC 599
DB 657 ATATATTAGAGGAGAAATGCCGACAGAAATTAGTACAAACCGAGATCTGCACCAATCC 716
QY 600 CAAGTAATTAATCTTGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACATGCCA 659
DB 717 TAGGCTAATTAACCTTGAGAGAGAGTGGGCAAAATCTCTGAGGCAATTCACATGCCA 659
QY 660 GAATGGGCTTTACCCAAACCACTGAGTATGATGACCAAGTACCAAGTATGAT 719
DB 777 CCAGAGACCTTTGCTAGTCCAAATTCACATGCAAGAGTAAATGCTTCCAAATTCAGTGT 836
QY 720 TCTTAGAGTGAATCAATCGTATGTCCTTAAGTA 764

DB 837 GTACAGTGTAGTATTAATCCCTATCATAGCTCTCATGTGTA 881

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Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA_Main.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1352	83.6	792	3	US-09-978-274A-3
3	1307	80.8	1092	3	US-09-978-274A-19
4	1235.5	76.4	1379	3	US-09-978-274A-30
5	1235.5	76.4	1379	10	US-11-106-187-1
6	1227.5	75.9	1368	3	US-09-978-274A-31
7	1224	75.9	1376	8	US-10-467-009-1

8	788	48.7	465	3	US-09-978-274A-5	Sequence 5, Appl1
9	564	34.9	333	3	US-09-978-274A-7	Sequence 7, Appl1
10	511	31.6	934	3	US-09-978-274A-32	Sequence 32, Appl1
11	511	31.6	934	10	US-11-106-187-3	Sequence 3, Appl1
12	480.5	29.7	855	10	US-11-106-187-20	Sequence 20, Appl1
13	378.5	23.4	935	9	US-10-919-750-4	Sequence 4, Appl1
14	361.5	22.4	804	3	US-09-861-257-38	Sequence 38, Appl1
15	361.5	22.4	804	6	US-10-189-360-23	Sequence 23, Appl1
16	357.5	22.1	804	3	US-09-861-257-35	Sequence 35, Appl1
17	357.5	22.1	804	3	US-09-861-257-35	Sequence 20, Appl1
18	356.5	22.0	804	6	US-10-189-360-20	Sequence 37, Appl1
19	356.5	22.0	804	6	US-10-189-360-22	Sequence 22, Appl1
20	355.5	22.0	804	3	US-09-861-257-36	Sequence 22, Appl1
21	355.5	22.0	804	3	US-09-861-257-36	Sequence 36, Appl1
22	355.5	22.0	804	6	US-10-189-360-19	Sequence 19, Appl1
23	355.5	22.0	804	6	US-10-189-360-21	Sequence 21, Appl1
24	348	21.5	999	3	US-09-792-793A-54	Sequence 54, Appl1
25	348	21.5	999	6	US-10-375-209A-54	Sequence 54, Appl1
26	345.5	21.4	993	3	US-09-792-793A-63	Sequence 63, Appl1
27	345.5	21.4	993	6	US-10-375-209A-63	Sequence 63, Appl1
28	344	21.3	765	3	US-09-792-793A-66	Sequence 66, Appl1
29	344	21.3	765	6	US-10-375-209A-66	Sequence 66, Appl1
30	344	21.3	984	3	US-09-792-793A-60	Sequence 60, Appl1
31	344	21.3	984	6	US-10-375-209A-60	Sequence 60, Appl1
32	344	21.3	999	3	US-09-792-793A-57	Sequence 57, Appl1
33	344	21.3	999	6	US-10-375-209A-57	Sequence 57, Appl1
34	339	21.0	1260	3	US-09-861-257-75	Sequence 75, Appl1
35	339	21.0	1260	6	US-10-189-360-72	Sequence 72, Appl1
36	337	20.8	1269	3	US-09-861-257-81	Sequence 81, Appl1
37	337	20.8	1269	6	US-10-189-360-78	Sequence 78, Appl1
38	337	20.8	1299	3	US-09-861-257-80	Sequence 80, Appl1
39	337	20.8	1299	6	US-10-189-360-77	Sequence 77, Appl1
40	335	20.7	765	3	US-09-861-257-23	Sequence 23, Appl1
41	335	20.7	765	6	US-10-189-360-79	Sequence 79, Appl1
42	335	20.7	1230	6	US-10-189-360-53	Sequence 53, Appl1
43	335	20.7	1233	3	US-09-861-257-24	Sequence 24, Appl1
44	335	20.7	1233	6	US-10-189-360-80	Sequence 80, Appl1
45	335	20.7	1251	3	US-09-861-257-77	Sequence 77, Appl1

ALIGNMENTS

RESULT 1
US-09-978-274A-1
; Sequence 1, Application US/09978274A
; Patent No. US2002016737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978,274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Phytolacca americana
US-09-978-274A-1

Alignment Scores:
Pred. No.: 6.75e-189
Score: 1617.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 3
Length: 945
Matches: 314
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-978-274A-2 (1-314) x US-09-978-274A-1 (1-945)

QY 1 MetLysValMetLeuValValValThrLeuIleAlaIlePheLeuIleAlaIleProThr 20
DB 1 ATGAAAGTATGCTTGTAGTGTGACCTTAATGCGGTGCTCATTTGCTGCACCACT 60

QY 21 SerThrCysAlaIleLeuThrIleThrPheAspAlaGlyAsnAlaThrIleLeuLysTy 40
DB 61 TCACCTGTGGCCATAATACGATCACCTTGATGCGAAATGCCACCATTAACAATAT 120

QY 41 AlaThrPheMetGlySerLeuArgAsnGlnAlaLysAspProLysPheLysCysTyGly 60
DB 121 GCCACCTTATGGAATCTCTCGTAATCAGCGAAAGATCCAAACCTTAATGCTATGCG 180

QY 11eProMetLeuProAspThrAsnSerThrProLysTyLeuLeuValLysLeuGlnGly 80
DB 181 ATACCAATGCTACTGATTAATTCGACCCCTTAAGTACTTAATGGTTAAGCTCCAAAGT 240

QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnLeuTyValMetGlyTy 100
DB 241 GCMAACCTTAAACCACTTACACTAATGCTGAGACGAATATTAATTATACGTGAGGCTAT 300

QY 101 SerAspProPheAsnGlnLysCysArgTyHisIlePheAsnAspIleThrSerThr 120
DB 301 TCTGATCCCTCAATGGCAATAGTGTCTTACCAATATTAATATATTAACACACACC 360

QY 121 GluArgThrAspValGluLeuThrLeuCysSerSerSerSerArgValAlaMetSer 140
DB 361 GAACGACATGATGTGAGAAATCTCTTGTCTCAAGTTCTAAGTTCTGTGTGCAATGTCC 420

QY 141 IleAsnTyAsnSerLeuTyProThrMetGluLysAlaGluValAsnSerArgAsn 160
DB 421 ATTAATCAACAATGCTTATATCCGACCATGAAAGAAAGCAAGAAATCAACAATAT 480

QY 161 GlnValGluLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
DB 481 CAAGTCCAAATGGGAATTCAAATATCTCAGACATGGCAAAATCTCTGAGTTGAT 540

QY 181 SerPheProValLysThrGluAlaPhePheLeuValAlaIleGlnMetValSerGlu 200
DB 541 TCATTCCTGTAAATCTGAGGCTTTTCTTCTGATGTCATCCAAATGCTTTCAGAG 600

QY 201 AlaAlaArgPheLysTyIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTy 220
DB 601 GCAGCCGCAATTCAGATACATAGAGAACCAAGTCAAGCTAATTTAATAGACATTCAC 660

QY 221 ProAspProLysValIleLeuLeuGluGluLysTyGlyLysIleSerGluAlaIleHis 240
DB 661 CCGATCCCAAAAGTAAATTAATTTGGAGAGAAAGTGGGGCAAAATCTCTGAGCAATTCAC 720

QY 241 AsnAlaLysAsnGlyValLeuProLysPheLeuGluLeuValAspAlaLysGlyThrLys 260
DB 721 AATGCCAAGAAATGGGCTTTATCCCAACCACTTGAGCTAGTGCATGCCAAAGTATCCAG 780

QY 261 TrpIleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyValAsn 280
DB 781 TGGATGTGTTCTTGAAGTGAATCAATCGATGTGGCACTCTTAAGTACGTTAAT 840

QY 281 GlyThrCysGlnThrThrTyrgIleAsnAlaMetPheSerGlnValIleIleSerThrTy 300
DB 841 GGAACCTGTACGACCACTTAACCAAAATGCGATGTCTCTCAAGTGTAAATTTCTACTTAT 900

QY 301 TyrAsnTyMetSerAsnLeuGlyAspLeuPheGluGlyPhe 314
DB 901 TATTAATTAATGTCTAATCTTGATGATCTAATTTGAAGGATTC 942

RESULT 2
US-09-978-274A-3
; Sequence No. Application US/0978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael

APPLICANT: Atkinson, Howard
APPLICANT: Neelam, Anil
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
FILE REFERENCE: 9341-028
CURRENT APPLICATION NUMBER: US/09/978,274A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 0025225.4
PRIOR FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 3
LENGTH: 792
TYPE: DNA
ORGANISM: *Phytolacca americana*
US-09-978-274A-3

Alignment Scores:
Pred. No.: 2,85e-156 Length: 792
Score: 1352.00 Matches: 262
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 83.6% Indels: 0
DB: 3 Gaps: 0

US-09-978-274A-2 (1-314) x US-09-978-274A-3 (1-792)

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QY 45 GluSerLeuArgAsnGlnAlaLysAspProLysLysCysTyGlyIleProMetLeu 64
DB 64 GAATCTCTCGTATATCAACGAAAGATCCAAATCTAAATGCTATGCGATACCAATGCTA 123

QY 65 ProAspThrAsnSerThrProLysTyLeuLeuValLysLeuGlnGlyValAlaLeuLys 84
DB 124 CCGATATCAATTAATCGACCCCTTAAGTATTAATGGTTAAGCTCCAAAGTCCAAACCTTAA 183

QY 85 ThrIleThrLeuMetLeuArgArgAsnLeuTyValMetGlyTySerAspProPhe 104
DB 184 ACATTAATCACTAATGCTGAGCAAGAAATATCTTAAGTGAATGGGCTATTCATCCCTTC 243

QY 105 AsnGlyAsnLysCysArgTyHisIlePheAsnAspIleThrSerThrGluArgThrAsp 124
DB 244 AATGGCAATAGATGTGTTACCATATTAATTAATTAATTAACAAGCACGAAAGCACTGAT 303

QY 125 ValGluAsnThrLeuCysSerSerSerSerSerArgValAlaMetSerIleAsnTyra 144
DB 304 GTGGAGAAATATCTCTTGTCTCAAGTTCTAAGTTCTGTGTGCAATGTCCATTAATCAAT 363

QY 145 SerLeuTyProThrMetGluLysLysValAlaLysSerArgAsnGlnValGlnLeu 164
DB 364 AGCTTAATATCCGACCATGGAAGAAAGCAAGATTAATCAAGAAATCAAGTCCAAATG 423

QY 165 GlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPheProVal 184
DB 424 GGAATTCAAATATCTCAGCATGTGCAATGAAATATCTCGAGTTGATTCATTCCTGTGA 483

QY 185 LysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPhe 204
DB 484 AAACCTGAGGCTTTTCTTACTGTGAGCATCCCAATGATGTTTCAGAGGACAGGCAATTC 543

QY 205 LysTyriIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTyProAspProLys 224
DB 544 AAGTACATAGAACCAAGTCAAGACTAATTTAATAGCAATTCATCCCTGATCCCAAA 603

QY 225 ValIleAsnLeuGluGluLysTyGlyLysIleSerGluAlaIleHisAsnAlaLysAsn 244
DB 604 GTAATTAATCTGAGAGGAAGTGGGCAAAATCTCTGAGGCAATTCACAATGCCAAAGAT 663

QY 245 GlyAlaLeuProLysProLeuGluLeuValAspAlaLysGlyThrLysTyTrpIleValLeu 264
DB 664 GGGGCTTATCCCAACCACTTGAAGTGAATGCCAAAGGATCCAAAGTGAATGTTCTT 723

Qy 265 ArgValAspGluIleAsnArgAspValAlaLeuLeuysTYrValAsnGlyThrCysGln 284
|||
Db 724 AGAGTGGATGAAATCAATCGATGATGGCACTCTTAAGTACGTTAATGAACTGTGAC 783
Qy 285 ThrThr 286
|||
Db 784 ACAACT 789
RESULT 3
US-09-978-274A-19
; Sequence 19, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Ackinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Unknown
; FEATURES:
; OTHER INFORMATION: PAP-S/Cystatin fusion
US-09-978-274A-19
Alignment Scores:
Pred. No.: 1.77e-150 Length: 1092
Score: 1307.00 Matches: 254
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 60.8% Indels: 0
Gaps: 0
DB: 3
US-09-978-274A-2 (1-314) x US-09-978-274A-19 (1-1092)
Qy 25 IleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnysTYrAlaThrPheMet 44
|||
Db 4 ATAAATACGATCACTTGTGATGCTGGAATGCAACCAATATATGCACTTTATG 63
Qy 45 GluSerLeuArgAsnGlnAlaIleAspProlysLeuysCysTYrGlyIleProMetLeu 64
|||
Db 64 GAATCTCTTGTATCAAGCAAGATCCAAATCTAAATGCTATGGCATACCAATGCTA 123
Qy 65 ProAspThrAsnSerThrProlysTYrLeuLeuValIleuGlnGlyAlaAsnLeuys 84
|||
Db 124 CCGATATCTAATTCGACCCCTTAAGTACTTATGTTAAGCTCCAAAGTGCAAACTTAAA 183
Qy 85 ThrIleThrLeuMetLeuArgAspAsnLeuTYrValMetGlyTYrSerAspProPhe 104
|||
Db 184 ACCATTACCTAATGCTGAGACGAAATTAATTAACGATGAGGCTATTCGATCCCTTC 243
Qy 105 AsnGlyAsnLeuysCysArgTYrHisIlePheAsnAspIleThrSerThrGluArgThrAsp 124
|||
Db 244 AATGGCAATAAGTGTCTTACCAATATTTATATTAATTAACACACGAAACGACATGAT 303
Qy 125 ValGluAsnThrLeuysCysSerSerSerSerArgValAlaMetSerIleAsnTYrAsn 144
|||
Db 304 GTGAGAAATCTCTTCTCAAGTTCTAGTCTCGTGTGCAATGTCATTAACTAACAAT 363
Qy 145 SerLeuTYrProThrMetGluValysAlaGluValAsnSerArgAsnGlnValGlnLeu 164
|||
Db 364 AGCTTAATATCCGACATGAAAGAAAGCAAGATTAATCTCAAAATCAAGTCCAATTG 423
Qy 165 GlyIleGlnIleLeuSerSerAspIleGlyIleSerGlyValAspSerPheProVal 184

Db 424 GGATTCAAATATACACACAGATTCGAAATATCTCGAGTTGATTCATTCCTCTA 483
Qy 185 LysThrGluAlaPhePheLeuValAlaIleGlnMetValSerGluAlaIleArgPhe 204
|||
Db 484 AAACCTAGGCTTTTCTTACTGTTAGCCATCCAAATGTTTCAGAGGCGCCGATTC 543
Qy 205 LysTYrIleGluAsnGlnValLysThrAsnPheAsnArgAlaPheTYrProAspProlys 224
|||
Db 544 AAGTACATAGAAACCAAGTCAGACTTAATTTAATAGACATTCATCCCTGATCCAAA 603
Qy 225 ValIleAsnLeuGluGluLysTYrGlyIleSerGluAlaIleHisAsnAlaIleAsn 244
|||
Db 604 GTATTATACCTTGACGAGAAAGTGGGCAAAATCTCTAGGCAATTCACATGCCAAGAT 663
Qy 245 GlyValLeuProlysProLeuGluLeuValAspAlaIleGlyTYrIleTYrIleValLeu 264
|||
Db 664 GGGGCTTTACCCAAACCACTTGAAGTGAATGCCAAAGGTACCAAGTGAATGTTCTT 723
Qy 265 ArgValAspGluIleAsnArgAspValAlaLeuLeuysTYr 278
|||
Db 724 AGAGTGGATGAAATCAATCGATGATGGCACTCTTAAGTAC 765
RESULT 4
US-09-978-274A-30
; Sequence 30, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Ackinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Phytolacca americana
US-09-978-274A-30
Alignment Scores:
Pred. No.: 1.79e-141 Length: 1379
Score: 1235.50 Matches: 239
Percent Similarity: 86.3% Conservative: 33
Best Local Similarity: 75.9% Mismatches: 40
Query Match: 76.4% Indels: 3
Gaps: 2
DB: 3
US-09-978-274A-2 (1-314) x US-09-978-274A-30 (1-1379)
Qy 1 MetLysValMetLeuValValValThrLeuIleAlaTrpLeuIleAlaIleProThr 20
|||
Db 225 ATGAAGTCGATGCTTGTGGAGCAATATCAATA-----TGGCTCATCTTGCACCACT 278
Qy 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTYr 40
|||
Db 279 TCAACTTGGGCTGTGATATCAATCATCTTACAAATGTTGAAAGTACCAACATTAAGCAATAC 338
Qy 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaIleAspProlysLeuysCysTYrGly 60
|||
Db 339 GCCACTTCTCGAATGATCTTCGTAATGAAGCAAAAGATCCAAAGTTTAAATGCTATGA 398
Qy 61 IleProMetLeuProAspThrAsnSerThrProlysTYrLeuLeuValIleuGlnGly 80
|||
Db 399 ATACCAATGTCTGCCATATACAAATCCAAAGTACCTGTGTGTAGCTCCAAAGGT 458
Qy 81 AlaAsnLeuysThrIleThrLeuMetLeuArgAsnAsnLeuTYrValMetGlyTYr 100

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Db      459  TCAAAATMAAAACCACTACACCTAATGCTAGAGCGAAACATTTGTATGATGCGTTAT 518
      101  SerAspProPheAnslYLeuAnslYsCYsArgYrHieIlePheAnslPliethrSerThr 120
      519  TCTGATCCCTTTGAAACCAATTAATGCTGTTACATATCTTTATGATGATCGGTACT 578
      121  GluArgThrAspValGluAnthrIleuCYsSerSerSerSerSerArgValAlaMetSer 140
      579  GAACGCCAAGATGTAGAGTACTCTTGGCCCAATGCCAATTCCTGCTGTAGTAAAAAC 638
      141  IleAnslYrAnserIleuYrProthrMetGluLysValAlaGluValAnserArgAnsl 160
      639  ATAACTTGTATGTGATATCCAACTTGAATCCAAACCGGAGTAAATCAAGAGT 698
      161  GluValGlnLeuGlyIleGlnIleLeuSerSerSerArgValIleSerGlyValAsp 180
      699  CAGGTCCAACTGGGAATTCAAATATCTGACAGTAAATTTGGAAAGATTTCTGGAGTATG 758
      181  SerPheProValIleYrThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
      759  TCATTCACCTGAGAAACCGAAGCCGAATTCCTATTGGTAGCCATTAACAAATGATATCAGAG 818
      201  AlaAlaArgPheIleYrIleGlnAnslValIleYrThrAnPheAnslArgAlaPheYr 220
      819  GCAGCAAGATTCAGATACATAGAGAAATCAGGTGAAAATTAATTTTAAACAGACATTCAC 878
      221  ProAspProLysValIleAnslLeuGlnGluLysTrpGlyLysIleSerGluAlaIleHis 240
      879  CTTAACTCCAAATCTTAATTTTGCAGAGACATGGGGTAAAGTTTTCACAGCAATTCAT 938
      241  AsnAlaLysAnslYAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLys 260
      939  GATGCCAAGATTCAGATTTTAACTTAACTCTGAGTAGTGGCACTGGGCGCAAG 998
      261  TrpIleValLeuArgValAspGluIleAnslArgAspValAlaLeuLeuLysYrValAsn 280
      999  TGGATAGTGTGAGAGTGAATTCAGAAATCCAGCTGATGACCTCTTAACTGCTGGT 1058
      281  GlyThrCYeGlnThrThrYr--GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
      1059  GGGAGCTGTCAAGCACTTAATACCAAAATGCCATGCTTTCTCACTTAATATGCTACT 1118
      300  TyrTyraAnslYrMetSerAnslLeuGlyAspLeuPheGlnGlyPhe 314
      1119  TATTATAATTAATCATGGTAACTTGGTGAATCTTAATTGAAGATTC 1163

```

RESULT 5
 US-11-106-187-1
 / Sequence 1, Application US/11106187
 / Publication No. US20050183162A1
 / GENERAL INFORMATION:
 / APPLICANT: TURNER, NITIGUN E.
 / APPLICANT: WANG, PINGR
 / TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
 / FILE REFERENCE: OCIRS 3.9-060 CONT
 / CURRENT APPLICATION NUMBER: US/11/106.187
 / PRIOR FILING DATE: 2005-04-14
 / PRIOR APPLICATION NUMBER: US/09/721.047
 / PRIOR FILING DATE: 2000-11-22
 / PRIOR APPLICATION NUMBER: PCT/US99/11301
 / PRIOR FILING DATE: 1999-05-21
 / PRIOR APPLICATION NUMBER: 60/086.374
 / PRIOR FILING DATE: 1998-05-22
 / NUMBER OF SEQ ID NOS: 21
 / SOFTWARE: PatentIn Ver. 3.3
 / SEQ ID NO 1
 / LENGTH: 1379
 / TYPE: DNA
 / ORGANISM: Phytolacca americana
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (225)..(1163)

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US-11-106-187-1
Alignment Scores:
Pred. No.: 1,79e-141 Length: 1,379
Score: 1235.50 Matches: 239
Percent Similarity: 86.3% Conservative: 33
Best Local Similarity: 75.9% Mismatches: 40
Query Match: 76.4% Indels: 3
DB: 10 Gaps: 2

US-09-978-274a-2 (1-314) x US-11-106-187-1 (1-1379)
      1  MetLysValMetLeuValValValThrLeuIleAlaTrpLeuIleAlaProthr 20
      225  ATGAGTTCAGATGCTTGTGTGATCAATATCAATATCAATATCAATATCAATATCAATATCA 278
      21  SerThrCYeAlaIleAnslThrIleThrPheAnslArgValAlaMetSer 40
      279  TCAACTGGGCTGTGATTCATCAATCAATGTTGGAAGTACCACTTACCAATATC 338
      41  AlaThrPheMetGlnSerLeuArgAnslAlaLysAspProLysCYsYrGly 60
      339  GCCACTTTCTGATATGATCTTCTGATATGAGCAAGATTCAGATTTAAATCTATGGA 398
      61  IleProMetLeuProAspThrAnslSerThrProLysYrLeuLeuValLysLeuGlnGly 80
      399  ATACCAATGCTGCGCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 458
      81  AlaAnslLeuYrThrIleThrLeuMetLeuArgAspAnslLeuYrValMetGlyYr 100
      459  TCAAAATMAAAACCACTACACCTAATGCTAGAGCGAAACATTTGTATGATGCGTTAT 518
      101  SerAspProPheAnslYLeuAnslYsCYsArgYrHieIlePheAnslPliethrSerThr 120
      519  TCTGATCCCTTTGAAACCAATTAATGCTGTTACATATCTTTATGATGATCGGTACT 578
      121  GluArgThrAspValGluAnthrIleuCYsSerSerSerSerSerArgValAlaMetSer 140
      579  GAACGCCAAGATGTAGAGTACTCTTGGCCCAATGCCAATTCCTGCTGTAGTAAAAAC 638
      141  IleAnslYrAnserIleuYrProthrMetGluLysValAlaGluValAnserArgAnsl 160
      639  ATAACTTGTATGTGATATCCAACTTGAATCCAAACCGGAGTAAATCAAGAGT 698
      161  GluValGlnLeuGlyIleGlnIleLeuSerSerSerArgValIleSerGlyValAsp 180
      699  CAGGTCCAACTGGGAATTCAAATATCTGACAGTAAATTTGGAAAGATTTCTGGAGTATG 758
      181  SerPheProValIleYrThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGlu 200
      759  TCATTCACCTGAGAAACCGAAGCCGAATTCCTATTGGTAGCCATTAACAAATGATATCAGAG 818
      201  AlaAlaArgPheIleYrIleGlnAnslValIleYrThrAnPheAnslArgAlaPheYr 220
      819  GCAGCAAGATTCAGATACATAGAGAAATCAGGTGAAAATTAATTTTAAACAGACATTCAC 878
      221  ProAspProLysValIleAnslLeuGlnGluLysTrpGlyLysIleSerGluAlaIleHis 240
      879  CTTAACTCCAAATCTTAATTTTGCAGAGACATGGGGTAAAGTTTTCACAGCAATTCAT 938
      241  AsnAlaLysAnslYAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLys 260
      939  GATGCCAAGATTCAGATTTTAACTTAACTCTGAGTAGTGGCACTGGGCGCAAG 998
      261  TrpIleValLeuArgValAspGluIleAnslArgAspValAlaLeuLeuLysYrValAsn 280
      999  TGGATAGTGTGAGAGTGAATTCAGAAATCCAGCTGATGACCTCTTAACTGCTGGT 1058
      281  GlyThrCYeGlnThrThrYr--GlnAsnAlaMetPheSerGlnValIleIleSerThr 299
      1059  GGGAGCTGTCAAGCACTTAATACCAAAATGCCATGCTTTCTCACTTAATATGCTACT 1118
      300  TyrTyraAnslYrMetSerAnslLeuGlyAspLeuPheGlnGlyPhe 314

```

Db 1119 TATTATAATACATGTTAATCTTGATCTATTGAAAGATTTC 1163

RESULT 6

US-09-978-274A-31
 ; Sequence 31, Application US/09978274A
 ; Patent No. US20020116737A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Christopher
 ; APPLICANT: McPherson, Michael
 ; APPLICANT: Atkinson, Howard
 ; APPLICANT: Neelam, Anil
 ; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
 ; FILE REFERENCE: 9341-028
 ; CURRENT APPLICATION NUMBER: US/09/978, 274A
 ; PRIOR FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 0025225.4
 ; PRIOR FILING DATE: 2000-10-14
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 31
 ; LENGTH: 1368
 ; TYPE: DNA
 ; ORGANISM: Phytolacca americana
 ; US-09-978-274A-31

Alignment Scores:

Pred. No.:	1.72e-140	Length:	1368
Score:	1227.50	Matches:	238
Percent Similarity:	86.0%	Conservative:	33
Best Local Similarity:	75.6%	Mismatches:	41
Query Match:	75.9%	Indels:	3
DB:	3	Gaps:	2

US-09-978-274A-2 (1-314) x US-09-978-274A-31 (1-1368)

Qy 1 MetLyValMetLeuValValValThreuleaLarPleuilealaProthr 20
 Db 225 ATGAAGCATGCTGGTGAGCAATCAATA-----TGGCTATTCTTGCACT 278
 Qy 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTy 40
 Db 279 TCAACTGGGCTGGATGATCATCATCTCAATGTGGAAGTACCACTATGCAATATAC 338
 Qy 41 AlaThrPheMetGlnSerLeuArgAsnGlnAlaIleAspProLysLeuLysCysTyGly 60
 Db 339 GCCACTTTTGGAAATGATCTTCTGTAATGAAGCGAAAGATCCAACTTTAAATGCTATGA 398
 Qy 61 IleProMetLeuProAspThrAsnSerThrProLysTyIleuLeuValLysLeuGlnGly 80
 Db 399 ATACCAATGCTGCCCATATCAATCAATCAATCAATCGTTGGTTGAGCTCCAAAGT 458
 Qy 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuTyValMetGlyTy 100
 Db 459 TCAAAATATAAAACCATCACACTATGCTGAGAGAAACATTTGTATGTGATGGTAT 518
 Qy 101 SerAspProPheAsnGlyAsnLysCysArgTyHisIlePheAsnAspIleThrSerThr 120
 Db 519 TCTGATCCCTTTGAAACCAATTAATGTCGTTACATATCTTATGATATCTCAGTACT 578
 Qy 121 GlnArgThrAspValGlnAsnThrLeuCysSerSerSerSerArgValAlaMetSer 140
 Db 579 GAACGCCAAGATGATGAGACTACTCTTGGCCAAATCCAAATTCGTTGTAAGAAAC 638
 Qy 141 IleAsnTyAsnSerLeuTyProThrMetGlnLysLysAlaGlnValAsnSerArgAsn 160
 Db 639 ATAACTTTGATGATGATATCAACATGGAATCAAAAGCGGAGTAATATCAAGAGT 698
 Qy 161 GlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAsp 180
 Db 699 CAGGTCCAACTGGAAATTCAAATATCTGACAGTAATTTGTGAAAGATTTCGAGTGATG 758
 Qy 181 SerPheProValLysThrGlnAlaPhePheLeuLeuValAlaIleGlnMetValSerGln 200

Db 759 TCATTCATGAGAAACCGAAGCCGATTCCTATGGTAGCATACAAATGATACAG 818

Qy 201 AlaAlaArgPheLysTyIleGlnAsnGlnValLysThrAsnPheAsnArgAlaPheTy 220

Db 819 GCAGCAAGATTCAGTACATAGAGATCAGGTGAAATCTAATTTTAAACAGCATTCAC 878

Qy 221 ProAspProLysValIleAsnLeuGlnLysTyIleGlyLysIleSerGlnAlaIleHis 240

Db 879 CCAATCCCAAGTACTTAATTTGCAAGACATGGGGTAAGATTCAACAGCAATTCAT 938

Qy 241 AsnAlaLysAsnGlyAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLys 260

Db 939 GATGCCAAGATGAGATTTTACCAGAACCTCTGAGCTATGATGTCAGTGGTCCAG 998

Qy 261 TrpIleValLeuArgValAspGluIleAsnArgAspValAlaLeuLysTyValAsn 280

Db 999 TGGATGCTGTGGAGAGGATGAATCAACGCTGATGATACCTTAACTACGTTGGT 1058

Qy 281 GlyThrCysGlnThrThrTyIleGlnAsnAlaMetPheSerGlnValIleIleSerThr 299

Db 1059 GGAGCTGCAAGCACTTAATTAACCAAAATGCCATGTTCTCAACTTAATATGCTACT 1118

Qy 300 TyrTyAsnTyIleMetSerAsnLeuGlyAspLeuPheGlnGlyPhe 314

Db 1119 TATTATAATACATGTTAATCTTGATCTATTGAAAGATTTC 1163

RESULT 7

US-10-467-009-1
 ; Sequence 1, Application US/10467009
 ; Publication No. US20040241673A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RUTGERS, THE STATE UNIVERSITY
 ; TITLE OF INVENTION: NON-CYTOTOXIC PAP MUTANTS
 ; FILE REFERENCE: OCIRS 3.4-076
 ; CURRENT APPLICATION NUMBER: US/10/467, 009
 ; PRIOR FILING DATE: 2003-08-01
 ; PRIOR APPLICATION NUMBER: 60/266,396
 ; PRIOR FILING DATE: 2001-02-02
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 1376
 ; TYPE: DNA
 ; ORGANISM: Phytolacca americana
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (225)..
 ; US-10-467-009-1

Alignment Scores:

Pred. No.:	4.7e-140	Length:	1376
Score:	1224.00 <td>Matches:</td> <td>239 </td>	Matches:	239
Percent Similarity:	86.0% <td>Conservative:</td> <td>32 </td>	Conservative:	32
Best Local Similarity:	75.9% <td>Mismatches:</td> <td>40 </td>	Mismatches:	40
Query Match:	75.7% <td>Indels:</td> <td>4 </td>	Indels:	4
DB:	8 <td>Gaps:</td> <td>3 </td>	Gaps:	3

US-09-978-274A-2 (1-314) x US-10-467-009-1 (1-1376)

Qy 1 MetLyValMetLeuValValValThreuleaLarPleuilealaProthr 20
 Db 225 ATGAAGCATGCTGGTGAGCAATCAATA-----TGGCTATTCTTGCACT 278
 Qy 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLysTy 40
 Db 279 TCAACTGGGCTGGATGATCATCATCTCAATGTGGAAGTACCACTTATGCAATATAC 338
 Qy 41 AlaThrPheMetGlnSerLeuArgAsnGlnAlaIleAspProLysLeuLysCysTyGly 60
 Db 339 GCCACTTTTGGAAATGATCTTCTGTAATGAAGCGAAAGATCCAACTTTAAATGCTATGA 398
 Qy 61 IleProMetLeuProAspThrAsnSerThrProLysTyIleuLeuValLysLeuGlnGly 80

US-09-978-274a-2 (1-314) x US-09-978-274a-7 (1-333)

QY 178 G|VAlaPsePheProValYThGluAlaPhePheLeuValAlaIleG|Met 197
 Db 4 GGAATTGATTCATTCCTCGTAAAGAGGCTTTTTCATCGTAGCCATCCAATG 63
 QY 198 ValSerGluAlaAlaArgPheLeuValYleGluAngluValYleThrAsnPheAsnArg 217
 Db 64 GTTTCAGAGGAGGCGCATTCAGTACATAGAGAACCAAGTCAGACATTAATTAAGA 123
 QY 218 AlaPheTyProAspProLeuValIleAsnLeuGluGluYleTPG|YleIleSerGlu 237
 Db 124 GCATTTCACCTGATCCCAAGTATTAATTGGAGAGAGAGTGGGGCAAAATCTCGAG 183
 QY 238 AlaIleIleAsnAlaValAsnGluValAlaLeuProLeuGluLeuValAspAlaVal 257
 Db 184 GCATTTCAGATGCAAGATGCGGGCTTTTACCAACCACTTGAGCTAGTGAGTCCAAA 243
 QY 258 G|YThyTrpIleValIleuArgValAspGluIleAsnArgAspValAlaLeuLeuVal 277
 Db 244 GGTACCAAGTGGATGATCTTTCAGATGATTAATCAATCTGATGCGACTCTTTAG 303
 QY 278 TyValAngluYThrYseGlnThrThr 286
 Db 304 TACGTTATGGAACCTGTCAAGCAACT 330

RESULT 10

US-09-978-274a-32
 ; Sequence 32, Application US/0978274A
 ; Patent No. US20020116737A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Christopher
 ; APPLICANT: McPherson, Michael
 ; APPLICANT: Atkinson, Howard
 ; APPLICANT: Neelan, Anil
 ; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
 ; FILE REFERENCE: 9341-028
 ; CURRENT APPLICATION NUMBER: US/09/978, 274A
 ; PRIOR FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 0025225.4
 ; PRIOR FILING DATE: 2000-10-14
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 32
 ; LENGTH: 934
 ; TYPE: DNA
 ; ORGANISM: Phytolacca americana
 ; US-09-978-274a-32

Alignment Scores:

Pred. No.: 3,28e-52 Length: 934
 Score: 511.00 Matches: 130
 Percent Similarity: 56.1% Conservative: 53
 Best Local Similarity: 39.9% Mismatches: 111
 Query Match: 31.6% Indels: 32
 DB: 3 Gaps: 14

US-09-978-274a-2 (1-314) x US-09-978-274a-32 (1-934)

QY 1 MetIyValMetLeuValValValThrLeuIleAlaTrpLeuIleAlaAlaProThr 20
 Db 7 ATGAGAGGTGATGAGAGGTGGTGGCATATCGATGAGTGGTTCACCAACCA 66
 QY 21 SerThrCyAlaIleAsnThrIleThrPheAspAlaGluValAsnAlaThrIleAsnLeuYr 40
 Db 67 -----GCTTCTTCAACATGCTGCTTGAAGCTTGAGATGCAACCAACCACTTAC 117
 QY 41 AlaThrPheMetGluSerLeuArgAsnGluAlaValAspProLeuLeuValYleYrGly 60
 Db 118 TCTAATTTTTCGACTAGTTCGCAAGAGCTGTGAAGAGCAAGAAATGACATGCAATGA 177
 QY 61 IleProMetLeuProAspThrAsnSerThrProLeuYrLeuLeuValYleGluGly 80

Db 178 ATGATATGGCCACCAACCTCACTGAACCAACCAAGATATGTGTTGACCTCAAAATTC 237

QY 81 AlaAsnLeuYrThrIleThrLeuMetLeuArgArgAsnLeuYrValMetGlyYr 100

Db 238 GGAATC---GGAACATTACATTAAGCAATGAGAGGGAACCTTAATTTTGAGAGGGCTAT 294

QY 101 SerAspProPheAsnGluValAsnLeuYrCyArgTyHisIlePheAsnAspIleThrSerThr 120

Db 295 TCTGACATTTTACATGGA---AAATGTCGTTATCGATCTTCAAGAT----- 339

QY 121 GluArgThrAspAlaGluAsnThrLeuCySerSerSerSerArg-----ValAla 138

Db 340 TCAGAATCCGATGCGCAAGAGACCGTTGCCCCGGGAGCAAAAGCAACCTGGACATCAG 399

QY 139 MetSerIleAsnTyTrAsnSerLeuYrProThrMetGluValYleValAlaAsnSer 158

Db 400 AATTAATATCCCTATGAAAAAGATTACAAAGGATGGAATCAAAAGGCT-----GGGGCT 453

QY 159 ArgAsnGluValGluLeuGlyIleGluIleLeuSerSerAspIleGlyYleIleSerGly 178

Db 454 AGAATTAATTAATGAGTTAGAGAAAGATTAACCTCAAGATGCAATGGTTAAATCTTACGC 513

QY 179 ValAspSerPhePro-----ValIleThrGluAlaPhePheLeuValAla 194

Db 514 AAGATGCAACGGATCAGAGCAGTATCAAAAAGAGGCTGAATTTCTTTATAGCC 573

QY 195 IleGluMetValSerGluAlaAlaArgPheLeuYrIleGluAngluValYleThrAsn 214

Db 574 GTTCAAAATGCTTACTGAGGATCAAGGTTCAAAATTAATTAAGCAAAAGTAAAGGCTTAA 633

QY 215 PheAsnArgAla-----PheTyProAspProLeuValIleAsnLeuGluGluYleYr 232

Db 634 TTTGATGATTCCTCAATGGTATTCAGCCAGATCTTAAGCTTAATTTCTTCAAGAAAAATGG 693

QY 233 GlyLeuIleSerGluAlaIleHisAsnAlaValAsnGly-----AlaLeu 247

Db 694 GACAGTGTTCCTAAGGTCATTT-----GCAAAAGTTGGACCTCCGGTATGATACGTT 747

QY 248 ProLeuPheLeuGluLeuValAspAlaValGlyThrIleYrIleValLeuValAsp 267

Db 748 ACTTACCTGAGACCTTAAAGATGAGATTAATTAACCTTGACCTACGGCACCATCAAC 807

QY 268 GluIleAsnArgAspVal-----AlaLeuLeuYrValAsnGlyThrYseGlnThrThr 286

Db 808 GACCTTAAGACACATTAATGCACTCTTAACCAAGCTT-----ACTTCAAGCTT--- 858

QY 287 TyGluAsnAlaMetPheSerGluValIleIleSerThrTyTrAsnTyrmSerAsn 306

Db 859 ---AAAAGTCCATGTTCCCTGAATTAATGCTATTAATTAAGACTAATTAATTAAC 915

QY 307 LeuGlyAspLeuPheGlu 312

Db 916 CTGGTGGA---TTCGAG 930

RESULT 11

US-11-106-187-3
 ; Sequence 3, Application US/11106187
 ; Publication No. US20050183162A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TUMER, NILGUN B.
 ; APPLICANT: WANG, PINGFENG
 ; TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN
 ; FILE REFERENCE: OCINS 3.9-060 CONT
 ; CURRENT APPLICATION NUMBER: US/11/106, 187
 ; PRIOR FILING DATE: 2005-04-14
 ; PRIOR APPLICATION NUMBER: US/09/721, 047
 ; PRIOR FILING DATE: 2000-11-22
 ; PRIOR APPLICATION NUMBER: PCT/US99/11301
 ; PRIOR FILING DATE: 1999-05-21
 ; PRIOR APPLICATION NUMBER: 60/086, 374
 ; PRIOR FILING DATE: 1998-05-22
 ; NUMBER OF SEQ ID NOS: 21

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/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 3
/ LENGTH: 934
/ TYPE: DNA
/ ORGANISM: Phytolacca americana
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: (1)..(75)
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: (76)..(930)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(930)
/ US-11-106-187-3

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Alignment Scores:

Pred. No.:	3,28e-52	Length:	934
Score:	511.00	Matches:	130
Percent Similarity:	56.1%	Conservative:	53
Best Local Similarity:	39.9%	Mismatches:	111
Query Match:	31.6%	Indels:	32
DB:	10	Gaps:	14

US-09-978-274a-2 (1-314) x US-11-106-187-3 (1-934)

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QY 1 MetLysValMetLeuValValValThrLeuIleAlaThrLeuIleAlaProThr 20
   |||||
DB 7 ATGAAAGTGTAAAGTAGTGGTGGCAATATCCATATGGCTGATCTTACACACCA 66
   |||||
QY 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGlyAsnAlaThrIleAsnLys 40
   |||||
DB 67 -----GCTTCTTCAACATAGTGTGGTGGAGTGGAGATGCCACACAGAACTTAC 117
   |||||
QY 41 AlaThrPheMetCysLeuSerLeuAlaGlnAlaLysPheProLysLeuLysCysTyrGly 60
   |||||
DB 118 TCTAATTTCTCTGCTAGTTGGCAGAGCTGTGAAAGACAAATTTGACATCCCATGGA 177
   |||||
QY 61 IleProMetLeuProAspThrAsnSerThrProLysTyrLeuValLysLeuGlnGly 80
   |||||
DB 178 ATGATATATGCCCAACCCCTCACTGAAACCCAGATATGTGTGGTGGCTTCAATTC 237
   |||||
QY 81 AlaAsnLeuLysThrIleThrLeuMetLeuArgArgAsnLeuLysTyrValMetGlyTyr 100
   |||||
DB 238 GGATCT---GGAACATTCATTCATAGCATCAGAAAGGGAATCTTATATTTGAGGGCTAT 294
   |||||
QY 101 SerAspProPheAsnGlnLysCysArgTyrHisIlePheAsnProIleThrSerThr 120
   |||||
DB 295 TCTGACATTTTACATGAGG---AATATGCTTATCGATCTTCAAGAT----- 339
   |||||
QY 121 GluArgThrAspValGluAsnThrLeuCysSerSerSerSerArg-----ValAla 138
   |||||
DB 340 TCGAATCCGATCCCAAGAGACCGTTGCCCGGGCAAAAGCAAGCTGCACTGAC 399
   |||||
QY 139 MetSerIleAsnTyrAsnSerLeuTyrProThrMetGluLysAlaGluValAsnSer 158
   |||||
DB 400 AATAATATATCCCATGAAAGAGTACAAAGGAGTGAATCAAAAGGCT-----GGGGCT 453
   |||||
QY 159 ArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGly 178
   |||||
DB 454 AGAAGCTAATATAGGTTAGGAAAGATTAACATCAAGAGTCAAGTGGTAAATCTACGGC 513
   |||||
QY 179 ValAspSerPhePro-----ValLysThrGluAlaPhePheLeuLeuValAla 194
   |||||
DB 514 AAGAGTCAACGATCAAGACGATATCAAAAAAAGAGGCTGAATTTCTTTATATAGCC 573
   |||||
QY 195 IleGlnMetValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThrAsn 214
   |||||
DB 574 GTTCAATATGTACTAGGATCAAGGATCAATATACATTGAGAAACAAGGAAAGGCTAA 633
   |||||
QY 215 PheAsnArgAla-----PheTyrProAspProLysValIleAsnLeuGlnGlyLysTyr 232
   |||||
DB 634 TTTGATGATGCCAATGGGTATCAGCCAGATCTTAAAGCTATTTCCCTAGAGAAATTTGG 693

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```

QY 233 GlyLysIleSerGluAlaIleHisAsnAlaLysAsnGly-----AlaLeu 247
   |||||
DB 694 GACAGTGTTCCTAAGGTCAAT-----GCAAAAGTTGGACCTCCGGTATGACTGTT 747
   |||||
QY 248 ProLysProLeuGluLeuValAspAlaLysGlyThrLysThrIleValLeuArgValAsp 267
   |||||
DB 748 ACTTATCTGAGACCTTAAGATGAGATTAATTAACCTTGGACTACGGCCACCATGAAC 807
   |||||
QY 268 GluIleAsnArgAspAla---AlaLeuLeuLysTyrValAsnGlyThrCysGlnThr 286
   |||||
DB 808 GACCTTAAGAACACATATATGATGCTTACCCACAGTT-----ACTTGCAAGT--- 858
   |||||
QY 287 TyrGlnAsnAlaMetPheSerGlnValIleIleSerThrTyrTyrAsnTyrMetSerAsn 306
   |||||
DB 859 ---AAAGTTCATATGTTCCCTGAATATATGCTATATATATATGACTATATATAC 915
   |||||
QY 307 LeuGlyAspLeuPheGlu 312
   |||||
DB 916 CTGGTGAA---TTCGAG 930
   |||||

```

RESULT 12

US-11-106-187-20

/ Sequence 20, Application US/11106187

/ Publication No. US20050183162A1

/ GENERAL INFORMATION:

/ APPLICANT: TOWNER, NITIGUN E.

/ TITLE OF INVENTION: TRANSGENIC PLANTS PRODUCING A PAP II PROTEIN

/ FILE REFERENCE: OCIRS 3.9-060 CONT

/ CURRENT FILING DATE: 2005-04-14

/ PRIOR APPLICATION NUMBER: US/09/721,047

/ PRIOR FILING DATE: 2000-11-22

/ PRIOR APPLICATION NUMBER: PCT/US99/11301

/ PRIOR FILING DATE: 1999-05-21

/ PRIOR APPLICATION NUMBER: 60/086,374

/ PRIOR FILING DATE: 1998-05-22

/ NUMBER OF SEQ ID NOS: 21

/ SOFTWARE: PatentIn Ver. 3.3

/ SEQ ID NO 20

/ LENGTH: 855

/ TYPE: DNA

/ ORGANISM: Phytolacca americana

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: (1)..(855)

/ US-11-106-187-20

US-09-978-274a-2 (1-314) x US-11-106-187-20 (1-855)

Alignment Scores:

Pred. No.:	1,67e-48	Length:	855
Score:	480.50	Matches:	121
Percent Similarity:	56.5%	Conservative:	48
Best Local Similarity:	40.5%	Mismatches:	101
Query Match:	29.7%	Indels:	29
DB:	10	Gaps:	13

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QY 28 IleThrPheAspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGluSerLeu 47
   |||||
DB 4 ATAGTGTGATGAGTGAAGATGCAACCAAGAACTACTCTAATTTCTGACTAGTTGG 63
   |||||
QY 48 ArgAsnGlnAlaLysAspProLysLeuLysCysTyrGlyIleProMetLeuProAspThr 67
   |||||
DB 64 CGAGAACTGTGAAAGACAAAGAAATTTGACATCCATGATATATATATATGCAACACCTC 123
   |||||
QY 68 AsnSerThrProLysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLysThrIleThr 87
   |||||
DB 124 ACTGAACAAACCAAGATATGTGTGGTGGACCTCAATTTGGATCT---GAAACATTCACA 180
   |||||
QY 88 LeuMetLeuArgArgAsnAsnLeuLysTyrValMetGlyTyrSerAspProPheAsnGlnLys 107
   |||||

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Db 181 TTACCAATCAGAGGGGAACTTATATTGGAGGCTATCTGACATTACATGA--- 237
 Qy 108 LysCysArgTyrHisIlePheAsnAspIleThrSerThrGluArgThrAspValGluAsn 127
 Db 238 AAATGTCGTTATCGGATCTTCAGAGT-----TCGAATCCGATGCCAAG 285
 Qy 128 ThrLeuCySerSerSerSerSerSerValAlaMetSerIleAsnTyrAsnSer 145
 Db 286 ACCGTTGCCCCGGGGCAGAAAGAGAGCGCTGACCTGAGAAATATATCCCTATGAAG 345
 Qy 146 LeuTyrProThrMetGluLysLeuValaGluValaAsnSerArgAsnGluValaGluLeuGly 165
 Db 346 AGTTACAAAGGAGATGGAATCAAAAGGT-----GGGCTAGAACTAAATTTAGGTTAGGA 399
 Qy 166 IleGlnIleLeuSerSerSerSerSerIleGlyLysIleSerGlyValaAspSerPhePro----- 183
 Db 400 AAGATACACTCAGAGTCGAGATGGGTAAATCTACGCGAAGAGATGACAGATCAGAG 459
 Qy 184 -----VallyrThrGluAlaPhePheLeuValaIleGlnMetValSerGluAla 201
 Db 460 CAGTATCAAAAATAATGAGCTGGAATTTCTTATAGCGTTCAAAATGTTACTAGAGCA 519
 Qy 202 AlaArgPheLysTyrIleGluAsnGlnVallyrThrAsnPheAsnArgAla-----Phe 219
 Db 520 TCAAGGTTCAAAATCATTGAGAACCAAGTGAAGGCTAAATTTGATGATGCCAATGGGTAT 579
 Qy 220 TyrProAspProLysValIleAsnLeuGluGlySerTyrGlyLysIleSerGluAlaIle 239
 Db 580 CAGCAGATCTTAAGCTATATTTCTTACAGAAAATTTGGAGACAGTGTTCATGAAGCTCAT 639
 Qy 240 HisAsnAlaLysAsnGly-----AlaLeuProLysProLeuGluLeuVal 254
 Db 640 -----GCAAAAGTTGGACCTCGGCTGATAGTACTGTACTTACCTGAGAGACTTAA 693
 Qy 255 AspAlaLysGlyThrLysTyrIleValLeuArgValaAspGluIleAsnArgAspVal--- 273
 Db 694 GATAGATATATTAACCTTGACTGACGCGACCATGAAAGCATTAAGAACAGCATTTATG 753
 Qy 274 AlaLeuLeuLysTyrValaAsnGlyThrCysGlnThrThrTyrGlnAsnAlaMetPheSer 293
 Db 754 GCATCTCCATACCCACGTT-----ACTTGCAAGGT-----AAAAGTTCATATGTTCCCT 801
 Qy 294 GlnValIleIleSerThrTyrTyrAsnTyrMetSerAsnLeuGlyAspLeuPheGlu 312
 Db 802 GAATTTATGTCCTTATATATAGACTATATAGTATAGTAACTTTGGTGA---TTGAG 855

RESULT 13
 US-10-919-750-4
 ; Sequence 4, Application US/10919750
 ; Publication No. US20050120414A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Diamond, Paul
 ; TITLE OR INVENTION: REGULATION OF POLYNUCLEIC ACID ACTIVITY AND EXPRESSION
 ; FILE REFERENCE: P1100-40S
 ; CURRENT APPLICATION NUMBER: US/10/919, 750
 ; PRIOR FILING DATE: 2004-08-16
 ; PRIOR APPLICATION NUMBER: US 10/644, 288
 ; PRIOR FILING DATE: 2003-08-20
 ; PRIOR APPLICATION NUMBER: US 10/354, 903
 ; PRIOR FILING DATE: 2003-01-29
 ; PRIOR APPLICATION NUMBER: US 60/352, 705
 ; PRIOR FILING DATE: 2002-01-29
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Microsoft Wordpad
 ; SEQ ID NO 4
 ; LENGTH: 935
 ; TYPE: DNA
 ; ORGANISM: Saponaria officinalis
 US-10-919-750-4

Alignment Scores: 7.82e-36 Length: 935
 Pred. No.: 378.50 Matches: 104
 Score:

Percent Similarity: 56.1% Conservative: 57
 Best Local Similarity: 36.2% Mismatches: 101
 Query Match: 23.4% Indels: 25
 Db: 9 Gaps: 11

US-09-978-274A-2 (1-314) x US-10-919-750-4 (1-935)

Qy 4 MetLeuValValValValThrLeuIleAlaThrLeuIle-----AlaAlaProThr 20
 Db 85 ATGAAGATATATGTTGTAACCAATATGATGATATCCGCTTCAATTTTCAGCTTGACA 144
 Qy 21 SerThrCysAlaIleAsnThrIleThrPheAspAlaGluAsnAlaThrIleAsnLysTyr 40
 Db 145 ACAATGATGCGGTACATCATCATCATTTAGATCTTAAATCCGACCGCGGTCAATAC 204
 Qy 41 AlaThrPheMetGluSerLeuArgAsnGlnAlaLysAspProLysLysCysTyrGly 60
 Db 205 TCATCTTTTGGATTAATAATCCGAACACCTAAAGATCCAAACTGAATATACGTTGCT 264
 Qy 61 IleProMet---LeuProAspThrAsnSerThrProLysTyrIleLeuValLysLeuGln 79
 Db 265 ACCGACATAGCCGATGATAGCCCACTTCAAGAAAATTTCTTAAATTAATTTCCAA 324
 Qy 80 GlyAlaAsnLeuLysThrIleThrLeuMetLeuArgAsnAsnLeuTyrValMetCly 99
 Db 325 AGTCCCGA---GGAACGCTCTCATCTGGCTTAAACGCCATTACTGTATGTGTCGCG 381
 Qy 100 Tyr-----SerAspProPheAsnGlyAsnLysCysArgTyrHisIlePheAsnAspIle 117
 Db 382 TATCTTCATATGATTAACAGAAATTTAATCGGCA---TATTACTTCAGATCAGAAAT 438
 Qy 118 ThrSerThrGluArgThrAspValGluAsnThrLeuCySerSerSerSerSerArgVal 137
 Db 439 ACTTCGCCGACGTCAACC-----GCCCTTTTCCAGAGGCCACACGTCAAT 486
 Qy 138 AlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGlyLysValaGluVal--- 156
 Db 487 CAGAAACTTTAGAAATACACAGAAATTTACAGTCATGAAAAGAAATGCCCAATAA 546
 Qy 157 -----AsnSerArgAsnGlnValaGluLeuGlyIleGlnIleLeuSerSerAspIle 173
 Db 547 CAAAGAGATCAAGATAGAAAAGAACTCGGTGGGATTTGACTTCACTTCAACGTCATG 606
 Qy 174 GlyLysIleSerGlyValaAspSerPheProValLysThrGluAlaPhePheLeuVal 193
 Db 607 GAACGACGTGAAC---AAGAAAGCACGTGGTTAAAGACAGAGTCAATTCCTTATATC 663
 Qy 194 AlaIleGlnMetValSerGluAlaAlaArgPheLysTyrIleGluAsnGlnValLysThr 213
 Db 664 GCTATTGAGATGACGCTGAGCGACGCCGATTTAGTACATCAAAACTTGTAATCAAG 723
 Qy 214 AsnPheAsnArgAlaPheTyrProAspProLysValIleAsnLeuGluLysTyrGly 233
 Db 724 AACTTTCACCAAGTTCAACTCGAACAAGAGATTCAGTTTGAGGTTAACTGAGAAA 783
 Qy 234 LysIleSerGluAlaIleHis---AsnAlaLysAsnGlyAlaLeuProLysProLeuGlu 252
 Db 784 AAAATTTCTACGGGAAATATACGGGGATGCCAAAACGGCGTTTAATTAAGATTATGAT 843
 Qy 253 LeuValaAspAlaLysGlyThrLysTyrIleValLeuArgValaAspGluIleAsnArgAsp 272
 Db 844 TTCCGGTTTGGAAA-----CTTAGCAGAGTGAAGACCTTG-----CAA 882
 Qy 273 ValAlaLeuLeuLysTyrVal 279
 Db 883 ATGGACTCTTATATGATTTG 903

RESULT 14
 US-09-861-257-38
 ; Sequence 38, Application US/09861257
 ; Publication No. US20030040496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chandler, Lois Ann

APPLICANT: Sosnowski, Barbara A.
APPLICANT: Baird, J. Andrew
APPLICANT: Pierce, Glenn
TITLE OF INVENTION: TREATMENT OF TUMORS USING
TITLE OF INVENTION: LIGAND-DIRECTED NUCLEIC ACID DELIVERY VEHICLES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/861,257
FILING DATE: 17-MAY-2001
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Christiansen Ph.D., William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 760100.423C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..804
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..804
OTHER INFORMATION: /note= "Nucleotide sequence
OTHER INFORMATION: corresponding to the clone M13 mp18-G9"
FEATURE:
NAME/KEY: mat peptide
LOCATION: 46..804
OTHER INFORMATION: /product= "Saporin"
US-09-861-257-38
Alignment Scores:
Pred. No.: 7.69e-34 Length: 804
Score: 361.50 Matches: 100
Percent Similarity: 56.1% Conservative: 56
Best Local Similarity: 36.0% Mismatches: 97
Query Match: 22.4% Indels: 25
DB: 3 Gaps: 11
US-09-978-274a-2 (1-314) x US-09-861-257-38 (1-804)
QY 13 AATATPLeuile-----AAlaIaProThSerThrCyAlaIleAenThrIleThr 29
DB 1 GCATGATCTCTGCTTCATATTTCAGCTTGACAACTGATCGCATCATCATCACA 60
QY 30 PheAspAlaGlyAsnAlaThrIleAsnLysTyAlaThrPheMetGluSerLeuArgAsn 49
DB 61 TTGATCTACTATAATCCGACCGCGGCTGACATCTCTTTGGATTAATCCGAAC 120
QY 50 GlnAlaLysAspProLysLeuLysCyTyGlyIleProMet---LeuProAspThrAsn 68
DB 121 AACGTAAAGGATCAACCTGAATAACGGGTGACGACATAGCCGCGAAGGCCACCT 180
QY 69 SerThrProLysTyLeuLeuValLysLeuGlnGlyAlaAsnLeuLysThrIleThrLeu 88

DB 181 TCTAAGAAAAATTCCTTAATTAATTCAGAAAGTCCGA---GGAAGGCTCACT 237
QY 89 MetLeuArgArgAsnLeuLysTyValMetGlyTyT-----SerAspProPheAsnGly 106
DB 238 GGCCTAAAGCAGTACTGTATGTCGCGTATCTTCGCAATGATTAACCAATGTT 297
QY 107 AsnLysCyAspArgTyTrHisIlePheAsnAspIleThSerThrGluArgThrAspValGlu 126
DB 298 AATCGGGA---TATTACTTCATGACAAATTAATCTCCGCGAGTTAAC----- 345
QY 127 AsnThrLeuCySerSerSerSerSerArgValAlaMetSerIleAsnTyAsnSerLeu 146
DB 346 ---GCCCTTTTCCAGAGCCACACATCGCAATCAGAAAGCTTTAAGAAATACACAGAAAT 402
QY 147 TyrProThMetGluLysLysAlaGluVal-----AsnSerArgAsnGlnVal 162
DB 403 TATCAGTCGATTAAAGAAATGCCAGTTAACACAGAGATCAAGATCAAGAAAGAAATC 462
QY 163 GlnLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPhe 182
DB 463 GCGTTGGGAGTTGACTTACTTCAAGCTCCATGAGACAGTGAC---AAGAGCGACGT 519
QY 183 ProValLysThrGluAlaPhePheLeuLeuValAlaIleGlnMetValSerGluAla 202
DB 520 GTGGTTAAAGACGACGATGATTCCTTATCGCTATTCAGATGACGCGTGAGCAGCG 579
QY 203 ArgPheLysTyTrIleGlnLeuGlnValLysTyAsnPheAsnArgAlaPheTyProAsp 222
DB 580 CGATTAGGTACATCAAACTTGTGTAATCAAGAACTTCCCAACAACTTCAACTCGGA 639
QY 223 ProLysValIleAsnLeuGluGluTyTrPglyLysIleSerGluAlaIleHis---Asn 241
DB 640 AACAAAGTATGATTCAGTTGAGTTAGCTGAAGAAATTTCTTACGCGCAATATACGGGAT 699
QY 242 AlaLysAsnGlyAlaLeuProLysPProLeuGluLeuValAspAlaLysGlyThrLysTyTr 261
DB 700 GCCAAAGACGCGCTGTTTAAAGATTAATGATTTTCGGGTTCGAAAA----- 747
QY 262 IleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyTrVal 279
DB 748 ---GTAGGACAGGTGAAGACTTG-----CAATGCACTCTTATGTATTTG 792
RESULT 15
US-10-189-360-23
Sequence 23, Application US/10189360
Publication No. US20030143217A1
GENERAL INFORMATION:
APPLICANT: Baird, J. Andrew
Chandler, Lois Ann
Sosnowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS
FOR THERAPE
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/189,360
FILING DATE: 02-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996

ATTORNEY/AGENT INFORMATION:
NAME: No. US20030143217Altenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.415C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..804
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..804
OTHER INFORMATION: /note= "Nucleotide sequence
corresponding to the clone m13 mp18-69 in Example I.B.2."
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 46..804
OTHER INFORMATION: /product= "Saporin"
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-189-360-23

Alignment Scores:

Pred. No.:	7,69e-34	Length:	804
Score:	361.50	Matches:	100
Percent Similarity:	56.1%	Conservative:	56
Best Local Similarity:	36.0%	Mismatches:	97
Query Match:	22.4%	Indels:	25
DB:	6	Gaps:	11

US-09-978-274A-2 (1-314) x US-10-189-360-23 (1-804)

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QY 13 AlATrLeuLeu-----AlAlAProThrSerThrCyBAAlaIleAenThrIleThr 29
DB 1 GCATGATCCGCTTCAATTTTCAGCTTGACCAACCACTGATGCGTCACATCATCACA 60
QY 30 PheAspAlaGlyAenAlaThrIleAsnLysTyAlaThrPheMetGluSerLeuArgAsn 49
DB 61 TTGATATTAGTAATTCGACCGCGGTCATATCTCATCTTTTGATTAATAATCCGAAC 120
QY 50 GluAlaLysAspProLysLeuLysCyAsTyrgIyIleProMet---LeuProAspThrAsn 68
DB 121 AACGTAAAGGATCCAAACCTGAATATACGGATACCGACATAGCCGTGATAGCCCACT 180
QY 69 SerThrProLysTyLeuLeuValLysLeuGlnGlyAlaAsnLeuLysThrIleThrLeu 88
DB 181 TCTAAAGAAAAATTCCTTAGAATTATTTCCAAAGTCCCGA---GGAACGGTCTCACTT 237
QY 89 MetLeuArgArgAenAenLeuTyValMetGlyTyT-----SerAspProPheAsnGly 106
DB 238 GGCCTTAACGCGATACCTTGATGTGTCGCGTATCTTGCAATGATTAACACGAATGTT 297
QY 107 AsnLysCyAsArgTyRHisIlePheAsnAspIleThrSerThrgIuArgThrAspValGlu 126
DB 298 AATCGGGCA---TATTACTTCAGATCAGAAATTACTTCCGCCGAGTTAAC----- 345
QY 127 AsnThrLeuCySerSerSerSerSerSerArgValAlaMetSerIleAsnTyRAsnSerLeu 146
DB 346 ---GCCCTTTTCCAGAGCCACAACTGCAAAATCAGAAAGCTTTAGATACACAGAAAT 402
QY 147 TyrProThrMetGluLysLysAlaGluVal-----AsnSerArgAsnGluVal 162
DB 403 TATCAATCATGATGAAAGATGCCAGATTAACACAGAGATCAAAAGTAGAAAAAATCTC 462
QY 163 GluLeuGlyIleGlnIleLeuSerSerAspIleGlyLysIleSerGlyValAspSerPhe 182
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DB 463 GGGTTGGGATGACTTACTTTCACAGTCCATGGAAGCAGTGAAC---AAGAAGCAGCT 519
QY 183 ProValLysThrGluAlaPhePheLeuValAlaIleGlnMetValSerGluAla 202
DB 520 GTGGTTAAAGACGAAGCTAGATTCCTTATGCTATTCAGATGACGGCTGAGGACGCG 579
QY 203 ArgPheLysTyRileGluAenGluValLysThrAsnPheAsnArgAlaPheTyRProAsp 222
DB 580 CGATTTAGGTACATACAAACTTGATATCAAGAACTTCCCAACAGTTCACTCGGA 639
QY 223 ProLysValIleAsnLeuGlnGluLysTyrgIyLysIleSerGluAlaIleHis---Asn 241
DB 640 AACAAAGTGAATTCAGTTGAGGTTAACTGGAATAAAATTTCTACGGCAATATACGGGAT 699
QY 242 AlaLysAsnGlyAlaLeuProLysProLeuGlnLeuValAspAlaLysGlyThrLysTrp 261
DB 700 GCCAAAAACGCGCTGTTTAAATTAAGATTATGATTTCCGGTTTGAAAA----- 747
QY 262 IleValLeuArgValAspGluIleAsnArgAspValAlaLeuLeuLysTyRVal 279
DB 748 ---GTGAGGCAAGTGAAAGACTTG-----CAATAGGACTCTTATGTAATTG 792
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Job time : 1129.2 secs

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 9, 2006, 01:48:26 ; Search time 823.643 Seconds
(without alignments)
1525.144 Million cell updates/sec

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Perfect score: 1617
Sequence: 1 MKWMLVVVTLTAMLIAPF.....VISTYYNYSNGLDPEEP 314

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 9267905 segs, 2000278028 residues
Total number of hits satisfying chosen parameters: 18535810

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-MAXLEN=200000000 -HOST=abse03p
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA_New:*
1: /SID5/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /SID5/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /SID5/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /SID5/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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15: /SID5/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	ID	Description
1	1235.5	76.4	1360	US-11-010-795-19	Sequence 19, Appl
2	511	31.6	934	US-11-010-795-21	Sequence 21, Appl

3	315.5	19.5	1855	8	US-10-893-584-95	Sequence 95, Appl
4	313.5	19.4	1855	8	US-10-893-584-92	Sequence 92, Appl
5	311	19.2	1855	8	US-10-893-584-35	Sequence 35, Appl
6	311	19.2	1855	8	US-10-893-584-74	Sequence 74, Appl
7	310.5	19.2	1855	8	US-10-893-584-39	Sequence 39, Appl
8	310.5	19.2	1855	8	US-10-893-584-50	Sequence 50, Appl
9	310	19.2	1855	8	US-10-893-584-125	Sequence 125, App
10	309	19.1	1813	8	US-10-893-584-245	Sequence 245, App
11	307.5	19.0	1810	8	US-10-893-584-168	Sequence 168, App
12	307.5	19.0	1855	8	US-10-893-584-80	Sequence 80, App
13	307.5	19.0	1807	8	US-10-893-584-196	Sequence 196, App
14	306.5	19.0	1855	8	US-10-893-584-3	Sequence 3, Appl
15	306.5	19.0	1855	8	US-10-893-584-5	Sequence 5, Appl
16	306.5	19.0	1855	8	US-10-893-584-7	Sequence 7, Appl
17	306.5	19.0	1855	8	US-10-893-584-9	Sequence 9, Appl
18	306.5	19.0	1855	8	US-10-893-584-13	Sequence 13, Appl
19	306.5	19.0	1855	8	US-10-893-584-15	Sequence 15, Appl
20	306.5	19.0	1855	8	US-10-893-584-17	Sequence 17, Appl
21	306.5	19.0	1855	8	US-10-893-584-19	Sequence 19, Appl
22	306.5	19.0	1855	8	US-10-893-584-21	Sequence 21, Appl
23	306.5	19.0	1855	8	US-10-893-584-23	Sequence 23, Appl
24	306.5	19.0	1855	8	US-10-893-584-25	Sequence 25, Appl
25	306.5	19.0	1855	8	US-10-893-584-27	Sequence 27, Appl
26	306.5	19.0	1855	8	US-10-893-584-29	Sequence 29, Appl
27	306.5	19.0	1855	8	US-10-893-584-31	Sequence 31, Appl
28	306.5	19.0	1855	8	US-10-893-584-33	Sequence 33, Appl
29	306.5	19.0	1855	8	US-10-893-584-37	Sequence 37, Appl
30	306.5	19.0	1855	8	US-10-893-584-48	Sequence 48, Appl
31	306.5	19.0	1855	8	US-10-893-584-52	Sequence 52, Appl
32	306.5	19.0	1855	8	US-10-893-584-54	Sequence 54, Appl
33	306.5	19.0	1855	8	US-10-893-584-77	Sequence 77, Appl
34	306.5	19.0	1855	8	US-10-893-584-83	Sequence 83, Appl
35	306.5	19.0	1855	8	US-10-893-584-86	Sequence 86, Appl
36	306.5	19.0	1855	8	US-10-893-584-89	Sequence 89, Appl
37	306.5	19.0	1855	8	US-10-893-584-98	Sequence 98, Appl
38	306.5	19.0	1855	8	US-10-893-584-101	Sequence 101, App
39	306.5	19.0	1855	8	US-10-893-584-104	Sequence 104, App
40	306.5	19.0	1855	8	US-10-893-584-110	Sequence 110, App
41	306.5	19.0	1855	8	US-10-893-584-113	Sequence 113, App
42	306.5	19.0	1855	8	US-10-893-584-116	Sequence 116, App
43	306.5	19.0	1855	8	US-10-893-584-119	Sequence 119, App
44	306.5	19.0	1855	8	US-10-893-584-122	Sequence 122, App
45	306.5	19.0	1861	8	US-10-893-584-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-11-010-795-19
; Sequence 19, Application US/11010795
; Publication No. US20060005271A1
; GENERAL INFORMATION:
; APPLICANT: TUMER, NITGUN E.
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING L3 DELTA PROTEINS ARE
; TITLE OF INVENTION: RESISTANT TO TRICHOECENE FUNGAL TOXINS
; FILE REFERENCE: OCINS 3.0-085
; CURRENT APPLICATION NUMBER: US/11/010,795
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,348
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 19
; LENGTH: 1360
; TYPE: DNA
; ORGANISM: *Phytolacca americana*
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (207)..(1145)
US-11-010-795-19
Alignment Scores:

Dh 514 AAGATGCAACGATGACGAAGACTATCAAAAAATGAGCTGAATTTCTTATAGCC 573
Qy 195 IlegImetValSerGluAlaAlaArgPheLeuTyrIleGluAenGlnValIleThrAsn 214
Dh 574 GTTCAATGGTACTGAGGCTCAAGGTTCAAAATTCATTGGAACAAAGTGAAGGCTTAA 633
Qy 215 PheAsnArgAla-----PheTyrProAspProIleValIleAenLeuGlnIleTyr 232
Dh 634 TTTGATGATGCGCAATGGGTATCAGCCAGATCTTAAAGCTATTTCTTGAAGAAAAATTGG 693
Qy 233 GLyLeuIleSerGluAlaIleHisAsnAlaIleValAsnGly-----AlaLeu 247
Dh 694 GACAGTGTTCATAGTCAAT-----GCAAAAGTTGCACTCCGGTGAATGATCACTGT 747
Qy 248 ProIleProLeuGlnLeuValAspAlaIleGlyThrIleTyrIleValIleValAspVal 267
Dh 748 ACTTACCTGAGAGCTTAAAGATGAGATTAATTAACCTTGAGCTAGCGGCAACATGAC 807
Qy 268 GlnIleAsnArgAspVal-----AlaLeuLeuIleTyrValAsnGlyThrCysGlnThr 286
Dh 808 GACCTTAAGAAGCATTAATGAGCACTCTTAACCAAGCTT-----ACTTGAAGGTT--- 858
Qy 287 TyrGlnAsnAlaMetPheSerGlnValIleIleSerThrTyrTyrAsnTyrMetSerAsn 306
Dh 859 ---AAAGTTCAGATGTCCTGAAATTAATGCTTATTAATAGACTAGATTAATGATAC 915
Qy 307 LeuGlyAspLeuPheGln 312
Dh 916 CTGGTGAA---TTGAG 930

RESULT 3

US-10-893-584-95
; Sequence 95, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admitr
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Richn-like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR APPLICATION NUMBER: 2004-07-19
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PAP-276 insert
US-10-893-584-95

Alignment Scores:

Pred. No.: 7,93e-26 Length: 1855
Score: 315.50 Matches: 95
Percent Similarity: 44.4% Conservative: 52
Best Local Similarity: 28.7% Mismatches: 115
Query Match: 19.5% Indels: 69
DB: 8 Gaps: 13

US-09-978-274A-2 (1-314) x US-10-893-584-95 (1-1855)

Qy 10 ThrLeuIleAlaTyrPheLeuIleAlaAlaProThrSerThrCysAlaIleAsnThr----- 27
Dh 25 ACTATTGTAAATGATGATGATGATGAGTGGCAACAGGCTTGTGTTGATCATCAGG 84

Qy 28 -----IleThrPhe 30
Dh 85 TGGCTTTCACTTAGAGATACACATATTCCTCCCAACATACCAATTAATAACTTT 144
Qy 31 AspAlaGlyAsnAlaThrIleAsnIleTyrAlaThrPheMetGluSerLeuArgAsnGln 50
Dh 145 ACCAAGCGGGGTGCTGAGCAAGCTGCAAGAGCTTATCAAACTTTATCAGAGCTTGGGGTCT 204
Qy 51 AlaIleAspProIleLeuIleCysTyrGlyIleProMetLeuProPheAsnGlyAsn 70
Dh 205 TTAACAACTGAGCTGATGAGACATGATATACAGTGTGCTCCAAACAGAGTGGTTTG 264
Qy 71 Pro-----LysTyrLeuLeuValIleLeuGlnIleValAsnLeuIleThrIleThr 87
Dh 265 CTTATTAACCAACGGTTTATTTATGTTGAACTCTCAAAATCATGACAGACTTCTGTATCA 324
Qy 88 LeuMetLeuArgArgAsnAsnLeuIleTyrValMetGlyTyrSerAspProPheAsnGlyAsn 107
Dh 325 TTAGCGGTGATGATCAACAAATGATATGATGTGGTACCGT-----GCTGAAAT 375
Qy 108 LysCysArgTyr-----HisIlePhe 114
Dh 376 AGCGCATATTTCTTCACTCTGACAAATCAGAAAGATCAGAAAGCATCATCTTTTC 435
Qy 115 AsnAspIleThrSerThrGluArgThrAspValGlnAsnThrLeuCysSerSerSerSer 134
Dh 436 -----ACTGATGTTCAAAAT----- 450
Qy 135 SerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGlnIleValAla 154
Dh 451 ---CGATATACATTCGCTTGGTGGTAAAT-----TATGATGACTTGAACAACCTTGC 501
Qy 155 GluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerArgPheGly 174
Dh 502 GGT---AATCTGAGAGAAATATCGAGTTGGAAATGCTCACTAGAGAGAGCATCTCA 558
Qy 175 LysIle-----SerGlyValAspSerPheProValIleThrGluAlaPhePhe 190
Dh 559 GCGCTTATTAATTAACGATCTGAGTGGTCACTGACCTTCACTGCTGCTGCTTCTT--- 615
Qy 191 LeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPheIleTyrIleGluAsnGln 210
Dh 616 ---ATATTTGCATTCCAATATGATTCAGAGCAAGATTCCAATATATTTGAGGAGAA 672
Qy 211 ValIleThr-----AsnPheAsnArgAlaPheTyrProAspProIleValIleAsnLeu 228
Dh 673 ATGCGCAGCAATTAAGTACAAACCGAGATCTGCACACGATCTTACGTAATTAACACTT 732
Qy 229 GlnGlnIleTyrPheGlyIleSerGluAlaIleHisAsnAlaIleValAsnGlyAlaLeuPro 248
Dh 733 GAGAAATGTTGGGGAGACTTTCACCTGCACTGCAATTCAGATTCACCAAGAGAGCTTTGCT 792
Qy 249 LysProLeuGlnLeuValAspAlaIleGlyThrIleTyrTyrIleValIleValAspVal 268
Dh 793 AGTCCAATTCAGATTCGAAAGACGTAATGTTTCCAAATTCAGTGTGATGATGATGATGATA 852
Qy 269 IleAsnArgAspValAlaLeuLeuIleTyrValAsnGlyThrCysGlnThrTyrGln 288
Dh 853 TTAATCCCTATCATAGCTCTCATGTGTAT-----AGATGCGCACTTCA---CCA 900

RESULT 4

US-10-893-584-92
; Sequence 92, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admitr

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APPLICANT: Stoll, Dominik
TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 92
LENGTH: 1855
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
US-10-893-584-92
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Alignment Scores:

Pred. No.:	1,35e-25	Length:	1855
Score:	313.50	Matches:	94
Percent Similarity:	44.5%	Conservative:	57
Best Local Similarity:	27.7%	Mismatches:	119
Query Match:	19.4%	Indels:	69
DB:	8	Gaps:	13

US-09-978-274A-2 (1-314) x US-10-893-584-92 (1-1855)

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DB 25 ACTATTGTATATATGATGTATGATGAGTGGCAACATGGCTTTGTTGGATCCACTCAGG 84
QY 28 -----11ethrPhe 30
DB 85 TGGTCTTCACATTAGAGATTAACAACATATTCGCCAACATACCCATATTATTAACCTTT 144
QY 31 AepAlaGlyAsnAlaThrIleAenLysTyraIleAthrPheMetGluSerLeuAryAenGln 50
DB 145 ACCACACGGGGTCCACTGTCGCAAGCTACACAACTTTATACAGAGCTGTGCGGCTGCT 204
QY 51 AlaLysAspProLysLeuLysCysTyrglyIleProMetLeuProAspThrAenSerThr 70
DB 205 TTAAACAACGTGAGCTGATGAGACATGATATACAGTGTGCGCAACAGAGTTGGTTTG 264
QY 71 Pro-----LysTyrlleuLeuValLysLeuGlnGlyAlaAenLysThrIleThr 87
DB 265 CCTATAAACCAACGGCTTTATTTTAGTGAACCTCAATCATGCAGAGCTTCTGTAC 324
QY 88 LeuMetLeuAryAenAenLysLeuValMetGlyTyrlleAenSerProPheAenGlyAen 107
DB 325 TTAGCGCTGATGTACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 375
QY 108 LysCysArgTyrlle-----HisIlePhe 114
DB 376 ACGCATATTTCTTCATCCTGACAAATCAGAAAGATGCAAGAACATCACTATCTTTTC 435
QY 115 AenAepIleThrSerThrGlnAryAenPheValGluAenThrLeuCysSerSerSerSer 134
DB 436 -----ACTGATGTTCAAAAT-----450
QY 135 SerArgValAlaMetSerIleAenTyrlleAenSerLeuTyrlleProThrMetGluLysAla 154
DB 451 ---CGATATACATGCGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 501
QY 155 GluValAenSerArgAenGlnValGlnLeuGlyIleGlnIleLeuSerSerAepIleGly 174
DB 502 GGT---AATCTGAGAGAAATATATCGAGTGGGAAATGATGATGATGATGATGATGATGAT 558
QY 175 LysIle-----SergIlyValAepSerPheProValLysThrGlnAlaPhePhe 190
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DB 559 GGCCTTATATTATACAGTACTGGGACTCAGCTTCCAACTGCGCTGCTCTT----- 615
QY 191 LeuLeuValAlaIleGlnMetValSergIlyAlaAlaAryAenTyrlleGluAenGln 210
DB 616 ---ATAATTGTCATCCAAATGATTTCAAGAGCAGAAAGATTCATATATTTGAGGGGAA 672
QY 211 ValIleThr-----AenPheAenArgAlaPheTyrlleProAspProLysValIleAenLeu 228
DB 673 ATGCGACGAGAAATTTAGTTCACACCGAGATCTGCACCAAGATCTTACCTGATTTACCTT 732
QY 229 GluGluLysTyrglyLysIleSergIlyAlaIleHisAenAlaLysAenGlyAlaLeuPro 248
DB 733 GAGAAATAGTGGGGGAGACTTTCACCTGCAATTCAGAGTCAACAGTCAACAGAGCTTGTCT 792
QY 249 LysPheLeuGluLeuValAenAlaLysGlyThrIleTyrlleValIleAenGlyValAenGln 268
DB 793 AGTCCAAATTCACCTGCAAGAGCTTAATGTTCCAAATTCAGTGTGACAGATGAGATATA 852
QY 269 IleAenArgAenValAlaLeuLeuLysTyrlleValAenGlyThrCysGlnThrThrTyrgln 288
DB 853 TTATCCCTATCATCTACTCATGCTGAT-----AGATCCGACCTCCA---CCA 900
QY 289 AsnAlaMetPheSergIlyValIleIleSerThrTyrlleAenTyrlleMetSerAenLeu 307
DB 901 TCGTCAAGATTTCTTTCTTTATATTCGGGTATCGGCTAATTTTATGCTGATGTT 957
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RESULT 5

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US-10-893-584-35
Sequence 35, Application US/10893584
Publication No. US20050272048A1
GENERAL INFORMATION:
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APPLICANT: Borgford, Thor
APPLICANT: Braun, Curtis
APPLICANT: Burac, Admir
APPLICANT: Stoll, Dominik
TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
LENGTH: 1855
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
US-10-893-584-35
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Alignment Scores:

Pred. No.:	2,63e-25	Length:	1855
Score:	311.00	Matches:	92
Percent Similarity:	43.2%	Conservative:	50
Best Local Similarity:	28.0%	Mismatches:	109
Query Match:	19.2%	Indels:	78
DB:	8	Gaps:	12

US-09-978-274A-2 (1-314) x US-10-893-584-35 (1-1855)

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DB 25 ACTATTGTATATATGATGTATGATGAGTGGCAACATGGCTTTGTTGGATCCACTCAGG 84
QY 28 -----11ethrPhe 30
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Db 85 TGCTCTTACATTAGAGATTAACAACATATTTCCCAACAAATCCCAATTATTAACCTT 144
Qy 31 AspaIaGlyAsnAlaThrIleAsnLysTyraIaThrPheMetGluSerLeuArgAsnGln 50
Db 145 ACCACAGGGGGTGCACCTGTGCAAGTACACAACTTATACAGCTGTGGCGGTGT 204
Qy 51 AlAlAspProLysLeuLysCysTyrglyIleProMetLeuProAspThrAsnSerThr 70
Db 205 TTAACAAGTGAAGCTGATGAGACATGATATACAGAGTGTGCCAAACAGAGTGGTTG 264
Qy 71 Pro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLysThrIleThr 87
Db 265 CCTTAAACCAACGCTTATATTATTTAGTGAACCTCAATCATGACAGACTTCTGTACA 324
Qy 88 LeuMetLeuArgArgAsnAsnLeuTyraIaMetGlyTyraSerAspProPheAsnGlyAsn 107
Db 325 TTACCGCTGATGATCAACCAATGATATGATGGCTACCGT-----GCTGAAT 375
Qy 108 LysCysArgTyrr-----HisIlePhe 114
Db 376 AGCGCATATTTCTTTCATCTGACATCAGGAAGATGCAAGCAATCAGCATCTTTTC 435
Qy 115 AsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSerSerSer 134
Db 436 -----ACTGATGTTCAAAAT----- 450
Qy 135 SerArgValAlaMetSerIleAsnTyraSerSerLeuTyrrProThrMetGluLysAla 154
Db 451 ----CGATATACATTCGCTTGGTGGTAAAT-----TATGATACAGCTTGAACAACTTGT 501
Qy 155 GluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGly 174
Db 502 GGT---AATCTGAGAGAAATATATGAGATGGGAATGGTCCATGAGAGAGGCTATCTCA 558
Qy 175 LysIle-----SerGlyValAspSerPheProValLysThrGluAlaPhePhe 190
Db 559 GCGCTTATATTAATACAGTACAGTACAGTCACTGCTTCCAGCTGCTGCTTCTT--- 615
Qy 191 LeuLeuValAlaIleGlnMetValSerGluAlaIaArgPheLysTyrrIleGluAsnGln 210
Db 616 ----ATAATTGTCATCCAAATATATTTCAAGACAGCAAGATTCAAATATATGAGAGAA 672
Qy 211 ValLysThr-----AsnPheAsnArgAlaPheTyrrProAspProLysValIleAsnLeu 228
Db 673 ATGGCAGCAGGAATTAAGTACACCGGAGATCTGCACAGATCTTAGGTATATACACTT 732
Qy 229 GluGluLysTyrglyLysIleSerGluAlaIleHisAsnAlaLysAsnGlyAlaLeuPro 248
Db 733 GAGAAATAGTTGGGGGAGACTTCCATGCAATTCAGAGTCTTACCAAGAGGCTTGGCT 792
Qy 249 LysProLeuGluLeuValAspAlaLysGlyTyrrIleTyrrIleValIleAsnArgValAspGln 268
Db 793 AGTCCAATTCACAGTCAAGACGTAATGTTCCAAATTCAGTGTGATCAGATGATGATA 852
Qy 269 IleAsnArgAspValAlaLeuLysLysTyrr----- 278
Db 853 TTATATCCCTATCATAGCTTCATGATGATATGATGCGACCTCCACCATCTCACAGTTT 912
Qy 279 -----ValAsnGlyThrCysGln 284
Db 913 TCTGGGGTGTGTAATGATCGTGTAGA 939
```

RESULT 6

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US-10-893-584-74
; Sequence 74, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
```

```
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
PRIOR FILING DATE: 2004-07-19/551,151
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 74
LENGTH: 1855
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PAP-262 Insert
US-10-893-584-74
```

Alignment Scores:

Pred. No.:	2,63e-25	Length:	1855
Score:	311.00	Matches:	93
Percent Similarity:	43.7%	Conservative:	52
Best Local Similarity:	28.0%	Mismatches:	119
Query Match:	19.2%	Indels:	68
DB:	8	Gaps:	12

US-09-978-274a-2 (1-314) x US-10-893-584-74 (1-1855)

```
Qy 10 ThrLeuIleAlaThrLeuIleAlaIaProThrSerThrCysAlaIleAsnThr----- 27
Db 25 ACTATTGTATATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 84
Qy 28 ----- 114
Db 85 TGCTCTTACATTAGAGATTAACAACATATTTCCCAACAAATCCCAATTATTAACCTT 144
Qy 31 AspaIaGlyAsnAlaThrIleAsnLysTyraIaThrPheMetGluSerLeuArgAsnGln 50
Db 145 ACCACAGGGGGTGCACCTGTGCAAGTACACAACTTATACAGCTGTGGCGGTGT 204
Qy 51 AlAlAspProLysLeuLysCysTyrglyIleProMetLeuProAspThrAsnSerThr 70
Db 205 TTAACAAGTGAAGCTGATGAGACATGATATACAGAGTGTGCCAAACAGAGTGGTTG 264
Qy 71 Pro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLysThrIleThr 87
Db 265 CCTTAAACCAACGCTTATATTATTTAGTGAACCTCAATCATGACAGACTTCTGTACA 324
Qy 88 LeuMetLeuArgArgAsnAsnLeuTyraIaMetGlyTyraSerAspProPheAsnGlyAsn 107
Db 325 TTACCGCTGATGATCAACCAATGATATGATGGCTACCGT-----GCTGAAT 375
Qy 108 LysCysArgTyrr-----HisIlePhe 114
Db 376 AGCGCATATTTCTTTCATCTGACATCAGGAAGATGCAAGCAATCAGCATCTTTTC 435
Qy 115 AsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSerSerSer 134
Db 436 -----ACTGATGTTCAAAAT----- 450
Qy 135 SerArgValAlaMetSerIleAsnTyraSerSerLeuTyrrProThrMetGluLysAla 154
Db 451 ----CGATATACATTCGCTTGGTGGTAAAT-----TATGATACAGCTTGAACAACTTGT 501
Qy 155 GluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGly 174
Db 502 GGT---AATCTGAGAGAAATATATGAGATGGGAATGGTCCATGAGAGAGGCTATCTCA 558
Qy 175 LysIle-----SerGlyValAspSerPheProValLysThrGluAlaPhePhe 190
Db 559 GCGCTTATATTAATACAGTACAGTACAGTCACTGCTTCCAGCTGCTGCTTCTT--- 615
```



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QY 51 AlAlaYAspProlybLeuYsCybYrGlyIleProMetLeuProAspThrAsnSerThr 70
DB 205 TTAAACAACGTGAGCTGATGAGCATGATATACAGTGTGCCAAACAGAGTTGGTTG 264
QY 71 Pro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuYsThrIleThr 87
DB 265 CCAATTAACCAACGCGTTTATTTAGTGAACCTCAAAATCAATGACAGAGCTTTCGTGACA 324
QY 88 LeuMetLeuArgArgAsnAsnLeuYrValMetGlyTyrSerAspProPheAsnGlyAsn 107
DB 325 TTAGCGCTGATGATGCACCAATGATGTGTGCGCTACCGT-----GCTGGAAT 375
QY 108 LysCyArgTyr-----ACTGATGTTCAAAAT-----HisIlePhe 114
DB 376 AGCGCATATTCTTTCACTCCTGACCAATCAGAAAGATCAGAAAGCAATCACTCATCTTTC 435
QY 115 AsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCySerSerSer 134
DB 436 -----ACTGATGTTCAAAAT----- 450
QY 135 SerArgValAlaMetSerIleAsnTyrAsnSerLeuYrProThrMetGlyLysVal 154
DB 451 ---CGATATACATTCGCTTGGTGGTAAT-----TATGATAGACTTGAACAACCTGCT 501
QY 155 GluValAsnSerArgAsnGlnValGlnLeuGlyTyrIleGlnIleLeuSerSerAspIleGly 174
DB 502 GGT---AATCTGAGAGAAATATCGAGTTGGAAATGTCCTCACTAGAGAGAGCTATCTCA 558
QY 175 LysIle-----SerGlyValAspSerPheProValLysThrGluAlaPhePhe 190
DB 559 GCGCTTATTTATTAACGATCTGGGCGCATCGACCTTCAACTGCTGCTGCTCTT--- 615
QY 191 LeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPheLysTyrIleGluAsnGln 210
DB 616 ---ATAATTGGATCCAAATGATTTGAGAGCAGCAAGATTCCAATATATGAGGAGAA 672
QY 211 ValLysThr-----AsnPheAsnArgAlaPheTyrProAspProLysValIleAsnLeu 228
DB 673 ATCGCAGCAGAAATTGATCAACCGGAGATGTCACACAGATCTCGATCGTAATTAACCTT 732
QY 229 GluGlnLysThrGlyLysIleSerGluAlaIleHisAsnAlaLysAsnGlyValAlaLeuPro 248
DB 733 GAAATATAGTGGGAGAGACTTCCATGCAATTCAGATTCAGAACCAAGAGGCTTGGCT 792
QY 249 LysProLeuGlnLeuValAspAlaLysGlyThrLysThrIleValLeuArgValAspGlu 268
DB 793 AGTCCAAATTCATCGCAAGAGCAATGATGTTCCAAATTCAGTGTGATGATGAGATATA 852
QY 269 IleAsnArgAspValAlaLeuLeuLysTyrValAsnGlyThrCys-GlnThrThrTyrGln 288
DB 853 TTAAATCCCTATCACTCATGCTCATGCTGAT-----AGATGCGCAGCTCCACCATCG 903
QY 288 AsnAlaMetPheSerGlnValIleIle 297
DB 904 TCACAGTTTTTCACAAAATATTGTATA 931
RESULT 10
US-10-893-584-245
; Sequence 245, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purec, Adam
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Richn-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
```

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; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 245
; LENGTH: 1813
; TYPE: DNA
; ORGANISM: E. coli
US-10-893-584-245
Alignment Scores:
Pred. No.: 4,36e-25 Length: 1813
Score: 309.00 Matches: 92
Percent Similarity: 43.5% Conservative: 48
Best Local Similarity: 28.6% Mismatches: 110
Query Match: 19.1% Indels: 72
DB: Gaps: 12
US-09-978-274A-2 (1-314) x US-10-893-584-245 (1-1813)
QY 10 ThrLeuIleAlaThrProLeuIleAlaIaProThrSerThrCysAlaIleAsnThr----- 27
DB 25 ACTATGTATATATGATGATGATGCGTGGCAACATGAGCTTGTGTGATCCACCTCAGG 84
QY 28 -----IleThrPhe 30
DB 85 TGCTTTCACTTAGAGATTAACAATATTTCCCAACCAATACCAATTAATTAATTT 144
QY 31 AspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGluSerLeuArgAsnGln 50
DB 145 ACCACAGCGGTGCCACTGTCGAAAGCTACACAACTTATATAGAGCTGTTCCGCGTCCGT 204
QY 51 AlAlaYAspProlybLeuYsCybYrGlyIleProMetLeuProAspThrAsnSerThr 70
DB 205 TTAAACAACGTGAGCTGATGAGCATGAAATTCAGTGTGCCAAACAGAGTTGGTTG 264
QY 71 Pro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuYsThrIleThr 87
DB 265 CCAATTAACCAACGCGTTTATTTAGTGAACCTCAAAATCAATGACAGAGCTTTCGTGACA 324
QY 88 LeuMetLeuArgArgAsnAsnLeuYrValMetGlyTyrSerAspProPheAsnGlyAsn 107
DB 325 TTAGCGCTGATGATGCACCAATGATGTGTGCGCTACCGT-----GCTGGAAT 375
QY 108 LysCyArgTyr-----ACTGATGTTCAAAAT-----HisIlePhe 114
DB 376 AGCGCATATTCTTTCACTCCTGACCAATCAGAAAGATCAGAAAGCAATCACTCATCTTTC 435
QY 115 AsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCySerSerSer 134
DB 436 -----ACTGATGTTCAAAAT----- 450
QY 135 SerArgValAlaMetSerIleAsnTyrAsnSerLeuYrProThrMetGlyLysVal 154
DB 451 ---CGATATACATTCGCTTGGTGGTAAT-----TATGATAGACTTGAACAACCTGCT 501
QY 155 GluValAsnSerArgAsnGlnValGlnLeuGlyTyrIleGlnIleLeuSerSerAspIleGly 174
DB 502 GGT---AATCTGAGAGAAATATCGAGTTGGAAATGTCCTCACTAGAGAGAGCTATCTCA 558
QY 175 LysIle-----SerGlyValAspSerPheProValLysThrGluAlaPhePhe 190
DB 559 GCGCTTATTTATTAACGATCTGGGCGCATCGACCTTCAACTGCTGCTGCTCTT--- 615
QY 191 LeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPheLysTyrIleGluAsnGln 210
DB 616 ---ATAATTGGATCCAAATGATTTGAGAGCAGCAAGATTCCAATATATGAGGAGAA 672
QY 211 ValLysThr-----AsnPheAsnArgAlaPheTyrProAspProLysValIleAsnLeu 228
DB 673 ATCGCAGCAGAAATTGATCAACCGGAGATGTCACACAGATCTCGATCGTAATTAACACTT 732
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: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: PAP-266 Insert
US-10-893-584-80

Alignment Scores:
Pred. No.: 6,7e-25 Length: 1855
Score: 307.50 Matches: 94
Percent Similarity: 43.8% Conservative: 53
Best Local Similarity: 28.0% Mismatches: 118
Query Match: 19.0% Indels: 71
DB: Gaps: 14

US-09-978-274a-2 (1-314) x US-10-893-584-80 (1-1855)

QY 10 ThrleuilealatrpleuilealaalaProthserThrcyalaileanThr----- 27
DB 25 ACTATTGTAAATATGATGTATGTCAGTGGCAACATGCGCTTTGTTGGATCCACCTCAGG 84
QY 28 -----ileThrPhe 30
DB 85 TGGCTTTTCACATTAGAGATTAACAATATCCCAACATCCCAATTAATTAATTT 144
QY 31 AspAlaGlyAsnAlaThrIleAsnLysTyraIaThrPheMetGluSerLeuArgAsnGln 50
DB 145 ACCACAGCGGGTCCACTGTGCAAGCTTACACAACTTTATCAGAGCTGTTCGGCGGT 204
QY 51 AlalaAspProLysLeuLysCysTyrglyIleProMetLeuProAspThrAsnSerThr 70
DB 205 TTAAACAACGTGAGCTGATGTGACATGATATACCAAGTGTGCCAAACAGAGTTGGTTG 264
QY 71 Pro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLysThrIleThr 87
DB 265 CCTATAAACCAAGCGTTATTTAGTTGAATCTCAATCATGACAGCTTCTCTTACA 324
QY 88 LeuMetLeuArgArgAsnAsnLeuTyraValMetGlyTyrsSerAspProPheAsnGlyAsn 107
DB 325 TTAGCGCTGATGTCAACCAATGATATGTGTGCGTACCGT-----GCTGGAAAT 375
QY 108 LysCysArgTYR-----HisIlePhe 114
DB 376 AGCGCATATTTCTTCTTCACTCTGACATCAGAAAGACAGAACATCACTCACTTCTTC 435
QY 115 AsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSerSerSer 134
DB 436 -----ACTGATGTTCAAAAT----- 450
QY 135 SerArgValAlaMetSerIleAsnTyraAsnSerLeuTyraProThrMetGluLysVala 154
DB 451 ---CGATATATACATTCGCTTGTGGTGAAT-----TATGATAGACTTGAACAACTTGT 501
QY 155 GluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGly 174
DB 502 GGT---AATCTGAGAGAAATATATCGAGTTGGAAATGTCCTACCTAGAGAGGCTATCTCA 558
QY 175 LysIle-----SerGlyValAspSerPheProValLysThrGluAlaPhePhe 190
DB 559 GCGCTTATATATTAACAGTACGTGGGACCTCAGCTTCCACTCGCTCTCTCTT--- 615
QY 191 LeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPheLysTyriIleGluAsnGln 210
DB 616 ---ATATATTTGCATTCCAAAATGATTTCAAGAGCAGCAAGATTCCAATATATTTAGGGAGAA 672
QY 211 ValLysThr-----AsnPheAsnArgAlaPheTyraProAspProLysValIleAsnLeu 228
DB 673 ATGCGCACGAGAAATTAAGTACCAACCGAGATCTGCACCAAGATCTTACGTAATTAACCTT 732
QY 229 GluGluLysIleTyrLysIleSerGluAlaIleIleAsnAlaLysAsnGlyAlaLeuPro 248
DB 733 GAGAAATAGTTGGGGAGACCTTCCACTGCAATTCAGAGCTTAACCAAGAGGCTTTGCT 792
QY 249 LysProLeuGluLeuValAspAlaLysGlyThrLysTrpIleValLeuArgValAspGlu 268

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DB 793 AGTCAATTCACCTGCAAGACGTAATGGTTCCAAATTCAGTGTGACGATGAGATATA 852
QY 269 IleAsnArgAspValAlaLeuLeuLysTyraValAsnGlyThrCysGlnThrTyrgln 288
DB 853 TTATCCCTATCTACGTCTCATGTGTAT-----AGATGCCACCTCCA---CCA 900
QY 289 AsnAlaMetPheSerGlnValIleIle-----SerThrTyraAsn 302
DB 901 TCGTCACAGTTTACAGACGTTGATATGTGTGCATGTCATTAAT 948

RESULT 13
US-10-893-584-196
: Sequence 196, Application US/10893584
: Publication No. US20050272048A1
: GENERAL INFORMATION:
: APPLICANT: Borgford, Thor
: APPLICANT: Braun, Curtis
: APPLICANT: Purac, Admir
: APPLICANT: Scoll, Dominik
: TITLE OR INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
: FILE REFERENCE: 10447-025
: CURRENT APPLICATION NUMBER: US/10/893,584
: PRIOR FILING DATE: 2004-07-19
: PRIOR APPLICATION NUMBER: US 09/551,151
: PRIOR FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: US 09/403,752
: PRIOR FILING DATE: 1999-10-29
: PRIOR APPLICATION NUMBER: US 10/089,058
: NUMBER OF SEQ ID NOS: 274
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 196
: LENGTH: 1807
: TYPE: DNA
: ORGANISM: E. coli
US-10-893-584-196

Alignment Scores:
Pred. No.: 7.39e-25 Length: 1807
Score: 307.00 Matches: 92
Percent Similarity: 43.8% Conservative: 48
Best Local Similarity: 28.8% Mismatches: 110
Query Match: 19.0% Indels: 70
DB: Gaps: 12

US-09-978-274a-2 (1-314) x US-10-893-584-196 (1-1807)

QY 10 ThrleuilealatrpleuilealaalaProthserThrcyalaileanThr----- 27
DB 25 ACTATTGTAAATATGATGTATGTCAGTGGCAACATGCGCTTTGTTGGATCCACCTCAGG 84
QY 28 -----ileThrPhe 30
DB 85 TGGCTTTTCACATTAGAGATTAACAATATTCCTCCAAACAATATTAATTAATTT 144
QY 31 AspAlaGlyAsnAlaThrIleAsnLysTyraIaThrPheMetGluSerLeuArgAsnGln 50
DB 145 ACCACAGCGGGTCCACTGTGCAAGCTTACACAACTTTATCAGAGCTGTTCGGCGGT 204
QY 51 AlalaAspProLysLeuLysCysTyrglyIleProMetLeuProAspThrAsnSerThr 70
DB 205 TTAAACAACGTGAGCTGATGTGACATGAAATACCAAGTGTTCGCAACAGAGTTGGTTG 264
QY 71 Pro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLysThrIleThr 87
DB 265 CCTATAAACCAAGCGTTATTTAGTTGAATCTCAATCATGACAGCTTCTCTTACA 324
QY 88 LeuMetLeuArgArgAsnAsnLeuTyraValMetGlyTyrsSerAspProPheAsnGlyAsn 107
DB 325 TTAGCGCTGATGTCAACCAATGATATGTGTGCGTACCGT-----GCTGGAAAT 375

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Qy 108 LysCysArgTyr-----HisIlePhe 114
Db 376 AGCCGATATTTCTTCAATCCTGACAAATGAGAAATGAGAAATGACATCATCTTTTC 435
Qy 115 AsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSerSerSer 134
Db 436 -----ACTGATGTTCAAAAT----- 450
Qy 135 SerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGluLysValAla 154
Db 451 ---CGATATACATTCGCTTGGTGGTGAAT---TATGATAGACTTGAACAACTTGTCT 501
Qy 155 GluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGly 174
Db 502 GGT---AATCTGAGAGAAATATGCAATGTTGGAAATGTCCTCAGAGAGAGCTTCTCA 558
Qy 175 LysIle-----SerGlyValAspSerPheProValLysThrGluAlaPhePhe 190
Db 559 GCGCTTATTTATTCAGTACTGCTGGCACTCAGCTTCCAACTTGGCTCGTTCTTT--- 615
Qy 191 LeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPheLysTyrIleGluAsnGln 210
Db 616 ---ATAATTCATTCCAATATATTTTTCAGAGACAGACAGATTCATATATTTAGAGGAGAA 672
Qy 211 ValLysThr-----AsnPheAsnArgAlaPheTyrProAspProLysValIleAsnLeu 228
Db 673 ATGGCAGCAGAAATTAAGTACACCGAGATCTGCACAGATCTTACGCTTAATTAACCTT 732
Qy 229 GluGluLysTyrGlyLysIleSerGluAlaIleHisAsnAlaLysAsnGlyValAlaLeuPro 248
Db 733 GAGAAATGTTGGGGAGACCTTCCACTGCAATTCAGAGCTTAACCAAGAGCCTTTGCT 792
Qy 249 LysProLeuGluLeuValAspAlaLysGlyThrLysTyrIleValLeuArgValAspGlu 268
Db 793 AGTCGAATTCACATGCAAAAGACGTAAATGTTCCAAATTCAGTGTACATGATGATGATATA 852
Qy 269 IleAsnArgAspValAlaLeuLeuLysTyr-----ValAsnGlyThrCys 283
Db 853 TTATTCCTATCATAGCTCTCATAGTGTATAGATGCCAGAGACAGATGATGCGGGGTGT 912

RESULT 14
US-10-893-584-3
; Sequence 3, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admitk
; APPLICANT: Scoll, Dominik
; TITLE OF INVENTION: Rizin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893, 584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Cathepsin B linker regions of PAP-214
US-10-893-584-3

Alignment Scores: 8,74e-25 Length: 1855
Pred. No.: 306,50 Matches: 89

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Percent Similarity: 44.2% Conservative: 48
Best Local Similarity: 28.7% Mismatches: 108
Query Match: 19.0% Indels: 65
Db: 8 Gaps: 11

US-09-978-274A-2 (1-314) x US-10-893-584-3 (1-1855)

Qy 10 ThrLeuIleAlaTProLleIleAlaLProThrSerThrCysAlaIleAsnThr----- 27
Db 25 ACTATGTATATATGATATGATATGATGAGCAACAGCTTGTGTGATTCAGACCTCAGGG 84
Qy 28 -----IleThrPhe 30
Db 85 TGGCTTTACATTTAGAGATTAACAATATATCCCAACAAATCCCAATATTAATTAATCTT 144
Qy 31 AspAlaGlyAsnAlaThrIleAsnLysTyrAlaThrPheMetGluSerLeuArgAsnGln 50
Db 145 ACCACAGCGGGGTGCACATGTCCAAAGCTACCAAACTTTATCAGAGCTGTTGGGGTCT 204
Qy 51 AlaLysAspProLysLysLysCysTyrGlyIleProMetLeuProAspThrAsnSerThr 70
Db 205 TTAACAACTGAGAGCTGATGTGAGACATGATATACAGTGTGCGCAACAGAGTTGGTTTG 264
Qy 71 Pro-----LysTyrLeuLeuValLysLeuGlnGlyAlaAsnLeuLysThrIleThr 87
Db 265 CCTATTAACCAACGCTTATTTATTTAGTGAATCTCAATCATGACAGAGCTTCTGTATCA 324
Qy 88 LeuMetLeuArgArgAsnAsnLeuTyrValMetGlyTyrSerAspProPheAsnGlyAsn 107
Db 325 TTACGCTGATGATGCACCAATGATATGTGTGGCTACCGT-----GCTGGAAT 375
Qy 108 LysCysArgTyr-----HisIlePhe 114
Db 376 AGCCGATATTTCTTCAATCCTGACAAATGAGAAATGAGAAATGACATCATCTTTTC 435
Qy 115 AsnAspIleThrSerThrGluArgThrAspValGluAsnThrLeuCysSerSerSer 134
Db 436 -----ACTGATGTTCAAAAT----- 450
Qy 135 SerArgValAlaMetSerIleAsnTyrAsnSerLeuTyrProThrMetGluLysValAla 154
Db 451 ---CGATATACATTCGCTTGGTGGTGAAT---TATGATAGACTTGAACAACTTGTCT 501
Qy 155 GluValAsnSerArgAsnGlnValGlnLeuGlyIleGlnIleLeuSerSerAspIleGly 174
Db 502 GGT---AATCTGAGAGAAATATGCAATGTTGGAAATGTCCTCAGAGAGGCTATCTCA 558
Qy 175 LysIle-----SerGlyValAspSerPheProValLysThrGluAlaPhePhe 190
Db 559 GCGCTTATTTATTCAGTACTGCTGGCACTCAGCTTCCAACTTGGCTCGTTCTTT--- 615
Qy 191 LeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPheLysTyrIleGluAsnGln 210
Db 616 ---ATAATTCATTCCAATATATTTTTCAGAGACAGACAGATTCATATATTTAGAGGAGAA 672
Qy 211 ValLysThr-----AsnPheAsnArgAlaPheTyrProAspProLysValIleAsnLeu 228
Db 673 ATGGCAGCAGAAATTAAGTACACCGAGATCTGCACAGATTCCTTACGTAATTAACCTT 732
Qy 229 GluGluLysTyrGlyLysIleSerGluAlaIleHisAsnAlaLysAsnGlyValAlaLeuPro 248
Db 733 GAGAAATGTTGGGGAGACCTTCCACTGCAATTCAGAGCTTAACCAAGAGAGCTTGTCT 792
Qy 249 LysProLeuGluLeuValAspAlaLysGlyThrLysTyrIleValLeuArgValAspGlu 268
Db 793 AGTCGAATTCACATGCAAAAGACGTAAATGTTCCAAATTCAGTGTATGATGATGATATA 852
Qy 269 IleAsnArgAspValAlaLeuLeuLysTyr-----ValAsnGlyThrCys 283
Db 853 TTATTCCTATCATAGCTCTCATAGTGTAT 882

RESULT 15
US-10-893-584-5

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/ Sequence 5, Application US/10893584
/ Publication No. US20050272048A1
/ GENERAL INFORMATION:
/ APPLICANT: Borgford, Thor
/ APPLICANT: Braun, Curtis
/ APPLICANT: Purac, Admit
/ APPLICANT: Stoll, Dominik
/ TITLE OF INVENTION: Rizin-Like Toxin Variants for Treatment of Cancer,
/ TITLE OF INVENTION: Viral or Parasitic Infections
/ FILE REFERENCE: 10447-025
/ CURRENT APPLICATION NUMBER: US/10/893,584
/ PRIOR APPLICATION NUMBER: US 09/551,151
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: US 09/403,752
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 10/089,058
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 274
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 1855
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: pap-216 insert
/ US-10-893-584-5
```

Alignment Scores:

Pred. No.:	8.74e-25	Length:	1855
Score:	306.50	Matches:	89
Percent Similarity:	44.2%	Conservative:	48
Best Local Similarity:	28.7%	Mismatches:	108
Query Match:	19.0%	Indels:	65
DB:	8	Gaps:	11

US-09-978-274a-2 (1-314) x US-10-893-584-5 (1-1855)

```
QY 10 ThrLeuIleAlaTTPLeuIleAlaIleAlaProThSerThrCysAlaIleAenThr----- 27
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 25 ACTATTGTATATGATGATGTATGCGAGTCAATGCGCTTTGTTGATCCACTCAGG 84
QY 28 -----11erhrphe 30
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 85 TGGTCTTTCACATTAGAGTAACAACATATCCCAACAATACCAATTATTAATCTT 144
QY 31 AepAlaGlyAsnAlaThrIleAenlyrTyAlaThrPheMetGluSerIleuArgAenGln 50
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 145 ACCACAGCGGGTCCACTGTGCAAGCTACCAAACTTATCAAGCTGTTCGCGGCTGT 204
QY 51 AlaIysAspProIysIleuIysCysTyGlyIleProMetLeuProAspThrAenSerThr 70
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 205 TTAACAACCTGAGCTGATGAGACATGATATACAGTGTTCGCAACAGAGTTGGTTG 264
QY 71 Pro-----LysTyIleuLeuValIysLeuGlnGlyAlaAenLeuIysThrIleThr 87
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 265 CCTATAACCAACGAGTTTATTTAGTTGAACCTCAATCATGCAGAGCTTCTGTATCA 324
QY 88 LeuMetLeuArgArgAenAenLeuTyValMetGlyTySerAspProPheAenGlyAen 107
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 325 TTAGCGCTGATGTACCAATGCAATATGTGTGCGTACCGT-----GCTGGAAT 375
QY 108 LysCysArgTy-----HisIlePhe 114
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 376 AGGCAATATTCTTTCATCTCGACAAATCAGGAAGATCAGAACATCACTCATCTTTC 435
QY 115 AsnAspIleThrSerThrgIuArgThrAspValGluAenThrIleuCysSerSerSer 134
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 436 -----ACTGATGTCAAAAT-----450
QY 135 SerArgValAlaMetSerIleAenTyAsnSerIleuTyProThrMetGluIysAla 154
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 451 ---CGATATATCATTCGCTTGTGTGTAAT-----TATGATAGACTTGAACAACTTGT 501
```

```
QY 155 GluValAsnSerArgAenGlnValGlnLeuGlyIleGlnIleuSerSerAspIleGly 174
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 502 GGT---AATCTGAGAGAAATATCTGAGTGGGAAATGCTCATAGAGAGGCTATCTCA 558
QY 175 LysIle-----SerGlyValAspSerPheProValIysThrgIuAlaPhePhe 190
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 559 GCGCTTATATTATTAAGTACTGGTGGCACTGAGCTCCAACTGCGTCTCTCTT---615
QY 191 LeuLeuValAlaIleGlnMetValSerGluAlaAlaArgPheIysTyIleGluAenGln 210
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 616 ---ATAATTGGCATCCAAATGATTTCAAGAGCAAGATTCCAATATATTTGAGGGAGAA 672
QY 211 ValIysThr-----AsnPheAsnArgAlaPheTyProAspProIysValIleAenLeu 228
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 673 ATGCGCAGAGAAATTAGTATCAACCGAGATCTGCACAGATCTTACGCTAATTACATT 732
QY 229 GluGluIysTrpGlyIysIleSerGluAlaIleHisAsnAlaIysAenGlyAlaLeuPro 248
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 733 GAGAAATAGTTGGGGGAGACTTTCACCTGCATTCAGAGCTTAACCAAGAGCCTTGTCT 792
QY 249 LysProLeuGluIleuValAspAlaIysGlyThrIysTrpIleValIleuArgValAspGln 268
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 793 AGTCAATTCACTGCAGAAAGACGTAAATGTTCCAAATTCAGTGTATCGATGTGAGTATA 852
QY 269 IleAsnArgAspValAlaLeuLeuIysTy 278
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 853 TTAATCCCTATCATAGCTCTCATGTGTAT 882
```

Search completed: April 9, 2006, 05:01:24
Job time : 832.643 secs